



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:06 PM GMT

PDB ID : 1WCE  
Title : Crystal structure of the T13 IBDV viral particle reveals a missing link in icosahedral viruses evolution  
Authors : Coulibaly, F.; Chevalier, C.; Gutsche, I.; Pous, J.; Bressanelli, S.; Navaza, J.; Delmas, B.; Rey, F.A.  
Deposited on : 2004-11-12  
Resolution : 7.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

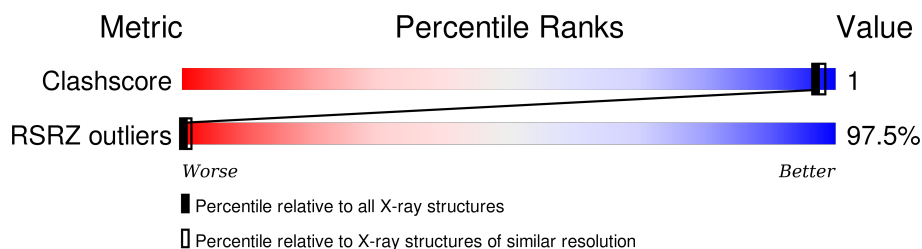
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

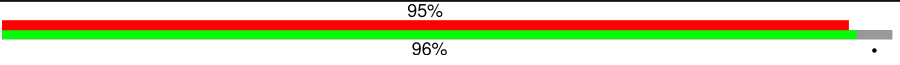
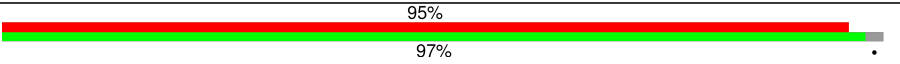
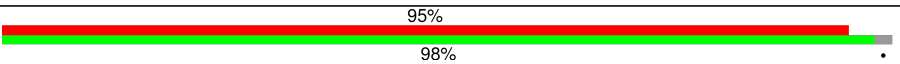
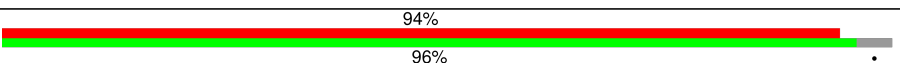
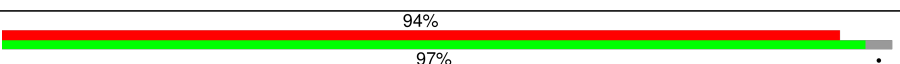
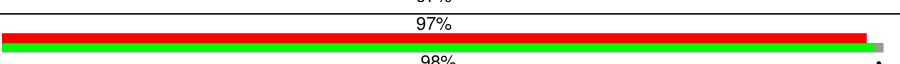
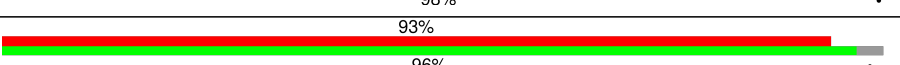
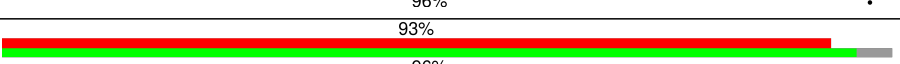
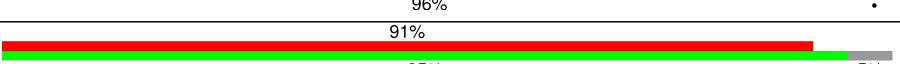
The reported resolution of this entry is 7.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	1063 (10.00-3.70)
RSRZ outliers	91569	1013 (9.50-3.66)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	441	
1	B	441	
1	C	441	
1	D	441	
1	E	441	
1	F	441	
1	G	441	
1	H	441	
1	I	441	

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Mol	Chain	Length	Quality of chain
1	J	441	<div><div></div><div>95%</div><div></div><div></div><div>96%</div><div></div><div>.</div></div>
1	K	441	<div><div></div><div>93%</div><div></div><div></div><div>94%</div><div></div><div>6%</div></div>
1	L	441	<div><div></div><div>95%</div><div></div><div></div><div>97%</div><div></div><div>.</div></div>
1	M	441	<div><div></div><div>94%</div><div></div><div></div><div>96%</div><div></div><div>.</div></div>

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 5533 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

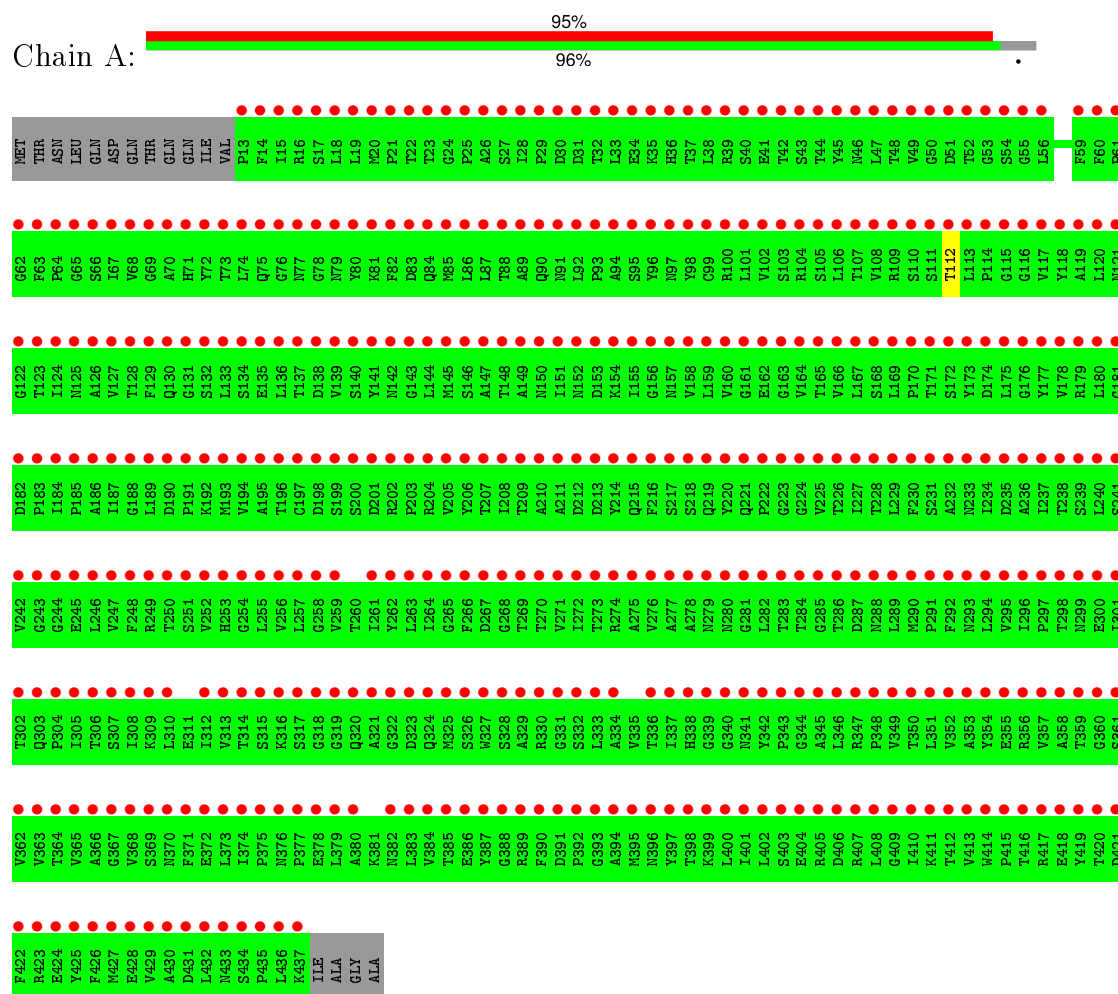
- Molecule 1 is a protein called MAJOR STRUCTURAL PROTEIN VP2.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
1	A	425	Total C 425 425	0	0	425
1	B	430	Total C 430 430	0	0	430
1	C	430	Total C 430 430	0	0	430
1	D	424	Total C 424 424	0	0	424
1	E	429	Total C 429 429	0	0	429
1	F	436	Total C 436 436	0	0	436
1	G	426	Total C 426 426	0	0	426
1	H	423	Total C 423 423	0	0	423
1	I	417	Total C 417 417	0	0	417
1	J	423	Total C 423 423	0	0	423
1	K	416	Total C 416 416	0	0	416
1	L	429	Total C 429 429	0	0	429
1	M	425	Total C 425 425	0	0	425

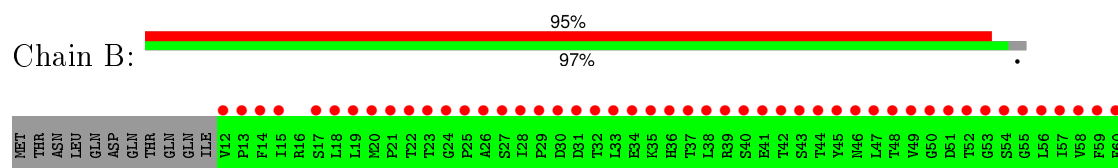
### 3 Residue-property plots

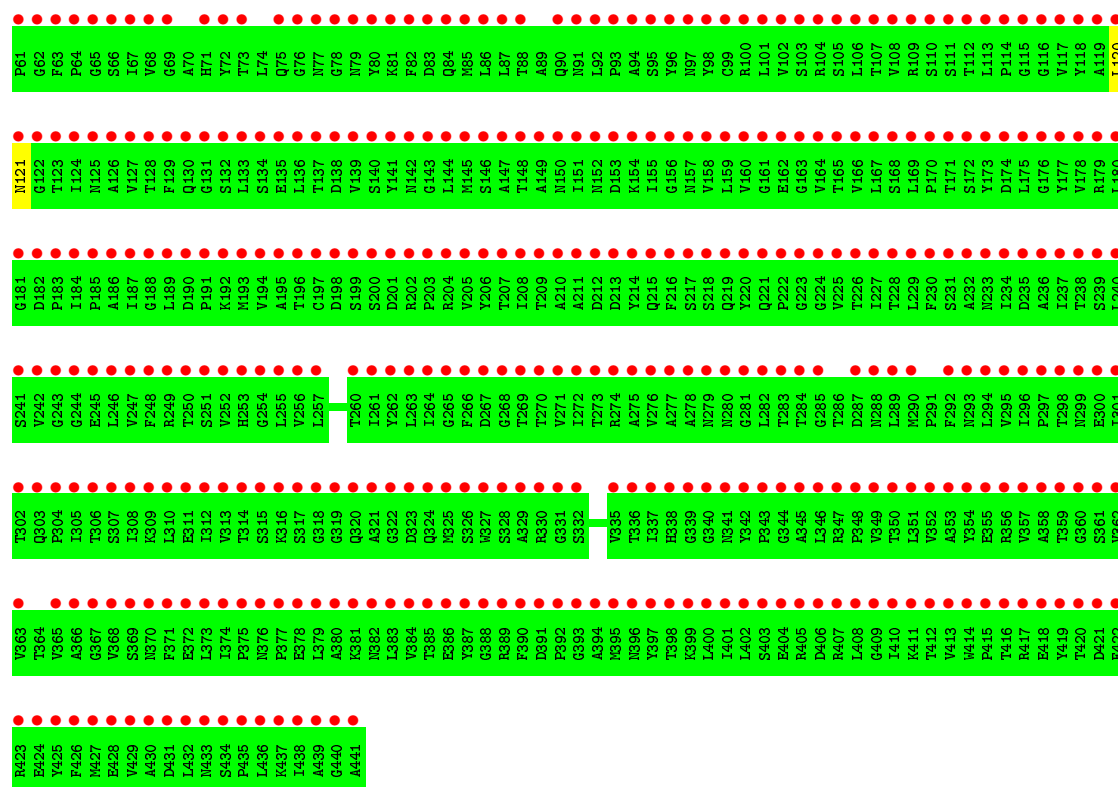
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $\text{RSRZ} > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

#### • Molecule 1: MAJOR STRUCTURAL PROTEIN VP2

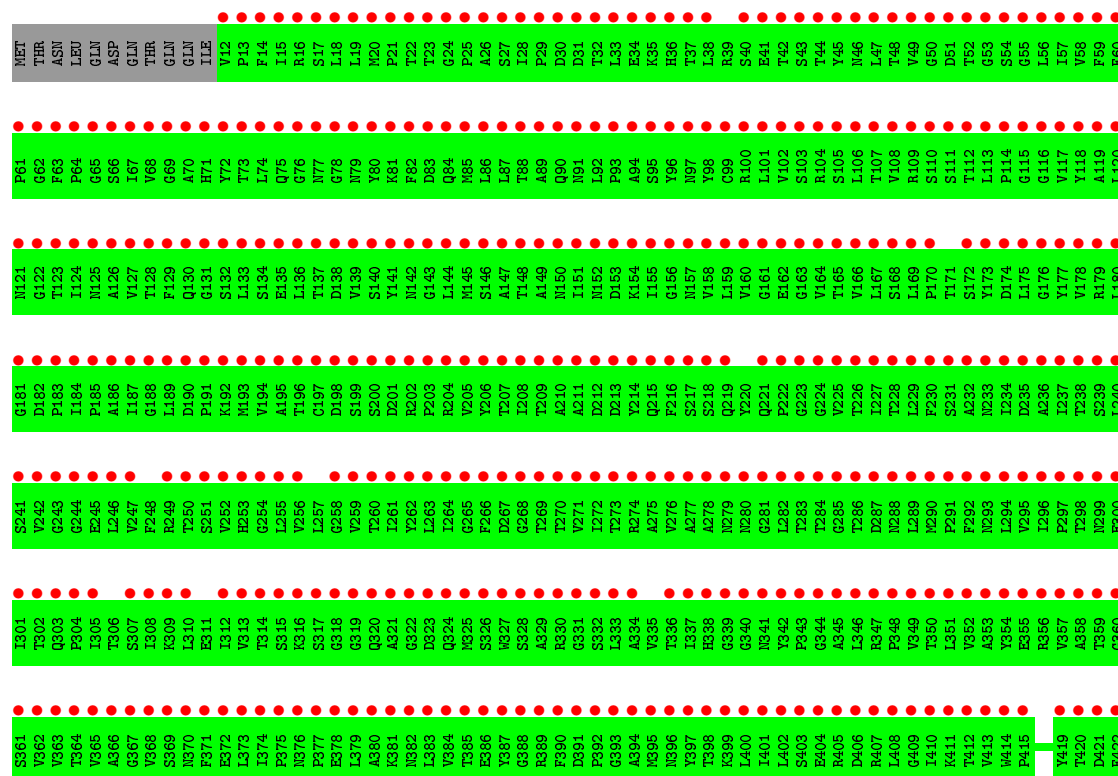


#### • Molecule 1: MAJOR STRUCTURAL PROTEIN VP2





### • Molecule 1: MAJOR STRUCTURAL PROTEIN VP2



R423  
E424  
Y425  
F426  
M427  
M428  
V429  
A430  
D431  
M432  
L433  
S434  
P435  
L436  
K437  
I438  
A439  
G440  
A441

● Molecule 1: MAJOR STRUCTURAL PROTEIN VP2

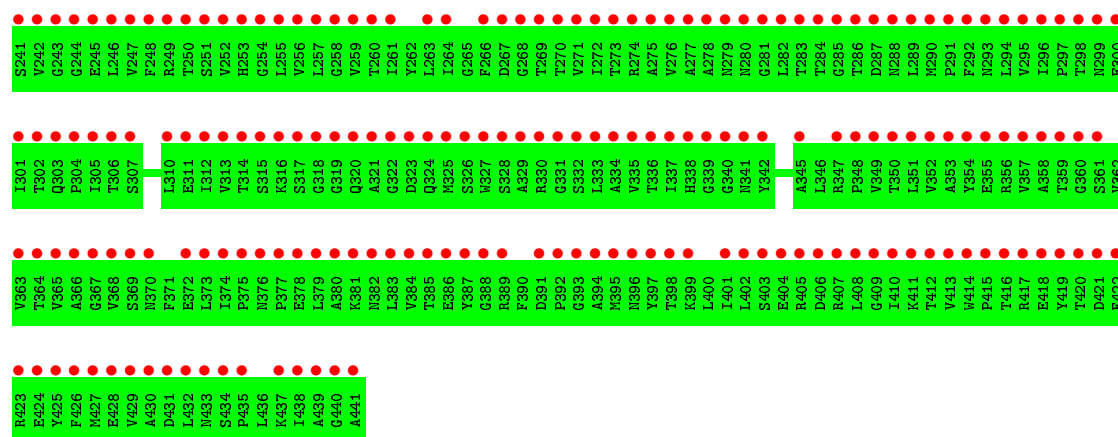
Chain D: 

MET THR ASN LEU GLN THR VAL P13 P14 P15 P16 P17 P18 P19 P20 P21 P22 P23 P24 P25 P26 P27 P28 P29 P30 P31 P32 P33 P34 P35 P36 P37 P38 P39 P40 P41 P42 P43 P44 P45 P46 P47 P48 P49 P50 P51 P52 P53 P54 P55 P56 P57 P58 P59 P60  
 P61 P62 P63 P64 P65 P66 P67 P68 P69 P70 P71 P72 P73 P74 P75 P76 P77 P78 P79 P80 P81 P82 P83 P84 P85 P86 P87 P88 P89 P90 P91 P92 P93 P94 P95 P96 P97 P98 P99 R100 R101 R102 R103 R104 R105 R106 R107 R108 R109 R110 R111 R112 R113 R114 R115 R116 R117 R118 R119 R120  
 M121 G122 G123 G124 G125 G126 G127 G128 G129 G130 G131 G132 G133 G134 G135 G136 G137 G138 G139 G140 G141 G142 G143 G144 G145 G146 G147 G148 G149 G150 G151 G152 G153 G154 G155 G156 G157 G158 G159 G160 G161 G162 G163 G164 G165 G166 G167 G168 G169 G170 G171 G172 G173 G174 G175 G176 G177 G178 G179 G180  
 G181 G182 G183 G184 G185 G186 G187 G188 G189 G190 G191 G192 G193 G194 G195 G196 G197 G198 G199 G200 G201 G202 G203 G204 G205 G206 G207 G208 G209 G210 G211 G212 G213 G214 G215 G216 G217 G218 G219 G220 G221 G222 G223 G224 G225 G226 G227 G228 G229 G230 G231 G232 G233 G234 G235 G236 G237 G238 G239 G240  
 S241 V242 G243 G244 G245 G246 G247 G248 G249 G250 G251 G252 G253 G254 G255 G256 G257 G258 G259 G260 G261 G262 G263 G264 G265 G266 G267 G268 G269 G270 G271 G272 G273 G274 G275 G276 G277 G278 G279 G280 G281 G282 G283 G284 G285 G286 G287 G288 G289 G290 G291 G292 G293 G294 G295 G296 G297 G298 G299 G300 G301  
 T302 Q303 P304 I305 E306 S307 I308 K309 K310 L311 E312 E313 V314 V315 S316 K317 K318 G319 G320 G321 G322 G323 G324 G325 G326 G327 G328 G329 G330 G331 G332 G333 G334 G335 G336 G337 G338 G339 G340 G341 G342 G343 G344 G345 G346 G347 G348 G349 G350 G351 G352 G353 G354 G355 G356 G357 G358 G359 G360 G361  
 V362 V363 V364 V365 V366 V367 V368 V369 V370 V371 V372 V373 V374 V375 V376 V377 V378 V379 V380 V381 V382 V383 V384 V385 V386 V387 V388 V389 V390 V391 V392 V393 V394 V395 V396 V397 V398 V399 V400 V401 V402 V403 V404 V405 V406 V407 V408 V409 V410 V411 V412 V413 V414 V415 V416 V417 V418 V419 V420 V421  
 F422 R423 E424 Y425 F426 M427 M428 V429 A430 D431 M432 L433 S434 P435 L436 LYS ILE ALA GLY ALA

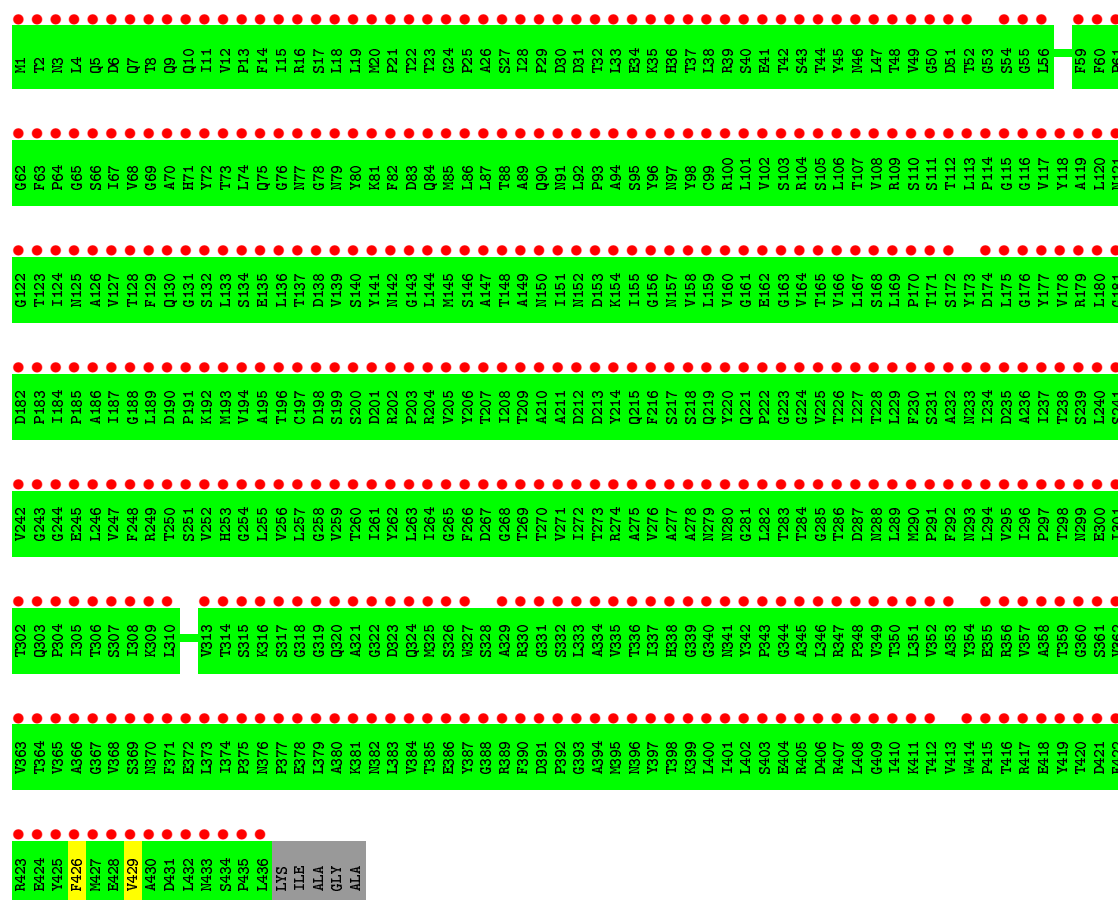
● Molecule 1: MAJOR STRUCTURAL PROTEIN VP2

Chain E: 

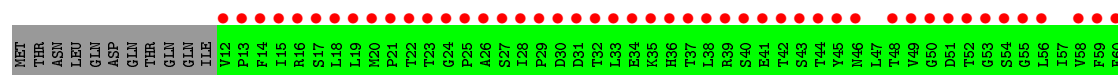
MET THR ASN LEU GLN THR VAL P13 P14 P15 P16 P17 P18 P19 P20 P21 P22 P23 P24 P25 P26 P27 P28 P29 P30 P31 P32 P33 P34 P35 P36 P37 P38 P39 P40 P41 P42 P43 P44 P45 P46 P47 P48 P49 P50 P51 P52 P53 P54 P55 P56 P57 P58 P59 P60  
 P61 P62 P63 P64 P65 P66 P67 P68 P69 P70 P71 P72 P73 P74 P75 P76 P77 P78 P79 P80 P81 P82 P83 P84 P85 P86 P87 P88 P89 P90 P91 P92 P93 P94 P95 P96 P97 P98 P99 R100 R101 R102 R103 R104 R105 R106 R107 R108 R109 R110 R111 R112 R113 R114 R115 R116 R117 R118 R119 R120  
 M121 G122 G123 G124 G125 G126 G127 G128 G129 G130 G131 G132 G133 G134 G135 G136 G137 G138 G139 G140 G141 G142 G143 G144 G145 G146 G147 G148 G149 G150 G151 G152 G153 G154 G155 G156 G157 G158 G159 G160 G161 G162 G163 G164 G165 G166 G167 G168 G169 G170 G171 G172 G173 G174 G175 G176 G177 G178 G179 G180  
 G181 G182 G183 G184 G185 G186 G187 G188 G189 G190 G191 G192 G193 G194 G195 G196 G197 G198 G199 G200 G201 G202 G203 G204 G205 G206 G207 G208 G209 G210 G211 G212 G213 G214 G215 G216 G217 G218 G219 G220 G221 G222 G223 G224 G225 G226 G227 G228 G229 G230 G231 G232 G233 G234 G235 G236 G237 G238 G239 G240



- Molecule 1: MAJOR STRUCTURAL PROTEIN VP2



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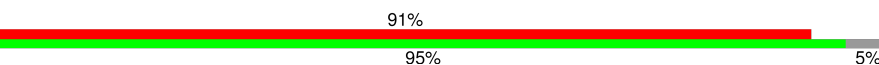






Y425	•
F426	•
M427	•
E428	•
V429	•
A430	•
D431	•
L432	•
M433	•
S434	•
P435	•
LEU	•
LYS	•
ILE	•
ALA	•
GLY	•

● Molecule 1: MAJOR STRUCTURAL PROTEIN VP2

Chain I: 

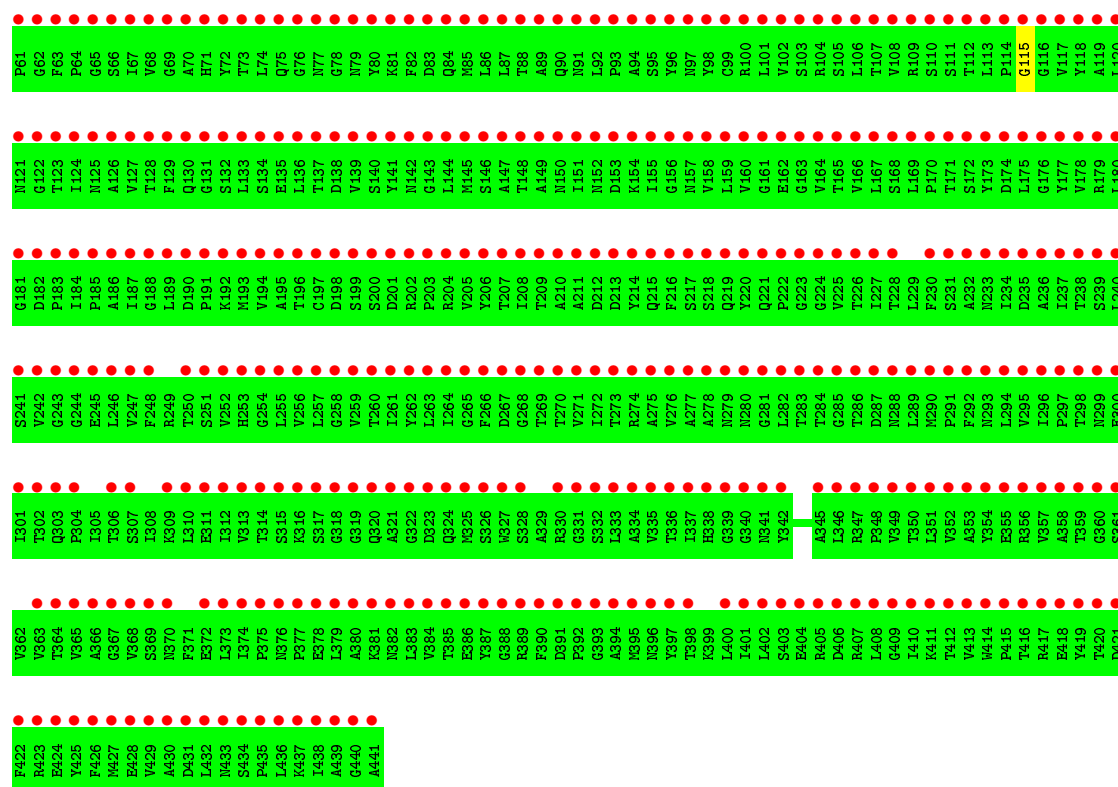
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L599	•
L600	•

● Molecule 1: MAJOR STRUCTURAL PROTEIN VP2

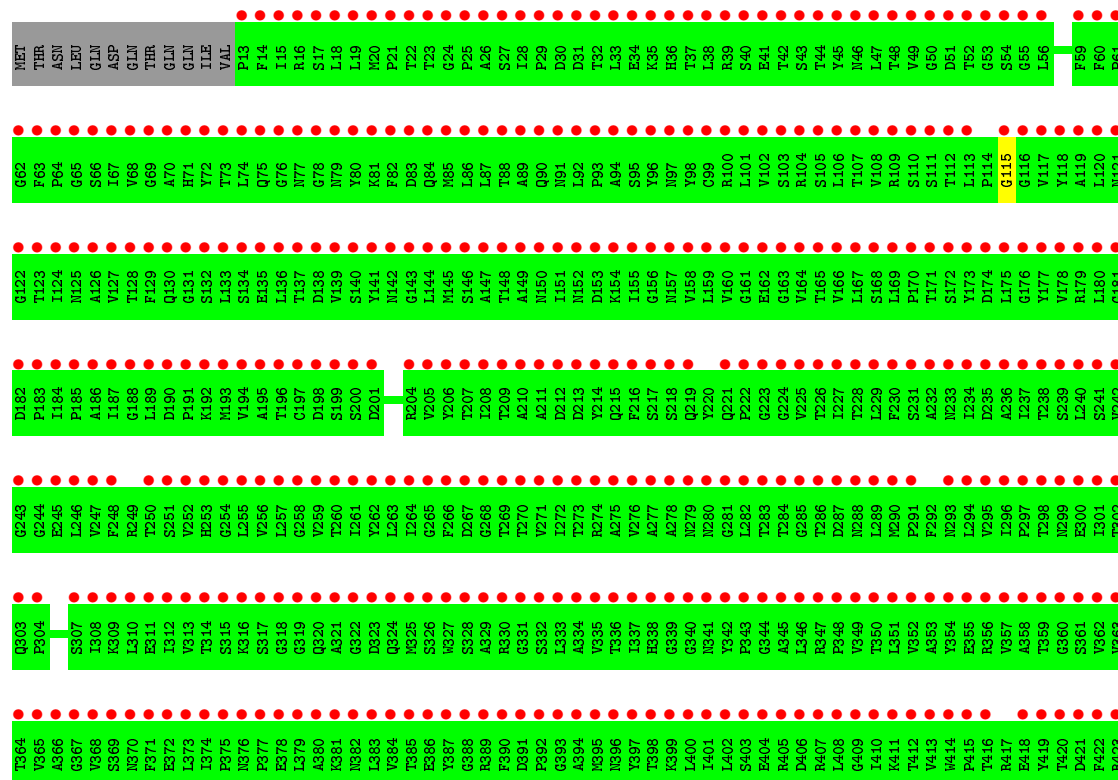
Chain J: 

RET	•
THR	•
ASN	•
LEU	•
GLN	•
ASP	•
GLN	•
THR	•
GLN	•
ILE	•
V12	•
P13	•
F14	•
I15	•
R16	•





### • Molecule 1: MAJOR STRUCTURAL PROTEIN VP2



E424	•
Y425	•
F426	•
M427	•
E428	•
V429	•
A430	•
D431	•
L432	•
N433	•
S434	•
P435	•
L436	•
LYS	
ILE	
A441	•
GLY	
ALA	

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	854.01Å 692.23Å 792.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 7.00 49.86 – 6.97	Depositor EDS
% Data completeness (in resolution range)	75.1 (50.00-7.00) 74.8 (49.86-6.97)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.90 (at 6.68Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	(Not available) , (Not available) 0.411 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	190.2	Xtriage
Anisotropy	0.155	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.41 , 27.2	EDS
Estimated twinning fraction	0.327 for -h,-k,l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.27$	Xtriage
Outliers	2 of 1089556 reflections (0.000%)	Xtriage
$F_o, F_c$ correlation	0.65	EDS
Total number of atoms	5533	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.97% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	425	0	0	2	0
1	B	430	0	0	2	0
1	C	430	0	0	0	0
1	D	424	0	0	1	0
1	E	429	0	0	1	0
1	F	436	0	0	1	0
1	G	426	0	0	1	0
1	H	423	0	0	0	0
1	I	417	0	0	0	0
1	J	423	0	0	1	0
1	K	416	0	0	1	0
1	L	429	0	0	1	0
1	M	425	0	0	1	0
All	All	5533	0	0	7	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

All (7) close contacts within the same asymmetric unit are listed below, sorted by their clash

magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:111:SER:CA	1:D:112:THR:CA	1.85	1.51
1:E:117:VAL:CA	1:M:115:GLY:CA	2.26	1.13
1:A:112:THR:CA	1:B:121:ASN:CA	2.64	0.76
1:K:118:TYR:CA	1:L:115:GLY:CA	2.82	0.58
1:A:112:THR:CA	1:B:120:LEU:CA	2.96	0.43
1:F:426:PHE:CA	1:F:429:VAL:CA	3.00	0.40
1:G:112:THR:CA	1:J:121:ASN:CA	2.99	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

### 5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.



## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	425/441 (96%)	7.27	419 (98%) 0 0	20, 47, 95, 99	0
1	B	430/441 (97%)	6.81	419 (97%) 0 1	20, 47, 95, 99	0
1	C	430/441 (97%)	6.88	419 (97%) 0 1	20, 47, 95, 99	0
1	D	424/441 (96%)	6.85	414 (97%) 0 1	20, 47, 95, 99	0
1	E	429/441 (97%)	6.77	416 (96%) 0 1	20, 47, 95, 99	0
1	F	436/441 (98%)	7.11	427 (97%) 0 1	20, 46, 95, 99	0
1	G	426/441 (96%)	6.86	409 (96%) 0 1	20, 47, 95, 99	0
1	H	423/441 (95%)	6.76	411 (97%) 0 1	20, 47, 95, 99	0
1	I	417/441 (94%)	7.04	402 (96%) 0 1	20, 47, 96, 99	0
1	J	423/441 (95%)	7.20	417 (98%) 0 0	20, 47, 95, 99	0
1	K	416/441 (94%)	6.70	408 (98%) 0 1	20, 47, 96, 99	0
1	L	429/441 (97%)	7.03	419 (97%) 0 1	20, 47, 95, 99	0
1	M	425/441 (96%)	6.97	414 (97%) 0 1	20, 47, 95, 99	0
All	All	5533/5733 (96%)	6.94	5394 (97%) 0 1	20, 47, 96, 99	0

All (5394) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	150	ASN	25.7
1	C	209	THR	25.7
1	A	64	PRO	23.9
1	F	83	ASP	23.4
1	D	391	ASP	23.1
1	M	209	THR	23.0
1	I	174	ASP	22.7
1	F	392	PRO	22.1
1	A	350	THR	22.1

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Mol	Chain	Res	Type	RSRZ
1	L	317	SER	21.7
1	B	212	ASP	21.4
1	C	396	ASN	21.3
1	G	208	ILE	21.2
1	B	83	ASP	20.8
1	L	83	ASP	20.4
1	L	166	VAL	20.3
1	F	103	SER	20.2
1	I	31	ASP	19.9
1	K	140	SER	19.8
1	A	391	ASP	19.7
1	J	389	ARG	19.7
1	M	181	GLY	19.6
1	E	32	THR	19.5
1	B	294	LEU	19.3
1	H	32	THR	19.0
1	A	207	THR	19.0
1	F	12	VAL	19.0
1	B	150	ASN	18.8
1	F	388	GLY	18.7
1	L	373	LEU	18.7
1	L	140	SER	18.7
1	C	26	ALA	18.7
1	J	64	PRO	18.6
1	F	315	SER	18.5
1	J	136	LEU	18.5
1	M	223	GLY	18.1
1	E	191	PRO	18.1
1	E	207	THR	18.1
1	B	84	GLN	18.0
1	A	54	SER	17.8
1	K	103	SER	17.8
1	H	207	THR	17.8
1	K	143	GLY	17.7
1	G	13	PRO	17.7
1	M	288	ASN	17.6
1	H	391	ASP	17.5
1	J	412	THR	17.5
1	L	45	TYR	17.5
1	D	315	SER	17.5
1	F	233	ASN	17.5
1	H	190	ASP	17.4

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Mol	Chain	Res	Type	RSRZ
1	D	183	PRO	17.4
1	M	22	THR	17.4
1	L	23	THR	17.3
1	F	111	SER	17.2
1	H	31	ASP	17.2
1	A	126	ALA	17.2
1	J	83	ASP	17.2
1	J	140	SER	17.1
1	J	226	THR	17.1
1	A	320	GLN	17.0
1	C	123	THR	17.0
1	M	207	THR	17.0
1	G	341	ASN	16.9
1	H	135	GLU	16.9
1	I	367	GLY	16.8
1	J	283	THR	16.7
1	F	287	ASP	16.7
1	J	317	SER	16.7
1	E	217	SER	16.7
1	F	89	ALA	16.7
1	J	149	ALA	16.7
1	L	84	GLN	16.6
1	K	209	THR	16.6
1	A	415	PRO	16.6
1	M	222	PRO	16.5
1	D	192	LYS	16.5
1	B	223	GLY	16.5
1	L	350	THR	16.5
1	D	150	ASN	16.5
1	E	208	ILE	16.5
1	I	190	ASP	16.5
1	J	286	THR	16.5
1	L	318	GLY	16.4
1	L	302	THR	16.4
1	D	375	PRO	16.3
1	F	150	ASN	16.3
1	J	19	LEU	16.3
1	L	341	ASN	16.3
1	H	151	ILE	16.2
1	F	341	ASN	16.2
1	G	196	THR	16.2
1	K	54	SER	16.2

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Mol	Chain	Res	Type	RSRZ
1	E	19	LEU	16.2
1	D	117	VAL	16.2
1	B	140	SER	16.1
1	D	32	THR	16.1
1	L	186	ALA	16.1
1	J	269	THR	16.1
1	H	430	ALA	16.1
1	J	341	ASN	16.1
1	C	378	GLU	16.0
1	J	42	THR	16.0
1	I	209	THR	16.0
1	B	192	LYS	16.0
1	C	207	THR	16.0
1	B	318	GLY	15.9
1	A	52	THR	15.9
1	L	44	THR	15.8
1	G	209	THR	15.8
1	D	29	PRO	15.8
1	M	150	ASN	15.8
1	L	174	ASP	15.7
1	M	135	GLU	15.7
1	C	297	PRO	15.7
1	B	208	ILE	15.7
1	I	155	ILE	15.7
1	L	274	ARG	15.6
1	A	94	ALA	15.6
1	I	297	PRO	15.6
1	J	282	LEU	15.6
1	E	302	THR	15.5
1	D	85	MET	15.5
1	A	181	GLY	15.5
1	J	369	SER	15.5
1	D	130	GLN	15.5
1	A	101	LEU	15.5
1	A	55	GLY	15.4
1	F	314	THR	15.4
1	H	112	THR	15.4
1	D	384	VAL	15.4
1	M	32	THR	15.4
1	K	415	PRO	15.4
1	I	142	ASN	15.3
1	L	224	GLY	15.3

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Mol	Chain	Res	Type	RSRZ
1	A	31	ASP	15.3
1	H	93	PRO	15.3
1	F	136	LEU	15.2
1	D	23	THR	15.2
1	A	241	SER	15.1
1	C	45	TYR	15.1
1	M	174	ASP	15.1
1	G	192	LYS	15.1
1	H	302	THR	15.1
1	M	302	THR	15.1
1	F	269	THR	15.1
1	A	166	VAL	15.1
1	C	176	GLY	15.1
1	E	273	THR	15.1
1	G	183	PRO	15.1
1	D	350	THR	15.0
1	M	286	THR	15.0
1	B	65	GLY	15.0
1	G	206	TYR	15.0
1	E	210	ALA	15.0
1	B	82	PHE	15.0
1	G	78	GLY	14.9
1	A	351	LEU	14.9
1	L	299	ASN	14.9
1	G	350	THR	14.9
1	G	96	TYR	14.9
1	D	385	THR	14.8
1	J	131	GLY	14.8
1	B	100	ARG	14.8
1	D	326	SER	14.8
1	F	112	THR	14.8
1	H	191	PRO	14.7
1	G	232	ALA	14.7
1	A	32	THR	14.7
1	A	251	SER	14.7
1	D	181	GLY	14.7
1	L	303	GLN	14.6
1	F	340	GLY	14.6
1	A	338	HIS	14.6
1	D	174	ASP	14.6
1	F	416	THR	14.6
1	B	209	THR	14.6

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Mol	Chain	Res	Type	RSRZ
1	D	360	GLY	14.5
1	E	31	ASP	14.5
1	G	392	PRO	14.5
1	M	206	TYR	14.5
1	D	376	ASN	14.5
1	B	226	THR	14.5
1	D	128	THR	14.5
1	G	352	VAL	14.5
1	L	194	VAL	14.5
1	D	374	ILE	14.5
1	C	13	PRO	14.4
1	G	302	THR	14.4
1	J	176	GLY	14.4
1	G	150	ASN	14.4
1	L	325	MET	14.4
1	J	221	GLN	14.4
1	A	206	TYR	14.3
1	E	295	VAL	14.3
1	F	35	LYS	14.3
1	H	152	ASN	14.3
1	K	321	ALA	14.3
1	D	31	ASP	14.3
1	H	195	ALA	14.3
1	H	388	GLY	14.3
1	A	128	THR	14.3
1	B	68	VAL	14.3
1	A	277	ALA	14.3
1	E	228	THR	14.3
1	A	30	ASP	14.3
1	C	385	THR	14.3
1	J	135	GLU	14.3
1	D	135	GLU	14.2
1	F	387	TYR	14.2
1	M	287	ASP	14.2
1	B	152	ASN	14.2
1	L	103	SER	14.2
1	M	208	ILE	14.2
1	K	299	ASN	14.2
1	F	13	PRO	14.2
1	B	141	TYR	14.2
1	M	151	ILE	14.2
1	A	13	PRO	14.2

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Mol	Chain	Res	Type	RSRZ
1	I	396	ASN	14.1
1	C	350	THR	14.1
1	G	77	ASN	14.1
1	L	136	LEU	14.1
1	A	318	GLY	14.1
1	B	19	LEU	14.0
1	C	421	ASP	14.0
1	H	321	ALA	14.0
1	J	315	SER	14.0
1	G	389	ARG	14.0
1	C	377	PRO	14.0
1	C	277	ALA	14.0
1	M	31	ASP	14.0
1	L	288	ASN	13.9
1	M	140	SER	13.9
1	I	43	SER	13.9
1	I	353	ALA	13.9
1	M	48	THR	13.9
1	K	295	VAL	13.9
1	K	116	GLY	13.8
1	H	130	GLN	13.8
1	F	79	ASN	13.8
1	M	303	GLN	13.8
1	F	104	ARG	13.7
1	J	61	PRO	13.7
1	J	147	ALA	13.7
1	M	178	VAL	13.7
1	G	435	PRO	13.7
1	I	389	ARG	13.7
1	L	369	SER	13.7
1	E	337	ILE	13.7
1	G	12	VAL	13.7
1	F	73	THR	13.6
1	C	296	ILE	13.6
1	C	32	THR	13.6
1	E	152	ASN	13.6
1	J	290	MET	13.6
1	C	147	ALA	13.6
1	G	369	SER	13.5
1	I	42	THR	13.5
1	L	415	PRO	13.5
1	A	193	MET	13.5

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Mol	Chain	Res	Type	RSRZ
1	J	375	PRO	13.5
1	F	281	GLY	13.5
1	C	206	TYR	13.5
1	I	152	ASN	13.4
1	L	187	ILE	13.4
1	G	378	GLU	13.4
1	G	321	ALA	13.4
1	K	52	THR	13.3
1	I	140	SER	13.3
1	I	205	VAL	13.3
1	C	250	THR	13.3
1	C	174	ASP	13.3
1	G	104	ARG	13.3
1	I	213	ASP	13.3
1	B	261	ILE	13.3
1	D	44	THR	13.3
1	F	44	THR	13.3
1	K	32	THR	13.3
1	E	52	THR	13.2
1	L	353	ALA	13.2
1	C	23	THR	13.2
1	F	72	TYR	13.2
1	M	110	SER	13.2
1	J	297	PRO	13.2
1	L	441	ALA	13.2
1	I	90	GLN	13.2
1	J	391	ASP	13.2
1	E	361	SER	13.2
1	G	19	LEU	13.2
1	D	24	GLY	13.2
1	M	83	ASP	13.1
1	F	22	THR	13.1
1	C	276	VAL	13.1
1	A	187	ILE	13.1
1	B	207	THR	13.1
1	G	207	THR	13.1
1	M	152	ASN	13.1
1	B	166	VAL	13.0
1	G	380	ALA	13.0
1	K	375	PRO	13.0
1	L	135	GLU	13.0
1	F	15	ILE	13.0

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Mol	Chain	Res	Type	RSRZ
1	B	372	GLU	13.0
1	I	30	ASP	13.0
1	E	168	SER	13.0
1	E	299	ASN	13.0
1	G	391	ASP	13.0
1	I	392	PRO	13.0
1	K	142	ASN	13.0
1	J	191	PRO	13.0
1	E	320	GLN	13.0
1	J	225	VAL	12.9
1	D	176	GLY	12.9
1	M	233	ASN	12.9
1	I	206	TYR	12.9
1	F	241	SER	12.9
1	A	61	PRO	12.9
1	I	269	THR	12.9
1	E	317	SER	12.9
1	B	314	THR	12.8
1	B	151	ILE	12.8
1	B	52	THR	12.8
1	E	64	PRO	12.8
1	J	23	THR	12.8
1	K	42	THR	12.8
1	F	261	ILE	12.8
1	E	251	SER	12.8
1	L	62	GLY	12.8
1	F	116	GLY	12.8
1	I	352	VAL	12.7
1	I	218	SER	12.7
1	D	139	VAL	12.7
1	K	213	ASP	12.7
1	L	110	SER	12.7
1	F	396	ASN	12.7
1	I	103	SER	12.7
1	B	183	PRO	12.7
1	E	83	ASP	12.7
1	I	143	GLY	12.7
1	I	131	GLY	12.7
1	I	50	GLY	12.7
1	M	136	LEU	12.7
1	G	361	SER	12.7
1	B	389	ARG	12.6

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Mol	Chain	Res	Type	RSRZ
1	K	270	THR	12.6
1	J	239	SER	12.6
1	F	302	THR	12.6
1	L	96	TYR	12.6
1	C	110	SER	12.6
1	K	374	ILE	12.6
1	J	65	GLY	12.6
1	M	186	ALA	12.6
1	D	228	THR	12.6
1	C	240	LEU	12.6
1	J	151	ILE	12.6
1	K	135	GLU	12.6
1	M	413	VAL	12.6
1	F	317	SER	12.6
1	M	164	VAL	12.6
1	A	395	MET	12.5
1	C	135	GLU	12.5
1	F	226	THR	12.5
1	K	300	GLU	12.5
1	M	340	GLY	12.5
1	F	293	ASN	12.5
1	K	130	GLN	12.5
1	D	86	LEU	12.5
1	J	103	SER	12.5
1	C	341	ASN	12.5
1	I	350	THR	12.5
1	A	100	ARG	12.5
1	I	164	VAL	12.5
1	J	200	SER	12.5
1	F	391	ASP	12.5
1	J	54	SER	12.5
1	B	81	LYS	12.5
1	J	195	ALA	12.5
1	C	195	ALA	12.5
1	J	222	PRO	12.4
1	E	231	SER	12.4
1	H	177	TYR	12.4
1	H	27	SER	12.4
1	A	208	ILE	12.4
1	M	269	THR	12.4
1	H	131	GLY	12.4
1	L	130	GLN	12.4

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Mol	Chain	Res	Type	RSRZ
1	A	165	THR	12.4
1	I	156	GLY	12.4
1	A	77	ASN	12.4
1	L	51	ASP	12.4
1	A	413	VAL	12.4
1	G	134	SER	12.3
1	L	231	SER	12.3
1	E	150	ASN	12.3
1	A	317	SER	12.3
1	B	146	SER	12.3
1	K	146	SER	12.3
1	B	133	LEU	12.3
1	K	303	GLN	12.3
1	A	182	ASP	12.3
1	L	389	ARG	12.3
1	M	177	TYR	12.3
1	H	96	TYR	12.3
1	H	48	THR	12.3
1	D	316	LYS	12.3
1	G	26	ALA	12.3
1	D	209	THR	12.2
1	E	112	THR	12.2
1	K	177	TYR	12.2
1	B	200	SER	12.2
1	G	164	VAL	12.2
1	D	15	ILE	12.2
1	I	77	ASN	12.2
1	H	269	THR	12.2
1	E	296	ILE	12.2
1	F	31	ASP	12.2
1	E	258	GLY	12.2
1	G	147	ALA	12.2
1	F	147	ALA	12.2
1	D	222	PRO	12.2
1	K	125	ASN	12.2
1	J	318	GLY	12.2
1	G	315	SER	12.2
1	E	142	ASN	12.1
1	E	293	ASN	12.1
1	C	162	GLU	12.1
1	J	275	ALA	12.1
1	I	173	TYR	12.1

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Mol	Chain	Res	Type	RSRZ
1	F	190	ASP	12.1
1	F	318	GLY	12.1
1	E	294	LEU	12.1
1	D	45	TYR	12.1
1	I	302	THR	12.1
1	E	385	THR	12.1
1	J	201	ASP	12.1
1	K	13	PRO	12.1
1	A	130	GLN	12.1
1	J	353	ALA	12.1
1	K	144	LEU	12.1
1	K	139	VAL	12.0
1	L	151	ILE	12.0
1	L	176	GLY	12.0
1	I	52	THR	12.0
1	C	77	ASN	12.0
1	D	389	ARG	12.0
1	H	411	LYS	12.0
1	B	147	ALA	12.0
1	M	415	PRO	12.0
1	H	247	VAL	12.0
1	C	31	ASP	12.0
1	K	217	SER	12.0
1	L	315	SER	12.0
1	B	340	GLY	12.0
1	F	206	TYR	12.0
1	G	171	THR	12.0
1	M	146	SER	12.0
1	G	30	ASP	12.0
1	C	213	ASP	12.0
1	H	23	THR	11.9
1	A	274	ARG	11.9
1	C	94	ALA	11.9
1	K	178	VAL	11.9
1	J	132	SER	11.9
1	K	65	GLY	11.9
1	F	199	SER	11.9
1	L	396	ASN	11.9
1	I	340	GLY	11.9
1	C	299	ASN	11.9
1	C	141	TYR	11.9
1	I	191	PRO	11.9

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Mol	Chain	Res	Type	RSRZ
1	J	130	GLN	11.9
1	A	221	GLN	11.9
1	D	133	LEU	11.9
1	I	51	ASP	11.9
1	A	115	GLY	11.9
1	J	12	VAL	11.9
1	C	190	ASP	11.8
1	H	153	ASP	11.8
1	H	314	THR	11.8
1	E	146	SER	11.8
1	J	224	GLY	11.8
1	H	384	VAL	11.8
1	I	125	ASN	11.8
1	I	227	ILE	11.8
1	D	396	ASN	11.8
1	F	146	SER	11.8
1	D	152	ASN	11.8
1	C	208	ILE	11.8
1	D	327	TRP	11.8
1	C	63	PHE	11.8
1	F	195	ALA	11.8
1	J	293	ASN	11.8
1	D	19	LEU	11.8
1	D	213	ASP	11.7
1	D	214	TYR	11.7
1	J	110	SER	11.7
1	J	302	THR	11.7
1	C	44	THR	11.7
1	E	65	GLY	11.7
1	M	297	PRO	11.7
1	J	52	THR	11.7
1	G	288	ASN	11.7
1	C	294	LEU	11.7
1	J	407	ARG	11.7
1	K	156	GLY	11.7
1	B	341	ASN	11.7
1	A	226	THR	11.7
1	J	350	THR	11.7
1	H	393	GLY	11.7
1	M	392	PRO	11.7
1	A	224	GLY	11.7
1	G	162	GLU	11.7

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Mol	Chain	Res	Type	RSRZ
1	B	415	PRO	11.7
1	C	175	LEU	11.6
1	H	209	THR	11.6
1	B	331	GLY	11.6
1	G	351	LEU	11.6
1	A	209	THR	11.6
1	E	206	TYR	11.6
1	D	134	SER	11.6
1	L	269	THR	11.6
1	A	233	ASN	11.6
1	A	252	VAL	11.6
1	C	379	LEU	11.6
1	J	213	ASP	11.5
1	B	79	ASN	11.5
1	F	288	ASN	11.5
1	C	239	SER	11.5
1	B	269	THR	11.5
1	M	176	GLY	11.5
1	I	393	GLY	11.5
1	I	160	VAL	11.5
1	K	126	ALA	11.5
1	C	322	GLY	11.5
1	C	355	GLU	11.5
1	B	213	ASP	11.5
1	B	53	GLY	11.5
1	B	119	ALA	11.5
1	D	207	THR	11.5
1	A	121	ASN	11.5
1	B	193	MET	11.5
1	I	166	VAL	11.5
1	J	112	THR	11.5
1	K	157	ASN	11.5
1	J	374	ILE	11.4
1	F	207	THR	11.4
1	L	314	THR	11.4
1	G	374	ILE	11.4
1	I	175	LEU	11.4
1	E	122	GLY	11.4
1	C	391	ASP	11.4
1	F	298	THR	11.4
1	D	317	SER	11.4
1	C	111	SER	11.4

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Mol	Chain	Res	Type	RSRZ
1	G	146	SER	11.4
1	I	135	GLU	11.4
1	K	152	ASN	11.4
1	K	136	LEU	11.4
1	E	338	HIS	11.4
1	K	176	GLY	11.4
1	A	293	ASN	11.4
1	A	161	GLY	11.4
1	L	42	THR	11.4
1	F	137	THR	11.4
1	F	240	LEU	11.4
1	I	390	PHE	11.4
1	D	166	VAL	11.3
1	C	151	ILE	11.3
1	G	172	SER	11.3
1	D	195	ALA	11.3
1	A	146	SER	11.3
1	J	159	LEU	11.3
1	J	251	SER	11.3
1	M	226	THR	11.3
1	A	253	HIS	11.3
1	A	396	ASN	11.3
1	G	195	ALA	11.3
1	J	95	SER	11.3
1	G	316	LYS	11.3
1	M	153	ASP	11.3
1	C	360	GLY	11.3
1	K	221	GLN	11.3
1	E	412	THR	11.3
1	E	235	ASP	11.3
1	A	183	PRO	11.3
1	F	196	THR	11.3
1	F	2	THR	11.3
1	F	165	THR	11.3
1	H	208	ILE	11.3
1	C	103	SER	11.3
1	K	251	SER	11.3
1	C	230	PHE	11.3
1	D	165	THR	11.3
1	K	48	THR	11.3
1	F	84	GLN	11.3
1	G	379	LEU	11.2

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Mol	Chain	Res	Type	RSRZ
1	D	240	LEU	11.2
1	K	117	VAL	11.2
1	F	46	ASN	11.2
1	G	138	ASP	11.2
1	F	254	GLY	11.2
1	L	352	VAL	11.2
1	M	44	THR	11.2
1	B	391	ASP	11.2
1	C	112	THR	11.2
1	B	350	THR	11.2
1	A	147	ALA	11.2
1	I	226	THR	11.2
1	L	323	ASP	11.2
1	I	316	LYS	11.2
1	B	142	ASN	11.2
1	E	240	LEU	11.2
1	M	191	PRO	11.1
1	I	375	PRO	11.1
1	G	406	ASP	11.1
1	G	31	ASP	11.1
1	L	24	GLY	11.1
1	C	212	ASP	11.1
1	L	139	VAL	11.1
1	D	196	THR	11.1
1	A	142	ASN	11.1
1	F	301	ILE	11.1
1	H	415	PRO	11.1
1	C	118	TYR	11.1
1	D	206	TYR	11.1
1	F	9	GLN	11.1
1	L	297	PRO	11.1
1	K	66	SER	11.1
1	K	218	SER	11.1
1	C	389	ARG	11.1
1	K	167	LEU	11.1
1	L	275	ALA	11.1
1	D	76	GLY	11.0
1	E	285	GLY	11.0
1	D	51	ASP	11.0
1	C	327	TRP	11.0
1	M	88	THR	11.0
1	E	303	GLN	11.0

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Mol	Chain	Res	Type	RSRZ
1	F	299	ASN	11.0
1	I	207	THR	11.0
1	D	322	GLY	11.0
1	J	392	PRO	11.0
1	I	153	ASP	11.0
1	J	287	ASP	11.0
1	M	61	PRO	11.0
1	D	118	TYR	11.0
1	J	207	THR	11.0
1	F	166	VAL	11.0
1	L	375	PRO	11.0
1	A	232	ALA	11.0
1	J	212	ASP	11.0
1	H	116	GLY	11.0
1	J	45	TYR	11.0
1	A	270	THR	11.0
1	H	392	PRO	11.0
1	I	239	SER	11.0
1	A	437	LYS	10.9
1	F	191	PRO	10.9
1	E	424	GLU	10.9
1	M	276	VAL	10.9
1	G	231	SER	10.9
1	D	162	GLU	10.9
1	A	110	SER	10.9
1	K	390	PHE	10.9
1	G	145	MET	10.9
1	L	290	MET	10.9
1	H	178	VAL	10.9
1	J	137	THR	10.9
1	A	164	VAL	10.9
1	G	218	SER	10.9
1	H	293	ASN	10.9
1	D	153	ASP	10.9
1	M	118	TYR	10.9
1	I	126	ALA	10.9
1	I	219	GLN	10.9
1	L	419	TYR	10.9
1	E	145	MET	10.9
1	E	276	VAL	10.9
1	L	150	ASN	10.9
1	B	61	PRO	10.9

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Mol	Chain	Res	Type	RSRZ
1	C	150	ASN	10.9
1	B	377	PRO	10.9
1	C	166	VAL	10.9
1	E	216	PHE	10.9
1	I	132	SER	10.9
1	A	47	LEU	10.9
1	G	251	SER	10.9
1	H	389	ARG	10.9
1	H	297	PRO	10.9
1	A	254	GLY	10.9
1	L	294	LEU	10.9
1	C	115	GLY	10.9
1	J	43	SER	10.9
1	J	214	TYR	10.9
1	I	336	THR	10.9
1	F	3	ASN	10.9
1	F	415	PRO	10.9
1	H	13	PRO	10.9
1	M	246	LEU	10.9
1	A	324	GLN	10.9
1	J	238	THR	10.8
1	M	431	ASP	10.8
1	G	97	ASN	10.8
1	F	186	ALA	10.8
1	E	23	THR	10.8
1	F	324	GLN	10.8
1	M	23	THR	10.8
1	M	363	VAL	10.8
1	J	253	HIS	10.8
1	M	216	PHE	10.8
1	D	235	ASP	10.8
1	D	302	THR	10.8
1	E	234	ILE	10.8
1	M	122	GLY	10.8
1	B	184	ILE	10.8
1	I	212	ASP	10.8
1	E	396	ASN	10.8
1	F	28	ILE	10.8
1	F	300	GLU	10.8
1	E	61	PRO	10.7
1	F	29	PRO	10.7
1	B	412	THR	10.7

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Mol	Chain	Res	Type	RSRZ
1	M	64	PRO	10.7
1	C	86	LEU	10.7
1	E	407	ARG	10.7
1	C	359	THR	10.7
1	J	153	ASP	10.7
1	E	275	ALA	10.7
1	I	372	GLU	10.7
1	H	385	THR	10.7
1	E	326	SER	10.7
1	D	84	GLN	10.7
1	A	379	LEU	10.7
1	D	293	ASN	10.7
1	F	228	THR	10.7
1	I	225	VAL	10.7
1	A	15	ILE	10.7
1	L	213	ASP	10.7
1	E	125	ASN	10.7
1	E	236	ALA	10.7
1	E	391	ASP	10.7
1	B	338	HIS	10.7
1	E	316	LYS	10.7
1	L	252	VAL	10.7
1	B	293	ASN	10.7
1	E	71	HIS	10.7
1	E	301	ILE	10.7
1	J	313	VAL	10.7
1	M	111	SER	10.7
1	M	149	ALA	10.7
1	D	28	ILE	10.6
1	G	240	LEU	10.6
1	K	183	PRO	10.6
1	K	376	ASN	10.6
1	L	232	ALA	10.6
1	A	78	GLY	10.6
1	K	179	ARG	10.6
1	D	233	ASN	10.6
1	C	73	THR	10.6
1	D	177	TYR	10.6
1	K	196	THR	10.6
1	H	100	ARG	10.6
1	M	245	GLU	10.6
1	A	62	GLY	10.6

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Mol	Chain	Res	Type	RSRZ
1	I	136	LEU	10.6
1	G	194	VAL	10.6
1	E	103	SER	10.6
1	G	296	ILE	10.6
1	G	434	SER	10.6
1	B	136	LEU	10.6
1	I	320	GLN	10.6
1	J	366	ALA	10.6
1	E	274	ARG	10.6
1	D	275	ALA	10.6
1	E	82	PHE	10.6
1	M	125	ASN	10.6
1	F	47	LEU	10.6
1	K	269	THR	10.6
1	B	325	MET	10.6
1	I	395	MET	10.6
1	E	35	LYS	10.6
1	E	272	ILE	10.6
1	G	266	PHE	10.6
1	E	190	ASP	10.5
1	A	76	GLY	10.5
1	I	104	ARG	10.5
1	I	391	ASP	10.5
1	A	414	TRP	10.5
1	F	39	ARG	10.5
1	E	376	ASN	10.5
1	I	73	THR	10.5
1	K	23	THR	10.5
1	E	141	TYR	10.5
1	E	252	VAL	10.5
1	L	185	PRO	10.5
1	H	276	VAL	10.5
1	M	319	GLY	10.5
1	L	155	ILE	10.5
1	C	397	TYR	10.5
1	K	118	TYR	10.5
1	M	139	VAL	10.5
1	M	145	MET	10.5
1	G	98	TYR	10.5
1	L	159	LEU	10.5
1	F	82	PHE	10.5
1	G	186	ALA	10.5

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Mol	Chain	Res	Type	RSRZ
1	I	68	VAL	10.5
1	I	296	ILE	10.5
1	G	213	ASP	10.5
1	H	394	ALA	10.5
1	K	95	SER	10.5
1	M	93	PRO	10.5
1	K	252	VAL	10.5
1	G	260	THR	10.5
1	E	133	LEU	10.4
1	E	356	ARG	10.4
1	B	219	GLN	10.4
1	J	44	THR	10.4
1	G	354	TYR	10.4
1	C	109	ARG	10.4
1	H	434	SER	10.4
1	B	330	ARG	10.4
1	A	230	PHE	10.4
1	A	103	SER	10.4
1	A	75	GLN	10.4
1	I	54	SER	10.4
1	K	328	SER	10.4
1	D	27	SER	10.4
1	J	194	VAL	10.4
1	M	200	SER	10.4
1	H	353	ALA	10.4
1	B	23	THR	10.4
1	F	260	THR	10.4
1	F	393	GLY	10.4
1	B	20	MET	10.4
1	F	227	ILE	10.4
1	A	105	SER	10.4
1	I	338	HIS	10.4
1	K	368	VAL	10.4
1	M	42	THR	10.4
1	B	295	VAL	10.3
1	I	415	PRO	10.3
1	H	85	MET	10.3
1	L	410	ILE	10.3
1	L	209	THR	10.3
1	C	369	SER	10.3
1	B	337	ILE	10.3
1	L	200	SER	10.3

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Mol	Chain	Res	Type	RSRZ
1	A	281	GLY	10.3
1	M	175	LEU	10.3
1	J	390	PHE	10.3
1	L	366	ALA	10.3
1	B	24	GLY	10.3
1	A	319	GLY	10.3
1	L	402	LEU	10.3
1	J	71	HIS	10.3
1	L	251	SER	10.3
1	E	46	ASN	10.3
1	B	319	GLY	10.3
1	C	64	PRO	10.3
1	D	112	THR	10.3
1	G	149	ALA	10.3
1	D	175	LEU	10.3
1	A	22	THR	10.3
1	H	102	VAL	10.3
1	L	131	GLY	10.3
1	B	361	SER	10.3
1	B	60	PHE	10.3
1	D	297	PRO	10.2
1	E	375	PRO	10.2
1	B	167	LEU	10.2
1	C	340	GLY	10.2
1	D	138	ASP	10.2
1	E	167	LEU	10.2
1	E	281	GLY	10.2
1	K	302	THR	10.2
1	M	284	THR	10.2
1	C	35	LYS	10.2
1	F	205	VAL	10.2
1	G	163	GLY	10.2
1	M	47	LEU	10.2
1	J	160	VAL	10.2
1	H	324	GLN	10.2
1	L	221	GLN	10.2
1	J	146	SER	10.2
1	M	195	ALA	10.2
1	A	174	ASP	10.2
1	G	144	LEU	10.2
1	L	338	HIS	10.2
1	C	186	ALA	10.2

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Mol	Chain	Res	Type	RSRZ
1	H	361	SER	10.2
1	A	436	LEU	10.2
1	K	36	HIS	10.2
1	E	147	ALA	10.2
1	F	374	ILE	10.2
1	G	152	ASN	10.2
1	D	193	MET	10.2
1	K	24	GLY	10.2
1	D	267	ASP	10.2
1	H	410	ILE	10.2
1	A	340	GLY	10.2
1	I	83	ASP	10.2
1	J	63	PHE	10.2
1	A	45	TYR	10.2
1	A	250	THR	10.2
1	B	253	HIS	10.1
1	G	24	GLY	10.1
1	I	163	GLY	10.1
1	D	387	TYR	10.1
1	A	345	ALA	10.1
1	D	411	LYS	10.1
1	K	324	GLN	10.1
1	A	294	LEU	10.1
1	J	82	PHE	10.1
1	K	244	GLY	10.1
1	C	95	SER	10.1
1	K	110	SER	10.1
1	H	81	LYS	10.1
1	H	49	VAL	10.1
1	M	341	ASN	10.1
1	I	78	GLY	10.1
1	G	326	SER	10.1
1	E	53	GLY	10.1
1	M	116	GLY	10.1
1	K	287	ASP	10.1
1	A	370	ASN	10.1
1	B	241	SER	10.1
1	K	395	MET	10.1
1	E	140	SER	10.1
1	G	393	GLY	10.0
1	B	238	THR	10.0
1	I	165	THR	10.0

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Mol	Chain	Res	Type	RSRZ
1	D	372	GLU	10.0
1	I	130	GLN	10.0
1	B	222	PRO	10.0
1	E	134	SER	10.0
1	J	36	HIS	10.0
1	K	335	VAL	10.0
1	J	86	LEU	10.0
1	K	236	ALA	10.0
1	K	297	PRO	10.0
1	M	384	VAL	10.0
1	H	26	ALA	10.0
1	K	288	ASN	10.0
1	F	232	ALA	10.0
1	E	55	GLY	10.0
1	K	296	ILE	10.0
1	D	144	LEU	10.0
1	B	108	VAL	10.0
1	H	175	LEU	10.0
1	I	388	GLY	10.0
1	E	174	ASP	10.0
1	F	198	ASP	10.0
1	D	89	ALA	10.0
1	K	278	ALA	10.0
1	D	30	ASP	10.0
1	B	55	GLY	10.0
1	A	194	VAL	10.0
1	B	431	ASP	10.0
1	J	231	SER	10.0
1	E	209	THR	10.0
1	D	182	ASP	10.0
1	K	348	PRO	10.0
1	D	274	ARG	10.0
1	M	436	LEU	10.0
1	A	298	THR	10.0
1	M	192	LYS	10.0
1	D	373	LEU	10.0
1	L	370	ASN	10.0
1	K	414	TRP	10.0
1	J	246	LEU	9.9
1	H	15	ILE	9.9
1	K	115	GLY	9.9
1	G	52	THR	9.9

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Mol	Chain	Res	Type	RSRZ
1	I	382	ASN	9.9
1	F	212	ASP	9.9
1	A	378	GLU	9.9
1	G	277	ALA	9.9
1	C	433	ASN	9.9
1	E	164	VAL	9.9
1	J	347	ARG	9.9
1	C	298	THR	9.9
1	C	76	GLY	9.9
1	H	30	ASP	9.9
1	I	195	ALA	9.9
1	I	298	THR	9.9
1	A	95	SER	9.9
1	A	261	ILE	9.9
1	E	49	VAL	9.9
1	F	407	ARG	9.9
1	A	93	PRO	9.9
1	L	192	LYS	9.9
1	E	132	SER	9.9
1	M	13	PRO	9.9
1	A	275	ALA	9.9
1	G	143	GLY	9.9
1	H	194	VAL	9.9
1	G	142	ASN	9.9
1	J	370	ASN	9.9
1	L	289	LEU	9.9
1	D	418	GLU	9.8
1	M	218	SER	9.8
1	B	123	THR	9.8
1	F	323	ASP	9.8
1	G	170	PRO	9.8
1	K	277	ALA	9.8
1	B	118	TYR	9.8
1	H	252	VAL	9.8
1	E	269	THR	9.8
1	A	276	VAL	9.8
1	F	406	ASP	9.8
1	J	123	THR	9.8
1	G	297	PRO	9.8
1	C	318	GLY	9.8
1	A	392	PRO	9.8
1	B	354	TYR	9.8

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	F	229	LEU	9.8
1	D	388	GLY	9.8
1	C	194	VAL	9.8
1	J	365	VAL	9.8
1	K	365	VAL	9.8
1	C	65	GLY	9.8
1	D	268	GLY	9.8
1	F	304	PRO	9.8
1	G	187	ILE	9.8
1	C	370	ASN	9.8
1	L	122	GLY	9.8
1	G	377	PRO	9.8
1	M	251	SER	9.7
1	J	107	THR	9.7
1	J	111	SER	9.7
1	A	125	ASN	9.7
1	F	174	ASP	9.7
1	C	191	PRO	9.7
1	H	192	LYS	9.7
1	A	192	LYS	9.7
1	L	27	SER	9.7
1	G	126	ALA	9.7
1	F	135	GLU	9.7
1	A	162	GLU	9.7
1	M	231	SER	9.7
1	E	241	SER	9.7
1	J	119	ALA	9.7
1	M	161	GLY	9.7
1	H	341	ASN	9.7
1	M	293	ASN	9.7
1	E	131	GLY	9.7
1	I	62	GLY	9.7
1	L	322	GLY	9.7
1	C	252	VAL	9.7
1	E	54	SER	9.7
1	H	429	VAL	9.7
1	L	70	ALA	9.7
1	G	225	VAL	9.7
1	L	208	ILE	9.7
1	L	321	ALA	9.7
1	D	88	THR	9.7
1	G	176	GLY	9.7

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Mol	Chain	Res	Type	RSRZ
1	H	187	ILE	9.7
1	L	384	VAL	9.7
1	G	422	PHE	9.7
1	G	275	ALA	9.7
1	F	389	ARG	9.7
1	A	176	GLY	9.6
1	M	194	VAL	9.6
1	M	350	THR	9.6
1	K	200	SER	9.6
1	A	280	ASN	9.6
1	M	213	ASP	9.6
1	A	65	GLY	9.6
1	B	232	ALA	9.6
1	M	52	THR	9.6
1	D	161	GLY	9.6
1	D	386	GLU	9.6
1	J	218	SER	9.6
1	L	286	THR	9.6
1	E	63	PHE	9.6
1	J	220	TYR	9.6
1	I	339	GLY	9.6
1	K	351	LEU	9.6
1	E	135	GLU	9.6
1	J	24	GLY	9.6
1	F	321	ALA	9.6
1	C	384	VAL	9.6
1	K	41	GLU	9.6
1	G	320	GLN	9.6
1	A	287	ASP	9.6
1	F	435	PRO	9.6
1	B	156	GLY	9.6
1	D	22	THR	9.6
1	F	297	PRO	9.6
1	E	30	ASP	9.6
1	A	412	THR	9.6
1	C	122	GLY	9.6
1	H	43	SER	9.6
1	L	412	THR	9.6
1	C	430	ALA	9.6
1	G	236	ALA	9.6
1	A	360	GLY	9.6
1	B	275	ALA	9.5

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Mol	Chain	Res	Type	RSRZ
1	L	41	GLU	9.5
1	M	165	THR	9.5
1	C	146	SER	9.5
1	E	155	ILE	9.5
1	G	247	VAL	9.5
1	H	253	HIS	9.5
1	F	248	PHE	9.5
1	C	124	ILE	9.5
1	H	42	THR	9.5
1	K	111	SER	9.5
1	I	178	VAL	9.5
1	A	145	MET	9.5
1	H	376	ASN	9.5
1	B	181	GLY	9.5
1	C	317	SER	9.5
1	H	35	LYS	9.5
1	F	364	THR	9.5
1	F	178	VAL	9.5
1	H	317	SER	9.5
1	L	388	GLY	9.5
1	H	420	THR	9.5
1	H	431	ASP	9.5
1	I	337	ILE	9.5
1	B	134	SER	9.5
1	G	276	VAL	9.5
1	C	395	MET	9.5
1	D	299	ASN	9.5
1	J	384	VAL	9.5
1	A	342	TYR	9.5
1	C	422	PHE	9.5
1	D	341	ASN	9.5
1	F	30	ASP	9.5
1	A	141	TYR	9.5
1	A	191	PRO	9.5
1	C	30	ASP	9.5
1	H	86	LEU	9.5
1	D	147	ALA	9.5
1	I	216	PHE	9.4
1	C	20	MET	9.4
1	L	413	VAL	9.4
1	C	337	ILE	9.4
1	K	279	ASN	9.4

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Mol	Chain	Res	Type	RSRZ
1	H	337	ILE	9.4
1	L	293	ASN	9.4
1	A	231	SER	9.4
1	G	219	GLN	9.4
1	J	409	GLY	9.4
1	L	170	PRO	9.4
1	M	210	ALA	9.4
1	L	13	PRO	9.4
1	L	144	LEU	9.4
1	J	173	TYR	9.4
1	H	134	SER	9.4
1	M	320	GLN	9.4
1	M	361	SER	9.4
1	F	219	GLN	9.4
1	C	323	ASP	9.4
1	C	181	GLY	9.4
1	J	240	LEU	9.4
1	K	232	ALA	9.4
1	M	126	ALA	9.4
1	E	24	GLY	9.4
1	F	280	ASN	9.4
1	M	137	THR	9.4
1	K	194	VAL	9.4
1	I	373	LEU	9.4
1	J	199	SER	9.4
1	I	383	LEU	9.4
1	B	313	VAL	9.4
1	G	385	THR	9.4
1	A	116	GLY	9.4
1	I	167	LEU	9.4
1	A	316	LYS	9.4
1	K	396	ASN	9.4
1	B	28	ILE	9.4
1	C	48	THR	9.3
1	M	19	LEU	9.3
1	B	336	THR	9.3
1	L	31	ASP	9.3
1	L	319	GLY	9.3
1	H	24	GLY	9.3
1	K	210	ALA	9.3
1	C	185	PRO	9.3
1	F	222	PRO	9.3

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Mol	Chain	Res	Type	RSRZ
1	E	369	SER	9.3
1	B	320	GLN	9.3
1	M	156	GLY	9.3
1	A	151	ILE	9.3
1	D	41	GLU	9.3
1	F	200	SER	9.3
1	M	289	LEU	9.3
1	A	152	ASN	9.3
1	L	295	VAL	9.3
1	G	116	GLY	9.3
1	J	13	PRO	9.3
1	J	34	GLU	9.3
1	C	81	LYS	9.3
1	C	261	ILE	9.3
1	H	103	SER	9.3
1	I	368	VAL	9.3
1	I	184	ILE	9.3
1	I	176	GLY	9.3
1	J	72	TYR	9.3
1	C	321	ALA	9.3
1	H	52	THR	9.3
1	L	273	THR	9.3
1	C	375	PRO	9.3
1	L	223	GLY	9.2
1	B	317	SER	9.2
1	H	386	GLU	9.2
1	I	199	SER	9.2
1	J	89	ALA	9.2
1	B	105	SER	9.2
1	L	222	PRO	9.2
1	G	115	GLY	9.2
1	B	80	TYR	9.2
1	I	13	PRO	9.2
1	M	296	ILE	9.2
1	H	356	ARG	9.2
1	D	59	PHE	9.2
1	I	208	ILE	9.2
1	M	162	GLU	9.2
1	A	132	SER	9.2
1	H	364	THR	9.2
1	L	55	GLY	9.2
1	C	412	THR	9.2

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Mol	Chain	Res	Type	RSRZ
1	D	423	ARG	9.2
1	I	428	GLU	9.2
1	E	130	GLN	9.2
1	F	417	ARG	9.2
1	M	82	PHE	9.2
1	I	41	GLU	9.2
1	B	225	VAL	9.2
1	D	101	LEU	9.2
1	C	62	GLY	9.2
1	I	122	GLY	9.2
1	G	179	ARG	9.2
1	M	180	LEU	9.2
1	J	209	THR	9.2
1	B	137	THR	9.2
1	C	231	SER	9.2
1	A	290	MET	9.1
1	E	432	LEU	9.1
1	I	288	ASN	9.1
1	E	244	GLY	9.1
1	I	233	ASN	9.1
1	L	175	LEU	9.1
1	C	25	PRO	9.1
1	G	253	HIS	9.1
1	I	283	THR	9.1
1	H	150	ASN	9.1
1	I	341	ASN	9.1
1	G	103	SER	9.1
1	I	252	VAL	9.1
1	F	390	PHE	9.1
1	A	299	ASN	9.1
1	D	83	ASP	9.1
1	B	375	PRO	9.1
1	M	332	SER	9.1
1	M	391	ASP	9.1
1	F	194	VAL	9.1
1	J	433	ASN	9.1
1	L	374	ILE	9.1
1	F	369	SER	9.1
1	J	133	LEU	9.1
1	H	60	PHE	9.1
1	H	303	GLN	9.1
1	J	77	ASN	9.1

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Mol	Chain	Res	Type	RSRZ
1	J	172	SER	9.1
1	K	104	ARG	9.1
1	B	424	GLU	9.1
1	G	175	LEU	9.1
1	D	136	LEU	9.1
1	E	298	THR	9.1
1	I	112	THR	9.1
1	G	281	GLY	9.1
1	I	24	GLY	9.1
1	C	270	THR	9.1
1	J	128	THR	9.1
1	H	148	THR	9.1
1	I	238	THR	9.1
1	M	283	THR	9.1
1	L	310	LEU	9.1
1	M	54	SER	9.1
1	I	192	LYS	9.1
1	F	270	THR	9.1
1	M	280	ASN	9.1
1	I	274	ARG	9.0
1	J	245	GLU	9.0
1	E	218	SER	9.0
1	E	315	SER	9.0
1	A	118	TYR	9.0
1	H	126	ALA	9.0
1	G	205	VAL	9.0
1	K	180	LEU	9.0
1	F	90	GLN	9.0
1	G	355	GLU	9.0
1	I	181	GLY	9.0
1	D	337	ILE	9.0
1	C	319	GLY	9.0
1	A	384	VAL	9.0
1	D	132	SER	9.0
1	H	218	SER	9.0
1	F	372	GLU	9.0
1	I	398	THR	9.0
1	K	166	VAL	9.0
1	A	388	GLY	9.0
1	H	286	THR	9.0
1	I	211	ALA	9.0
1	G	293	ASN	9.0

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Mol	Chain	Res	Type	RSRZ
1	J	156	GLY	9.0
1	A	354	TYR	9.0
1	A	297	PRO	9.0
1	G	83	ASP	9.0
1	M	72	TYR	9.0
1	A	42	THR	9.0
1	F	132	SER	9.0
1	G	317	SER	9.0
1	C	285	GLY	9.0
1	I	15	ILE	9.0
1	I	86	LEU	9.0
1	E	227	ILE	9.0
1	F	130	GLN	9.0
1	F	255	LEU	9.0
1	K	353	ALA	9.0
1	D	223	GLY	9.0
1	C	235	ASP	9.0
1	B	128	THR	9.0
1	G	420	THR	9.0
1	H	239	SER	9.0
1	H	260	THR	9.0
1	A	240	LEU	9.0
1	H	214	TYR	9.0
1	L	351	LEU	9.0
1	B	392	PRO	9.0
1	M	79	ASN	9.0
1	M	212	ASP	9.0
1	E	223	GLY	9.0
1	E	348	PRO	9.0
1	B	272	ILE	9.0
1	D	323	ASP	9.0
1	H	99	CYS	9.0
1	H	327	TRP	9.0
1	I	357	VAL	9.0
1	M	378	GLU	9.0
1	C	293	ASN	8.9
1	E	138	ASP	8.9
1	A	238	THR	8.9
1	B	390	PHE	8.9
1	M	117	VAL	8.9
1	F	71	HIS	8.9
1	I	157	ASN	8.9

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Mol	Chain	Res	Type	RSRZ
1	C	83	ASP	8.9
1	A	24	GLY	8.9
1	J	208	ILE	8.9
1	A	119	ALA	8.9
1	I	228	THR	8.9
1	I	358	ALA	8.9
1	I	281	GLY	8.9
1	K	384	VAL	8.9
1	F	277	ALA	8.9
1	M	163	GLY	8.9
1	M	24	GLY	8.9
1	A	421	ASP	8.9
1	E	50	GLY	8.9
1	B	145	MET	8.9
1	E	15	ILE	8.9
1	F	296	ILE	8.9
1	F	373	LEU	8.9
1	L	57	ILE	8.9
1	F	218	SER	8.9
1	M	141	TYR	8.9
1	I	137	THR	8.9
1	A	160	VAL	8.9
1	L	409	GLY	8.9
1	I	200	SER	8.9
1	A	321	ALA	8.9
1	D	70	ALA	8.9
1	D	158	VAL	8.9
1	L	354	TYR	8.9
1	C	388	GLY	8.9
1	M	253	HIS	8.9
1	F	313	VAL	8.9
1	L	25	PRO	8.9
1	L	218	SER	8.9
1	D	243	GLY	8.9
1	H	240	LEU	8.8
1	D	239	SER	8.8
1	E	62	GLY	8.8
1	A	120	LEU	8.8
1	J	274	ARG	8.8
1	B	216	PHE	8.8
1	F	361	SER	8.8
1	F	75	GLN	8.8

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Mol	Chain	Res	Type	RSRZ
1	G	188	GLY	8.8
1	M	224	GLY	8.8
1	M	282	LEU	8.8
1	M	185	PRO	8.8
1	E	334	ALA	8.8
1	B	386	GLU	8.8
1	J	314	THR	8.8
1	B	396	ASN	8.8
1	J	323	ASP	8.8
1	M	193	MET	8.8
1	J	76	GLY	8.8
1	E	350	THR	8.8
1	J	178	VAL	8.8
1	L	147	ALA	8.8
1	G	381	LYS	8.8
1	H	412	THR	8.8
1	I	67	ILE	8.8
1	L	431	ASP	8.8
1	F	80	TYR	8.8
1	B	327	TRP	8.8
1	L	281	GLY	8.8
1	C	281	GLY	8.8
1	H	367	GLY	8.8
1	K	102	VAL	8.8
1	K	304	PRO	8.8
1	K	338	HIS	8.8
1	K	370	ASN	8.8
1	B	260	THR	8.8
1	A	407	ARG	8.7
1	B	12	VAL	8.7
1	B	95	SER	8.7
1	G	325	MET	8.7
1	A	369	SER	8.7
1	F	145	MET	8.7
1	K	293	ASN	8.7
1	J	37	THR	8.7
1	J	326	SER	8.7
1	G	174	ASP	8.7
1	H	409	GLY	8.7
1	M	270	THR	8.7
1	G	61	PRO	8.7
1	A	167	LEU	8.7

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Mol	Chain	Res	Type	RSRZ
1	H	160	VAL	8.7
1	K	153	ASP	8.7
1	J	320	GLN	8.7
1	M	298	THR	8.7
1	I	410	ILE	8.7
1	A	288	ASN	8.7
1	B	401	ILE	8.7
1	M	196	THR	8.7
1	I	261	ILE	8.7
1	J	254	GLY	8.7
1	G	178	VAL	8.7
1	B	378	GLU	8.7
1	B	130	GLN	8.7
1	E	178	VAL	8.7
1	B	367	GLY	8.7
1	E	163	GLY	8.7
1	F	131	GLY	8.7
1	J	406	ASP	8.7
1	G	233	ASN	8.7
1	J	104	ARG	8.7
1	D	208	ILE	8.7
1	B	29	PRO	8.7
1	E	297	PRO	8.7
1	G	148	THR	8.7
1	K	195	ALA	8.7
1	E	418	GLU	8.7
1	H	34	GLU	8.7
1	K	145	MET	8.7
1	D	69	GLY	8.7
1	F	356	ARG	8.7
1	G	204	ARG	8.7
1	M	409	GLY	8.7
1	M	147	ALA	8.6
1	C	159	LEU	8.6
1	F	375	PRO	8.6
1	M	375	PRO	8.6
1	C	12	VAL	8.6
1	L	26	ALA	8.6
1	K	421	ASP	8.6
1	I	232	ALA	8.6
1	K	204	ARG	8.6
1	M	422	PHE	8.6

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Mol	Chain	Res	Type	RSRZ
1	G	214	TYR	8.6
1	A	19	LEU	8.6
1	H	20	MET	8.6
1	H	147	ALA	8.6
1	J	152	ASN	8.6
1	F	213	ASP	8.6
1	D	140	SER	8.6
1	J	268	GLY	8.6
1	J	385	THR	8.6
1	M	183	PRO	8.6
1	G	68	VAL	8.6
1	B	407	ARG	8.6
1	I	253	HIS	8.6
1	H	243	GLY	8.6
1	I	179	ARG	8.6
1	H	326	SER	8.6
1	J	68	VAL	8.6
1	J	227	ILE	8.6
1	B	303	GLN	8.6
1	I	303	GLN	8.6
1	F	386	GLU	8.6
1	M	374	ILE	8.6
1	A	236	ALA	8.6
1	K	315	SER	8.6
1	C	134	SER	8.6
1	B	164	VAL	8.6
1	F	76	GLY	8.6
1	M	94	ALA	8.6
1	J	270	THR	8.6
1	C	163	GLY	8.6
1	D	141	TYR	8.6
1	L	435	PRO	8.6
1	C	324	GLN	8.6
1	D	91	ASN	8.6
1	J	145	MET	8.6
1	E	48	THR	8.6
1	M	273	THR	8.6
1	L	418	GLU	8.6
1	G	167	LEU	8.5
1	I	275	ALA	8.5
1	J	236	ALA	8.5
1	G	318	GLY	8.5

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	G	125	ASN	8.5
1	D	82	PHE	8.5
1	C	136	LEU	8.5
1	K	112	THR	8.5
1	K	250	THR	8.5
1	L	298	THR	8.5
1	K	141	TYR	8.5
1	H	375	PRO	8.5
1	B	159	LEU	8.5
1	M	290	MET	8.5
1	E	431	ASP	8.5
1	C	437	LYS	8.5
1	J	192	LYS	8.5
1	F	100	ARG	8.5
1	K	27	SER	8.5
1	J	148	THR	8.5
1	B	157	ASN	8.5
1	G	32	THR	8.5
1	M	45	TYR	8.5
1	M	142	ASN	8.5
1	C	278	ALA	8.5
1	D	281	GLY	8.5
1	B	51	ASP	8.5
1	I	60	PHE	8.5
1	C	117	VAL	8.5
1	E	84	GLN	8.5
1	D	61	PRO	8.5
1	G	51	ASP	8.5
1	I	419	TYR	8.5
1	B	373	LEU	8.5
1	F	1	MET	8.5
1	G	323	ASP	8.5
1	D	226	THR	8.4
1	E	72	TYR	8.4
1	D	18	LEU	8.4
1	F	197	CYS	8.4
1	H	188	GLY	8.4
1	G	203	PRO	8.4
1	H	44	THR	8.4
1	C	78	GLY	8.4
1	D	77	ASN	8.4
1	D	285	GLY	8.4

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Mol	Chain	Res	Type	RSRZ
1	D	303	GLN	8.4
1	H	296	ILE	8.4
1	A	51	ASP	8.4
1	E	156	GLY	8.4
1	K	147	ALA	8.4
1	F	290	MET	8.4
1	M	160	VAL	8.4
1	A	80	TYR	8.4
1	C	125	ASN	8.4
1	K	155	ILE	8.4
1	J	219	GLN	8.4
1	K	317	SER	8.4
1	D	164	VAL	8.4
1	L	241	SER	8.4
1	I	64	PRO	8.4
1	F	51	ASP	8.4
1	F	66	SER	8.4
1	J	398	THR	8.4
1	B	101	LEU	8.4
1	D	276	VAL	8.4
1	E	224	GLY	8.4
1	A	256	VAL	8.4
1	L	104	ARG	8.4
1	L	128	THR	8.4
1	A	131	GLY	8.4
1	G	212	ASP	8.4
1	M	294	LEU	8.4
1	M	279	ASN	8.3
1	F	65	GLY	8.3
1	G	313	VAL	8.3
1	G	353	ALA	8.3
1	I	27	SER	8.3
1	G	331	GLY	8.3
1	M	25	PRO	8.3
1	E	239	SER	8.3
1	D	410	ILE	8.3
1	L	56	LEU	8.3
1	I	299	ASN	8.3
1	M	138	ASP	8.3
1	J	377	PRO	8.3
1	M	51	ASP	8.3
1	B	206	TYR	8.3

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Mol	Chain	Res	Type	RSRZ
1	E	192	LYS	8.3
1	E	366	ALA	8.3
1	E	411	LYS	8.3
1	K	33	LEU	8.3
1	I	61	PRO	8.3
1	M	75	GLN	8.3
1	F	162	GLU	8.3
1	L	246	LEU	8.3
1	B	406	ASP	8.3
1	D	60	PHE	8.3
1	E	193	MET	8.3
1	E	77	ASN	8.3
1	G	153	ASP	8.3
1	J	40	SER	8.3
1	A	48	THR	8.3
1	D	179	ARG	8.3
1	H	320	GLN	8.3
1	J	325	MET	8.3
1	L	377	PRO	8.3
1	A	155	ILE	8.3
1	A	219	GLN	8.3
1	C	348	PRO	8.3
1	D	414	TRP	8.3
1	E	397	TYR	8.3
1	H	308	ILE	8.3
1	B	276	VAL	8.3
1	G	345	ALA	8.3
1	I	14	PHE	8.3
1	M	277	ALA	8.3
1	K	355	GLU	8.3
1	J	413	VAL	8.3
1	H	47	LEU	8.3
1	J	388	GLY	8.3
1	H	316	LYS	8.3
1	A	188	GLY	8.3
1	H	22	THR	8.3
1	L	256	VAL	8.3
1	M	414	TRP	8.3
1	H	318	GLY	8.2
1	K	29	PRO	8.2
1	F	276	VAL	8.2
1	H	72	TYR	8.2

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Mol	Chain	Res	Type	RSRZ
1	B	73	THR	8.2
1	C	59	PHE	8.2
1	A	157	ASN	8.2
1	B	30	ASP	8.2
1	G	155	ILE	8.2
1	C	72	TYR	8.2
1	K	205	VAL	8.2
1	I	159	LEU	8.2
1	M	227	ILE	8.2
1	I	229	LEU	8.2
1	M	20	MET	8.2
1	C	70	ALA	8.2
1	F	23	THR	8.2
1	J	31	ASP	8.2
1	A	303	GLN	8.2
1	G	25	PRO	8.2
1	H	184	ILE	8.2
1	L	167	LEU	8.2
1	G	141	TYR	8.2
1	M	197	CYS	8.2
1	E	353	ALA	8.2
1	F	424	GLU	8.2
1	B	125	ASN	8.2
1	G	132	SER	8.2
1	E	229	LEU	8.2
1	E	321	ALA	8.2
1	M	342	TYR	8.2
1	D	62	GLY	8.2
1	K	407	ARG	8.2
1	L	191	PRO	8.2
1	I	369	SER	8.2
1	A	63	PHE	8.2
1	M	30	ASP	8.2
1	L	146	SER	8.2
1	F	294	LEU	8.2
1	K	82	PHE	8.2
1	M	239	SER	8.2
1	C	24	GLY	8.2
1	C	404	GLU	8.2
1	E	325	MET	8.2
1	M	295	VAL	8.2
1	A	374	ILE	8.2

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Mol	Chain	Res	Type	RSRZ
1	B	302	THR	8.2
1	C	22	THR	8.2
1	F	164	VAL	8.1
1	I	217	SER	8.1
1	C	366	ALA	8.1
1	F	253	HIS	8.1
1	K	391	ASP	8.1
1	C	196	THR	8.1
1	M	112	THR	8.1
1	G	324	GLN	8.1
1	K	245	GLU	8.1
1	J	193	MET	8.1
1	J	419	TYR	8.1
1	L	376	ASN	8.1
1	I	144	LEU	8.1
1	B	132	SER	8.1
1	M	187	ILE	8.1
1	I	278	ALA	8.1
1	F	337	ILE	8.1
1	G	252	VAL	8.1
1	I	220	TYR	8.1
1	I	414	TRP	8.1
1	J	378	GLU	8.1
1	E	79	ASN	8.1
1	F	410	ILE	8.1
1	G	67	ILE	8.1
1	J	187	ILE	8.1
1	E	176	GLY	8.1
1	J	186	ALA	8.1
1	I	44	THR	8.1
1	C	291	PRO	8.1
1	K	190	ASP	8.1
1	K	358	ALA	8.1
1	A	28	ILE	8.1
1	J	261	ILE	8.1
1	A	196	THR	8.1
1	H	287	ASP	8.1
1	H	390	PHE	8.1
1	A	156	GLY	8.1
1	L	61	PRO	8.1
1	G	151	ILE	8.1
1	J	217	SER	8.1

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Mol	Chain	Res	Type	RSRZ
1	J	179	ARG	8.1
1	C	313	VAL	8.1
1	G	235	ASP	8.1
1	J	185	PRO	8.0
1	K	385	THR	8.0
1	C	226	THR	8.0
1	C	290	MET	8.0
1	I	196	THR	8.0
1	C	43	SER	8.0
1	E	153	ASP	8.0
1	J	66	SER	8.0
1	E	148	THR	8.0
1	D	146	SER	8.0
1	H	261	ILE	8.0
1	I	324	GLN	8.0
1	K	28	ILE	8.0
1	K	327	TRP	8.0
1	K	393	GLY	8.0
1	C	27	SER	8.0
1	H	61	PRO	8.0
1	H	82	PHE	8.0
1	I	29	PRO	8.0
1	M	367	GLY	8.0
1	G	250	THR	8.0
1	C	392	PRO	8.0
1	E	47	LEU	8.0
1	F	409	GLY	8.0
1	M	258	GLY	8.0
1	J	51	ASP	8.0
1	K	44	THR	8.0
1	F	259	VAL	8.0
1	G	280	ASN	8.0
1	G	154	LYS	8.0
1	K	138	ASP	8.0
1	G	226	THR	8.0
1	A	217	SER	8.0
1	J	75	GLN	8.0
1	A	366	ALA	8.0
1	C	71	HIS	8.0
1	H	71	HIS	8.0
1	H	315	SER	8.0
1	I	146	SER	8.0

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Mol	Chain	Res	Type	RSRZ
1	E	44	THR	8.0
1	E	419	TYR	8.0
1	L	38	LEU	8.0
1	F	380	ALA	8.0
1	I	277	ALA	8.0
1	I	72	TYR	8.0
1	M	43	SER	8.0
1	A	296	ILE	8.0
1	B	138	ASP	8.0
1	B	196	THR	8.0
1	I	188	GLY	8.0
1	D	294	LEU	8.0
1	I	273	THR	8.0
1	H	183	PRO	8.0
1	H	138	ASP	8.0
1	D	126	ALA	8.0
1	G	286	THR	8.0
1	J	241	SER	8.0
1	A	150	ASN	8.0
1	L	300	GLU	8.0
1	D	253	HIS	7.9
1	I	402	LEU	7.9
1	K	18	LEU	7.9
1	M	15	ILE	7.9
1	I	183	PRO	7.9
1	M	154	LYS	7.9
1	C	19	LEU	7.9
1	C	105	SER	7.9
1	F	192	LYS	7.9
1	G	91	ASN	7.9
1	B	250	THR	7.9
1	D	395	MET	7.9
1	D	342	TYR	7.9
1	D	416	THR	7.9
1	F	95	SER	7.9
1	M	34	GLU	7.9
1	B	404	GLU	7.9
1	C	198	ASP	7.9
1	I	116	GLY	7.9
1	F	236	ALA	7.9
1	K	20	MET	7.9
1	E	144	LEU	7.9

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Mol	Chain	Res	Type	RSRZ
1	F	275	ALA	7.9
1	L	391	ASP	7.9
1	M	421	ASP	7.9
1	C	90	GLN	7.9
1	E	286	THR	7.9
1	F	42	THR	7.9
1	K	261	ILE	7.9
1	L	438	ILE	7.9
1	M	235	ASP	7.9
1	H	66	SER	7.9
1	B	205	VAL	7.9
1	C	142	ASN	7.9
1	I	250	THR	7.9
1	G	334	ALA	7.9
1	H	232	ALA	7.9
1	K	318	GLY	7.9
1	M	299	ASN	7.9
1	L	190	ASP	7.9
1	J	35	LYS	7.9
1	L	385	THR	7.9
1	D	397	TYR	7.9
1	J	338	HIS	7.9
1	B	423	ARG	7.9
1	D	279	ASN	7.9
1	L	238	THR	7.9
1	B	176	GLY	7.9
1	K	31	ASP	7.9
1	D	331	GLY	7.9
1	D	252	VAL	7.9
1	F	358	ALA	7.9
1	J	90	GLN	7.9
1	C	199	SER	7.9
1	E	427	MET	7.8
1	I	279	ASN	7.8
1	F	352	VAL	7.8
1	L	37	THR	7.8
1	C	423	ARG	7.8
1	D	241	SER	7.8
1	L	179	ARG	7.8
1	M	95	SER	7.8
1	G	43	SER	7.8
1	J	277	ALA	7.8

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Mol	Chain	Res	Type	RSRZ
1	B	374	ILE	7.8
1	D	123	THR	7.8
1	E	378	GLU	7.8
1	J	285	GLY	7.8
1	B	376	ASN	7.8
1	I	231	SER	7.8
1	K	150	ASN	7.8
1	M	91	ASN	7.8
1	C	316	LYS	7.8
1	F	148	THR	7.8
1	I	23	THR	7.8
1	B	352	VAL	7.8
1	A	122	GLY	7.8
1	G	388	GLY	7.8
1	H	133	LEU	7.8
1	D	379	LEU	7.8
1	L	357	VAL	7.8
1	G	274	ARG	7.8
1	J	393	GLY	7.8
1	J	139	VAL	7.8
1	J	402	LEU	7.8
1	K	199	SER	7.8
1	I	154	LYS	7.8
1	I	351	LEU	7.8
1	B	110	SER	7.8
1	H	309	LYS	7.8
1	G	23	THR	7.8
1	F	185	PRO	7.8
1	K	237	ILE	7.8
1	C	128	THR	7.8
1	K	240	LEU	7.8
1	C	386	GLU	7.8
1	A	273	THR	7.7
1	C	274	ARG	7.7
1	I	272	ILE	7.7
1	J	122	GLY	7.7
1	H	54	SER	7.7
1	C	402	LEU	7.7
1	B	360	GLY	7.7
1	F	176	GLY	7.7
1	L	50	GLY	7.7
1	D	142	ASN	7.7

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Mol	Chain	Res	Type	RSRZ
1	A	159	LEU	7.7
1	H	236	ALA	7.7
1	K	354	TYR	7.7
1	H	176	GLY	7.7
1	E	420	THR	7.7
1	J	204	ARG	7.7
1	J	376	ASN	7.7
1	B	178	VAL	7.7
1	I	323	ASP	7.7
1	K	175	LEU	7.7
1	B	236	ALA	7.7
1	D	234	ILE	7.7
1	L	312	ILE	7.7
1	B	353	ALA	7.7
1	A	331	GLY	7.7
1	G	130	GLN	7.7
1	H	95	SER	7.7
1	H	146	SER	7.7
1	L	164	VAL	7.7
1	I	293	ASN	7.7
1	K	373	LEU	7.7
1	K	364	THR	7.7
1	L	71	HIS	7.7
1	D	282	LEU	7.7
1	F	134	SER	7.7
1	I	327	TRP	7.7
1	A	377	PRO	7.7
1	E	403	SER	7.7
1	L	272	ILE	7.7
1	F	303	GLN	7.7
1	H	219	GLN	7.7
1	H	298	THR	7.7
1	E	56	LEU	7.7
1	K	280	ASN	7.7
1	L	414	TRP	7.7
1	B	163	GLY	7.7
1	E	398	THR	7.7
1	D	129	PHE	7.7
1	C	140	SER	7.7
1	F	316	LYS	7.7
1	E	90	GLN	7.7
1	F	221	GLN	7.7

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Mol	Chain	Res	Type	RSRZ
1	G	375	PRO	7.7
1	E	43	SER	7.7
1	A	216	PHE	7.7
1	F	61	PRO	7.7
1	L	440	GLY	7.7
1	C	52	THR	7.7
1	I	201	ASP	7.7
1	K	77	ASN	7.7
1	M	382	ASN	7.7
1	D	157	ASN	7.7
1	E	13	PRO	7.7
1	H	28	ILE	7.7
1	K	330	ARG	7.7
1	M	334	ALA	7.6
1	G	161	GLY	7.6
1	H	186	ALA	7.6
1	K	420	THR	7.6
1	B	129	PHE	7.6
1	H	65	GLY	7.6
1	L	40	SER	7.6
1	J	67	ILE	7.6
1	B	411	LYS	7.6
1	E	78	GLY	7.6
1	H	206	TYR	7.6
1	L	296	ILE	7.6
1	L	48	THR	7.6
1	L	195	ALA	7.6
1	H	231	SER	7.6
1	L	215	GLN	7.6
1	H	338	HIS	7.6
1	H	51	ASP	7.6
1	J	141	TYR	7.6
1	J	397	TYR	7.6
1	B	85	MET	7.6
1	I	151	ILE	7.6
1	J	79	ASN	7.6
1	E	116	GLY	7.6
1	G	284	THR	7.6
1	H	378	GLU	7.6
1	D	159	LEU	7.6
1	I	348	PRO	7.6
1	K	94	ALA	7.6

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Mol	Chain	Res	Type	RSRZ
1	J	18	LEU	7.6
1	K	298	THR	7.6
1	M	412	THR	7.6
1	A	422	PHE	7.6
1	K	51	ASP	7.6
1	M	182	ASP	7.6
1	F	50	GLY	7.6
1	E	426	PHE	7.6
1	H	419	TYR	7.6
1	I	89	ALA	7.6
1	E	91	ASN	7.6
1	L	125	ASN	7.6
1	G	93	PRO	7.6
1	D	296	ILE	7.6
1	L	193	MET	7.6
1	I	285	GLY	7.6
1	M	166	VAL	7.6
1	F	138	ASP	7.6
1	B	339	GLY	7.6
1	C	405	ARG	7.6
1	F	250	THR	7.6
1	C	21	PRO	7.6
1	A	46	ASN	7.6
1	B	91	ASN	7.6
1	F	249	ARG	7.5
1	B	422	PHE	7.5
1	D	426	PHE	7.5
1	D	57	ILE	7.5
1	F	48	THR	7.5
1	H	181	GLY	7.5
1	H	435	PRO	7.5
1	K	243	GLY	7.5
1	F	327	TRP	7.5
1	I	141	TYR	7.5
1	F	382	ASN	7.5
1	J	182	ASP	7.5
1	D	314	THR	7.5
1	L	420	THR	7.5
1	F	279	ASN	7.5
1	C	353	ALA	7.5
1	F	235	ASP	7.5
1	K	186	ALA	7.5

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Mol	Chain	Res	Type	RSRZ
1	F	231	SER	7.5
1	I	280	ASN	7.5
1	J	174	ASP	7.5
1	K	96	TYR	7.5
1	G	327	TRP	7.5
1	H	387	TYR	7.5
1	L	378	GLU	7.5
1	A	326	SER	7.5
1	G	332	SER	7.5
1	K	369	SER	7.5
1	K	197	CYS	7.5
1	D	168	SER	7.5
1	D	403	SER	7.5
1	J	337	ILE	7.5
1	B	126	ALA	7.5
1	E	270	THR	7.5
1	I	32	THR	7.5
1	D	290	MET	7.5
1	G	16	ARG	7.5
1	K	131	GLY	7.5
1	K	325	MET	7.5
1	M	266	PHE	7.5
1	E	169	LEU	7.5
1	J	294	LEU	7.5
1	C	137	THR	7.5
1	I	286	THR	7.5
1	J	205	VAL	7.5
1	L	19	LEU	7.5
1	I	147	ALA	7.5
1	H	179	ARG	7.5
1	I	56	LEU	7.5
1	B	177	TYR	7.5
1	B	220	TYR	7.5
1	B	168	SER	7.5
1	E	384	VAL	7.5
1	E	81	LYS	7.5
1	E	143	GLY	7.5
1	G	314	THR	7.5
1	L	32	THR	7.5
1	M	101	LEU	7.5
1	F	214	TYR	7.5
1	L	109	ARG	7.5

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Mol	Chain	Res	Type	RSRZ
1	H	159	LEU	7.5
1	M	60	PHE	7.5
1	A	278	ALA	7.5
1	H	213	ASP	7.5
1	I	405	ARG	7.4
1	A	113	LEU	7.4
1	A	302	THR	7.4
1	C	61	PRO	7.4
1	C	183	PRO	7.4
1	D	199	SER	7.4
1	F	45	TYR	7.4
1	H	119	ALA	7.4
1	I	26	ALA	7.4
1	M	173	TYR	7.4
1	J	129	PHE	7.4
1	K	372	GLU	7.4
1	A	341	ASN	7.4
1	M	285	GLY	7.4
1	G	287	ASP	7.4
1	M	377	PRO	7.4
1	E	45	TYR	7.4
1	H	335	VAL	7.4
1	E	336	THR	7.4
1	G	44	THR	7.4
1	E	166	VAL	7.4
1	K	231	SER	7.4
1	L	199	SER	7.4
1	L	148	THR	7.4
1	B	27	SER	7.4
1	C	106	LEU	7.4
1	K	424	GLU	7.4
1	B	281	GLY	7.4
1	I	187	ILE	7.4
1	B	279	ASN	7.4
1	I	210	ALA	7.4
1	L	330	ARG	7.4
1	A	406	ASP	7.4
1	I	235	ASP	7.4
1	A	134	SER	7.4
1	I	81	LYS	7.4
1	L	198	ASP	7.4
1	M	373	LEU	7.4

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Mol	Chain	Res	Type	RSRZ
1	A	314	THR	7.4
1	A	117	VAL	7.4
1	M	357	VAL	7.4
1	G	265	GLY	7.4
1	B	299	ASN	7.4
1	B	357	VAL	7.4
1	H	395	MET	7.4
1	I	162	GLU	7.4
1	B	93	PRO	7.4
1	A	20	MET	7.4
1	A	214	TYR	7.4
1	A	383	LEU	7.4
1	H	115	GLY	7.4
1	H	342	TYR	7.4
1	M	268	GLY	7.4
1	M	281	GLY	7.4
1	I	204	ARG	7.4
1	M	430	ALA	7.4
1	D	286	THR	7.4
1	L	280	ASN	7.4
1	K	255	LEU	7.3
1	D	321	ALA	7.3
1	G	237	ILE	7.3
1	H	101	LEU	7.3
1	E	268	GLY	7.3
1	J	288	ASN	7.3
1	B	385	THR	7.3
1	H	221	GLN	7.3
1	F	394	ALA	7.3
1	K	366	ALA	7.3
1	H	46	ASN	7.3
1	B	224	GLY	7.3
1	F	113	LEU	7.3
1	L	316	LYS	7.3
1	D	194	VAL	7.3
1	I	282	LEU	7.3
1	F	32	THR	7.3
1	L	85	MET	7.3
1	H	295	VAL	7.3
1	B	265	GLY	7.3
1	M	236	ALA	7.3
1	L	436	LEU	7.3

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Mol	Chain	Res	Type	RSRZ
1	M	127	VAL	7.3
1	F	24	GLY	7.3
1	B	351	LEU	7.3
1	I	260	THR	7.3
1	A	90	GLN	7.3
1	A	289	LEU	7.3
1	J	215	GLN	7.3
1	D	42	THR	7.3
1	G	224	GLY	7.3
1	D	39	ARG	7.3
1	F	10	GLN	7.3
1	C	160	VAL	7.3
1	E	314	THR	7.3
1	H	222	PRO	7.3
1	C	167	LEU	7.3
1	H	50	GLY	7.3
1	M	198	ASP	7.3
1	J	167	LEU	7.3
1	I	119	ALA	7.3
1	J	368	VAL	7.3
1	B	215	GLN	7.3
1	C	184	ILE	7.3
1	F	266	PHE	7.3
1	J	20	MET	7.3
1	C	330	ARG	7.3
1	K	347	ARG	7.3
1	B	64	PRO	7.3
1	C	376	ASN	7.3
1	L	43	SER	7.3
1	C	85	MET	7.3
1	L	395	MET	7.3
1	K	208	ILE	7.3
1	L	201	ASP	7.3
1	H	370	ASN	7.3
1	D	178	VAL	7.3
1	B	117	VAL	7.3
1	C	157	ASN	7.3
1	J	29	PRO	7.2
1	K	69	GLY	7.2
1	A	249	ARG	7.2
1	M	76	GLY	7.2
1	H	398	THR	7.2

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Mol	Chain	Res	Type	RSRZ
1	G	193	MET	7.2
1	M	215	GLN	7.2
1	C	229	LEU	7.2
1	D	180	LEU	7.2
1	J	340	GLY	7.2
1	K	64	PRO	7.2
1	K	222	PRO	7.2
1	H	136	LEU	7.2
1	I	87	LEU	7.2
1	L	326	SER	7.2
1	C	201	ASP	7.2
1	B	416	THR	7.2
1	G	398	THR	7.2
1	I	420	THR	7.2
1	F	101	LEU	7.2
1	E	110	SER	7.2
1	L	240	LEU	7.2
1	L	304	PRO	7.2
1	C	138	ASP	7.2
1	E	213	ASP	7.2
1	G	38	LEU	7.2
1	J	249	ARG	7.2
1	H	285	GLY	7.2
1	G	71	HIS	7.2
1	L	157	ASN	7.2
1	A	144	LEU	7.2
1	A	215	GLN	7.2
1	L	320	GLN	7.2
1	F	243	GLY	7.2
1	J	25	PRO	7.2
1	I	189	LEU	7.2
1	C	218	SER	7.2
1	I	265	GLY	7.2
1	L	327	TRP	7.2
1	G	255	LEU	7.2
1	D	143	GLY	7.2
1	B	48	THR	7.2
1	B	182	ASP	7.2
1	D	38	LEU	7.2
1	D	229	LEU	7.2
1	H	68	VAL	7.2
1	H	282	LEU	7.2

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Mol	Chain	Res	Type	RSRZ
1	H	294	LEU	7.2
1	K	45	TYR	7.2
1	F	320	GLN	7.2
1	A	33	LEU	7.2
1	L	261	ILE	7.2
1	C	367	GLY	7.2
1	D	149	ALA	7.2
1	K	191	PRO	7.2
1	K	137	THR	7.2
1	G	27	SER	7.2
1	L	156	GLY	7.2
1	E	230	PHE	7.2
1	G	249	ARG	7.2
1	A	255	LEU	7.1
1	A	200	SER	7.1
1	B	90	GLN	7.1
1	I	84	GLN	7.1
1	C	96	TYR	7.1
1	D	271	VAL	7.1
1	F	105	SER	7.1
1	E	282	LEU	7.1
1	D	361	SER	7.1
1	B	114	PRO	7.1
1	F	183	PRO	7.1
1	H	84	GLN	7.1
1	K	282	LEU	7.1
1	C	435	PRO	7.1
1	E	386	GLU	7.1
1	K	182	ASP	7.1
1	L	47	LEU	7.1
1	J	181	GLY	7.1
1	K	76	GLY	7.1
1	H	397	TYR	7.1
1	A	91	ASN	7.1
1	E	188	GLY	7.1
1	L	63	PHE	7.1
1	B	430	ALA	7.1
1	G	436	LEU	7.1
1	J	431	ASP	7.1
1	H	79	ASN	7.1
1	K	336	THR	7.1
1	D	167	LEU	7.1

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Mol	Chain	Res	Type	RSRZ
1	B	122	GLY	7.1
1	E	59	PHE	7.1
1	H	199	SER	7.1
1	L	434	SER	7.1
1	D	236	ALA	7.1
1	H	110	SER	7.1
1	L	247	VAL	7.1
1	I	394	ALA	7.1
1	F	60	PHE	7.1
1	H	156	GLY	7.1
1	K	371	PHE	7.1
1	M	324	GLN	7.1
1	A	185	PRO	7.1
1	D	217	SER	7.1
1	D	308	ILE	7.1
1	M	410	ILE	7.1
1	B	369	SER	7.1
1	F	403	SER	7.1
1	K	184	ILE	7.1
1	B	31	ASP	7.1
1	F	353	ALA	7.1
1	L	88	THR	7.1
1	B	67	ILE	7.1
1	K	43	SER	7.1
1	F	376	ASN	7.1
1	F	418	GLU	7.1
1	M	247	VAL	7.1
1	B	274	ARG	7.1
1	B	239	SER	7.1
1	J	206	TYR	7.1
1	M	351	LEU	7.1
1	K	323	ASP	7.1
1	K	334	ALA	7.1
1	C	223	GLY	7.0
1	F	379	LEU	7.0
1	B	199	SER	7.0
1	D	325	MET	7.0
1	K	413	VAL	7.0
1	A	257	LEU	7.0
1	J	355	GLU	7.0
1	G	124	ILE	7.0
1	L	233	ASN	7.0

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Mol	Chain	Res	Type	RSRZ
1	A	27	SER	7.0
1	L	342	TYR	7.0
1	B	18	LEU	7.0
1	A	235	ASP	7.0
1	B	247	VAL	7.0
1	J	420	THR	7.0
1	K	63	PHE	7.0
1	H	107	THR	7.0
1	C	221	GLN	7.0
1	I	198	ASP	7.0
1	C	216	PHE	7.0
1	C	431	ASP	7.0
1	G	270	THR	7.0
1	H	215	GLN	7.0
1	J	237	ILE	7.0
1	J	266	PHE	7.0
1	L	219	GLN	7.0
1	C	354	TYR	7.0
1	A	129	PHE	7.0
1	D	266	PHE	7.0
1	M	63	PHE	7.0
1	B	440	GLY	7.0
1	E	410	ILE	7.0
1	A	358	ALA	7.0
1	F	149	ALA	7.0
1	M	143	GLY	7.0
1	F	436	LEU	7.0
1	G	423	ARG	7.0
1	H	288	ASN	7.0
1	J	415	PRO	7.0
1	L	196	THR	7.0
1	H	267	ASP	7.0
1	C	415	PRO	7.0
1	B	273	THR	7.0
1	G	133	LEU	7.0
1	G	246	LEU	7.0
1	K	266	PHE	7.0
1	H	323	ASP	7.0
1	A	355	GLU	7.0
1	G	222	PRO	7.0
1	G	376	ASN	7.0
1	L	28	ILE	7.0

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Mol	Chain	Res	Type	RSRZ
1	F	295	VAL	7.0
1	J	276	VAL	7.0
1	A	83	ASP	7.0
1	J	62	GLY	7.0
1	L	141	TYR	7.0
1	G	267	ASP	7.0
1	I	315	SER	7.0
1	L	214	TYR	7.0
1	E	66	SER	7.0
1	F	27	SER	7.0
1	K	352	VAL	7.0
1	A	245	GLU	6.9
1	K	181	GLY	6.9
1	A	416	THR	6.9
1	K	350	THR	6.9
1	F	278	ALA	6.9
1	A	86	LEU	6.9
1	G	339	GLY	6.9
1	J	352	VAL	6.9
1	G	73	THR	6.9
1	I	326	SER	6.9
1	K	70	ALA	6.9
1	I	63	PHE	6.9
1	I	134	SER	6.9
1	J	408	LEU	6.9
1	M	69	GLY	6.9
1	B	99	CYS	6.9
1	G	201	ASP	6.9
1	B	379	LEU	6.9
1	F	419	TYR	6.9
1	H	348	PRO	6.9
1	K	19	LEU	6.9
1	K	294	LEU	6.9
1	A	295	VAL	6.9
1	B	139	VAL	6.9
1	C	275	ALA	6.9
1	H	299	ASN	6.9
1	J	144	LEU	6.9
1	A	177	TYR	6.9
1	C	130	GLN	6.9
1	C	211	ALA	6.9
1	F	62	GLY	6.9

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Mol	Chain	Res	Type	RSRZ
1	E	136	LEU	6.9
1	G	239	SER	6.9
1	G	65	GLY	6.9
1	L	77	ASN	6.9
1	A	426	PHE	6.9
1	G	90	GLN	6.9
1	K	75	GLN	6.9
1	C	236	ALA	6.9
1	B	315	SER	6.9
1	C	82	PHE	6.9
1	A	242	VAL	6.9
1	A	348	PRO	6.9
1	L	401	ILE	6.9
1	I	270	THR	6.9
1	K	320	GLN	6.9
1	A	140	SER	6.9
1	A	210	ALA	6.9
1	D	367	GLY	6.9
1	E	29	PRO	6.9
1	I	85	MET	6.9
1	M	274	ARG	6.9
1	B	439	ALA	6.9
1	J	142	ASN	6.9
1	F	368	VAL	6.9
1	M	189	LEU	6.9
1	D	37	THR	6.9
1	L	165	THR	6.9
1	B	76	GLY	6.9
1	G	216	PHE	6.9
1	H	421	ASP	6.9
1	H	142	ASN	6.8
1	F	385	THR	6.8
1	L	439	ALA	6.8
1	B	419	TYR	6.8
1	C	342	TYR	6.8
1	E	423	ARG	6.8
1	J	411	LYS	6.8
1	D	415	PRO	6.8
1	F	338	HIS	6.8
1	J	189	LEU	6.8
1	E	414	TRP	6.8
1	A	352	VAL	6.8

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Mol	Chain	Res	Type	RSRZ
1	F	350	THR	6.8
1	I	48	THR	6.8
1	B	326	SER	6.8
1	L	217	SER	6.8
1	B	368	VAL	6.8
1	D	340	GLY	6.8
1	J	60	PHE	6.8
1	H	201	ASP	6.8
1	A	279	ASN	6.8
1	H	225	VAL	6.8
1	D	16	ARG	6.8
1	E	111	SER	6.8
1	G	112	THR	6.8
1	M	71	HIS	6.8
1	E	197	CYS	6.8
1	G	202	ARG	6.8
1	B	277	ALA	6.8
1	C	241	SER	6.8
1	H	363	VAL	6.8
1	H	64	PRO	6.8
1	H	226	THR	6.8
1	B	135	GLU	6.8
1	G	110	SER	6.8
1	M	199	SER	6.8
1	M	87	LEU	6.8
1	I	121	ASN	6.8
1	M	205	VAL	6.8
1	H	217	SER	6.8
1	I	374	ILE	6.8
1	I	427	MET	6.8
1	L	87	LEU	6.8
1	C	193	MET	6.8
1	M	179	ARG	6.8
1	E	175	LEU	6.8
1	I	145	MET	6.8
1	B	43	SER	6.8
1	E	200	SER	6.8
1	E	211	ALA	6.8
1	I	223	GLY	6.8
1	E	406	ASP	6.8
1	A	339	GLY	6.8
1	C	104	ARG	6.8

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Mol	Chain	Res	Type	RSRZ
1	K	339	GLY	6.8
1	J	188	GLY	6.8
1	M	89	ALA	6.8
1	B	198	ASP	6.8
1	C	374	ILE	6.8
1	F	395	MET	6.8
1	D	258	GLY	6.8
1	F	252	VAL	6.8
1	I	91	ASN	6.8
1	D	125	ASN	6.8
1	F	291	PRO	6.8
1	G	370	ASN	6.8
1	A	170	PRO	6.8
1	E	374	ILE	6.8
1	L	197	CYS	6.7
1	A	29	PRO	6.7
1	A	195	ALA	6.7
1	F	351	LEU	6.7
1	J	235	ASP	6.7
1	C	434	SER	6.7
1	L	82	PHE	6.7
1	A	72	TYR	6.7
1	L	227	ILE	6.7
1	A	404	GLU	6.7
1	B	428	GLU	6.7
1	B	387	TYR	6.7
1	E	181	GLY	6.7
1	G	340	GLY	6.7
1	J	96	TYR	6.7
1	F	170	PRO	6.7
1	B	280	ASN	6.7
1	M	214	TYR	6.7
1	G	37	THR	6.7
1	A	243	GLY	6.7
1	D	301	ILE	6.7
1	D	295	VAL	6.7
1	E	51	ASP	6.7
1	F	402	LEU	6.7
1	M	318	GLY	6.7
1	D	338	HIS	6.7
1	D	173	TYR	6.7
1	G	283	THR	6.7

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Mol	Chain	Res	Type	RSRZ
1	H	40	SER	6.7
1	C	126	ALA	6.7
1	C	173	TYR	6.7
1	E	318	GLY	6.7
1	B	432	LEU	6.7
1	D	392	PRO	6.7
1	F	217	SER	6.7
1	G	217	SER	6.7
1	H	238	THR	6.7
1	A	387	TYR	6.7
1	I	129	PHE	6.7
1	M	188	GLY	6.7
1	C	253	HIS	6.7
1	F	102	VAL	6.7
1	G	168	SER	6.7
1	D	353	ALA	6.7
1	A	376	ASN	6.7
1	H	29	PRO	6.7
1	M	121	ASN	6.7
1	A	227	ILE	6.7
1	I	150	ASN	6.7
1	J	316	LYS	6.7
1	M	115	GLY	6.7
1	F	117	VAL	6.7
1	B	187	ILE	6.7
1	D	378	GLU	6.7
1	L	390	PHE	6.7
1	F	77	ASN	6.7
1	H	373	LEU	6.7
1	I	47	LEU	6.7
1	L	266	PHE	6.7
1	G	198	ASP	6.7
1	A	218	SER	6.7
1	B	195	ALA	6.7
1	A	237	ILE	6.7
1	J	175	LEU	6.7
1	L	129	PHE	6.7
1	K	148	THR	6.7
1	H	357	VAL	6.7
1	I	384	VAL	6.7
1	K	227	ILE	6.6
1	H	105	SER	6.6

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Mol	Chain	Res	Type	RSRZ
1	C	260	THR	6.6
1	B	233	ASN	6.6
1	L	424	GLU	6.6
1	D	218	SER	6.6
1	C	14	PHE	6.6
1	C	414	TRP	6.6
1	H	118	TYR	6.6
1	H	396	ASN	6.6
1	J	300	GLU	6.6
1	K	132	SER	6.6
1	E	405	ARG	6.6
1	E	415	PRO	6.6
1	H	140	SER	6.6
1	A	41	GLU	6.6
1	H	67	ILE	6.6
1	A	337	ILE	6.6
1	F	81	LYS	6.6
1	E	319	GLY	6.6
1	I	300	GLU	6.6
1	M	55	GLY	6.6
1	G	234	ILE	6.6
1	H	350	THR	6.6
1	J	101	LEU	6.6
1	E	388	GLY	6.6
1	H	300	GLU	6.6
1	L	245	GLU	6.6
1	B	414	TRP	6.6
1	E	73	THR	6.6
1	H	36	HIS	6.6
1	H	117	VAL	6.6
1	I	354	TYR	6.6
1	D	324	GLN	6.6
1	M	315	SER	6.6
1	G	407	ARG	6.6
1	I	22	THR	6.6
1	K	212	ASP	6.6
1	C	219	GLN	6.6
1	C	425	TYR	6.6
1	G	211	ALA	6.6
1	L	423	ARG	6.6
1	A	359	THR	6.6
1	B	175	LEU	6.6

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Mol	Chain	Res	Type	RSRZ
1	D	189	LEU	6.6
1	A	163	GLY	6.6
1	C	372	GLU	6.6
1	H	369	SER	6.6
1	G	86	LEU	6.6
1	G	129	PHE	6.6
1	G	322	GLY	6.6
1	G	337	ILE	6.6
1	H	233	ASN	6.6
1	M	435	PRO	6.6
1	B	116	GLY	6.6
1	C	49	VAL	6.6
1	D	212	ASP	6.6
1	E	183	PRO	6.6
1	I	12	VAL	6.6
1	J	93	PRO	6.6
1	K	107	THR	6.6
1	K	337	ILE	6.6
1	M	335	VAL	6.6
1	F	422	PHE	6.6
1	L	101	LEU	6.6
1	M	411	LYS	6.6
1	L	29	PRO	6.6
1	E	25	PRO	6.5
1	H	55	GLY	6.5
1	A	14	PHE	6.5
1	C	225	VAL	6.5
1	F	93	PRO	6.5
1	D	284	THR	6.5
1	A	300	GLU	6.5
1	A	418	GLU	6.5
1	I	182	ASP	6.5
1	E	413	VAL	6.5
1	L	154	LYS	6.5
1	E	373	LEU	6.5
1	A	239	SER	6.5
1	J	210	ALA	6.5
1	I	268	GLY	6.5
1	D	260	THR	6.5
1	D	155	ILE	6.5
1	F	43	SER	6.5
1	L	287	ASP	6.5

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Mol	Chain	Res	Type	RSRZ
1	K	72	TYR	6.5
1	D	160	VAL	6.5
1	D	356	ARG	6.5
1	F	325	MET	6.5
1	L	142	ASN	6.5
1	L	152	ASN	6.5
1	K	37	THR	6.5
1	K	59	PHE	6.5
1	J	177	TYR	6.5
1	I	19	LEU	6.5
1	L	235	ASP	6.5
1	L	182	ASP	6.5
1	L	255	LEU	6.5
1	M	429	VAL	6.5
1	M	393	GLY	6.5
1	E	41	GLU	6.5
1	J	336	THR	6.5
1	L	53	GLY	6.5
1	M	322	GLY	6.5
1	C	46	ASN	6.5
1	C	88	THR	6.5
1	F	156	GLY	6.5
1	K	134	SER	6.5
1	C	60	PHE	6.5
1	L	225	VAL	6.5
1	A	135	GLU	6.5
1	H	200	SER	6.5
1	H	336	THR	6.5
1	E	139	VAL	6.5
1	G	405	ARG	6.5
1	J	299	ASN	6.5
1	D	390	PHE	6.5
1	G	421	ASP	6.5
1	L	121	ASN	6.5
1	A	325	MET	6.5
1	G	336	THR	6.5
1	M	130	GLN	6.5
1	A	44	THR	6.4
1	D	298	THR	6.4
1	F	41	GLU	6.4
1	G	215	GLN	6.4
1	M	301	ILE	6.4

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Mol	Chain	Res	Type	RSRZ
1	C	156	GLY	6.4
1	J	78	GLY	6.4
1	L	421	ASP	6.4
1	B	249	ARG	6.4
1	K	340	GLY	6.4
1	A	398	THR	6.4
1	F	154	LYS	6.4
1	A	262	TYR	6.4
1	D	137	THR	6.4
1	E	279	ASN	6.4
1	M	90	GLN	6.4
1	B	66	SER	6.4
1	I	128	THR	6.4
1	I	313	VAL	6.4
1	I	294	LEU	6.4
1	A	427	MET	6.4
1	C	358	ALA	6.4
1	E	20	MET	6.4
1	I	236	ALA	6.4
1	B	78	GLY	6.4
1	B	393	GLY	6.4
1	E	360	GLY	6.4
1	J	330	ARG	6.4
1	G	191	PRO	6.4
1	L	133	LEU	6.4
1	A	365	VAL	6.4
1	E	381	LYS	6.4
1	J	319	GLY	6.4
1	D	435	PRO	6.4
1	H	83	ASP	6.4
1	M	364	THR	6.4
1	H	241	SER	6.4
1	J	232	ALA	6.4
1	L	134	SER	6.4
1	K	165	THR	6.4
1	F	85	MET	6.4
1	L	380	ALA	6.4
1	I	317	SER	6.4
1	L	188	GLY	6.4
1	K	185	PRO	6.4
1	C	390	PHE	6.4
1	E	177	TYR	6.4

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Mol	Chain	Res	Type	RSRZ
1	G	117	VAL	6.4
1	M	46	ASN	6.4
1	A	229	LEU	6.4
1	G	384	VAL	6.4
1	K	322	GLY	6.4
1	E	28	ILE	6.4
1	E	284	THR	6.4
1	M	102	VAL	6.4
1	M	106	LEU	6.4
1	L	22	THR	6.4
1	M	441	ALA	6.4
1	C	217	SER	6.4
1	G	105	SER	6.4
1	M	396	ASN	6.4
1	J	250	THR	6.4
1	J	339	GLY	6.4
1	L	358	ALA	6.4
1	C	373	LEU	6.4
1	E	33	LEU	6.4
1	L	237	ILE	6.4
1	J	183	PRO	6.4
1	G	248	PHE	6.4
1	G	390	PHE	6.4
1	K	163	GLY	6.3
1	L	34	GLU	6.3
1	G	81	LYS	6.3
1	E	69	GLY	6.3
1	E	312	ILE	6.3
1	H	33	LEU	6.3
1	I	312	ILE	6.3
1	I	364	THR	6.3
1	B	251	SER	6.3
1	F	167	LEU	6.3
1	J	94	ALA	6.3
1	F	239	SER	6.3
1	H	14	PHE	6.3
1	G	173	TYR	6.3
1	H	372	GLU	6.3
1	C	286	THR	6.3
1	D	105	SER	6.3
1	A	389	ARG	6.3
1	H	280	ASN	6.3

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Mol	Chain	Res	Type	RSRZ
1	E	22	THR	6.3
1	K	219	GLN	6.3
1	E	104	ARG	6.3
1	F	163	GLY	6.3
1	G	210	ALA	6.3
1	M	65	GLY	6.3
1	M	376	ASN	6.3
1	G	88	THR	6.3
1	H	108	VAL	6.3
1	H	212	ASP	6.3
1	L	430	ALA	6.3
1	F	40	SER	6.3
1	B	94	ALA	6.3
1	D	198	ASP	6.3
1	F	433	ASN	6.3
1	J	30	ASP	6.3
1	A	23	THR	6.3
1	I	230	PHE	6.3
1	M	370	ASN	6.3
1	A	66	SER	6.3
1	C	232	ALA	6.3
1	B	42	THR	6.3
1	E	225	VAL	6.3
1	F	421	ASP	6.3
1	K	151	ILE	6.3
1	I	376	ASN	6.3
1	H	132	SER	6.3
1	B	420	THR	6.3
1	F	267	ASP	6.3
1	F	381	LYS	6.3
1	I	185	PRO	6.3
1	J	55	GLY	6.3
1	M	355	GLU	6.3
1	F	193	MET	6.3
1	G	309	LYS	6.3
1	K	35	LYS	6.3
1	K	316	LYS	6.3
1	A	112	THR	6.3
1	D	111	SER	6.3
1	I	100	ARG	6.3
1	K	425	TYR	6.3
1	I	366	ALA	6.3

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Mol	Chain	Res	Type	RSRZ
1	K	15	ILE	6.3
1	A	186	ALA	6.3
1	G	60	PHE	6.3
1	G	165	THR	6.3
1	A	269	THR	6.3
1	E	173	TYR	6.3
1	I	18	LEU	6.3
1	L	177	TYR	6.3
1	B	210	ALA	6.3
1	B	174	ASP	6.2
1	H	73	THR	6.3
1	J	109	ARG	6.3
1	K	85	MET	6.3
1	G	223	GLY	6.2
1	A	104	ARG	6.2
1	A	197	CYS	6.2
1	C	251	SER	6.2
1	H	235	ASP	6.2
1	J	88	THR	6.2
1	M	427	MET	6.2
1	C	387	TYR	6.2
1	H	92	LEU	6.2
1	H	379	LEU	6.2
1	K	133	LEU	6.2
1	B	158	VAL	6.2
1	G	69	GLY	6.2
1	I	55	GLY	6.2
1	E	121	ASN	6.2
1	F	110	SER	6.2
1	G	140	SER	6.2
1	H	265	GLY	6.2
1	I	409	GLY	6.2
1	H	56	LEU	6.2
1	J	202	ARG	6.2
1	E	280	ASN	6.2
1	G	338	HIS	6.2
1	H	205	VAL	6.2
1	J	258	GLY	6.2
1	A	403	SER	6.2
1	D	221	GLN	6.2
1	H	432	LEU	6.2
1	K	249	ARG	6.2

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Mol	Chain	Res	Type	RSRZ
1	G	64	PRO	6.2
1	H	141	TYR	6.2
1	L	137	THR	6.2
1	L	183	PRO	6.2
1	A	322	GLY	6.2
1	D	116	GLY	6.2
1	D	131	GLY	6.2
1	F	142	ASN	6.2
1	E	185	PRO	6.2
1	J	373	LEU	6.2
1	H	433	ASN	6.2
1	M	267	ASP	6.2
1	M	275	ALA	6.2
1	A	225	VAL	6.2
1	B	188	GLY	6.2
1	B	255	LEU	6.2
1	B	283	THR	6.2
1	D	197	CYS	6.2
1	H	38	LEU	6.2
1	D	187	ILE	6.2
1	I	25	PRO	6.2
1	E	232	ALA	6.2
1	L	123	THR	6.2
1	H	158	VAL	6.2
1	C	93	PRO	6.2
1	F	180	LEU	6.2
1	I	397	TYR	6.2
1	J	47	LEU	6.2
1	E	105	SER	6.2
1	L	153	ASP	6.2
1	C	161	GLY	6.2
1	F	16	ARG	6.2
1	I	158	VAL	6.2
1	F	177	TYR	6.2
1	F	208	ILE	6.2
1	G	70	ALA	6.2
1	I	46	ASN	6.2
1	A	71	HIS	6.2
1	H	88	THR	6.2
1	J	309	LYS	6.2
1	L	291	PRO	6.2
1	A	327	TRP	6.2

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Mol	Chain	Res	Type	RSRZ
1	C	295	VAL	6.2
1	G	282	LEU	6.2
1	I	224	GLY	6.2
1	D	249	ARG	6.2
1	M	128	THR	6.2
1	M	50	GLY	6.2
1	E	126	ALA	6.2
1	B	417	ARG	6.2
1	F	151	ILE	6.2
1	H	91	ASN	6.2
1	M	148	THR	6.2
1	M	250	THR	6.2
1	A	133	LEU	6.1
1	G	368	VAL	6.1
1	H	69	GLY	6.1
1	K	360	GLY	6.1
1	M	432	LEU	6.1
1	H	174	ASP	6.1
1	C	403	SER	6.1
1	I	66	SER	6.1
1	J	50	GLY	6.1
1	C	287	ASP	6.1
1	H	128	THR	6.1
1	I	377	PRO	6.1
1	I	111	SER	6.1
1	A	432	LEU	6.1
1	L	158	VAL	6.1
1	M	327	TRP	6.1
1	F	326	SER	6.1
1	L	126	ALA	6.1
1	I	259	VAL	6.1
1	L	18	LEU	6.1
1	F	6	ASP	6.1
1	H	273	THR	6.1
1	L	181	GLY	6.1
1	A	136	LEU	6.1
1	G	358	ALA	6.1
1	A	420	THR	6.1
1	D	428	GLU	6.1
1	M	252	VAL	6.1
1	J	116	GLY	6.1
1	M	107	THR	6.1

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Mol	Chain	Res	Type	RSRZ
1	H	223	GLY	6.1
1	L	265	GLY	6.1
1	A	425	TYR	6.1
1	B	323	ASP	6.1
1	B	425	TYR	6.1
1	K	164	VAL	6.1
1	M	134	SER	6.1
1	B	221	GLN	6.1
1	C	145	MET	6.1
1	B	107	THR	6.1
1	C	329	ALA	6.1
1	D	366	ALA	6.1
1	K	403	SER	6.1
1	C	187	ILE	6.1
1	D	184	ILE	6.1
1	M	78	GLY	6.1
1	B	418	GLU	6.1
1	B	59	PHE	6.1
1	B	278	ALA	6.1
1	K	394	ALA	6.1
1	H	256	VAL	6.1
1	C	165	THR	6.1
1	C	197	CYS	6.1
1	I	40	SER	6.1
1	L	95	SER	6.1
1	C	303	GLN	6.1
1	K	108	VAL	6.1
1	D	67	ILE	6.1
1	H	149	ALA	6.1
1	G	85	MET	6.1
1	H	129	PHE	6.1
1	K	201	ASP	6.1
1	L	66	SER	6.1
1	L	311	GLU	6.1
1	D	119	ALA	6.1
1	H	196	THR	6.1
1	M	14	PHE	6.1
1	J	327	TRP	6.1
1	E	102	VAL	6.1
1	I	177	TYR	6.1
1	L	365	VAL	6.1
1	I	240	LEU	6.1

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Mol	Chain	Res	Type	RSRZ
1	M	103	SER	6.1
1	A	431	ASP	6.1
1	L	236	ALA	6.1
1	I	321	ALA	6.1
1	K	233	ASN	6.1
1	K	253	HIS	6.1
1	B	35	LYS	6.1
1	C	131	GLY	6.1
1	C	91	ASN	6.0
1	F	181	GLY	6.0
1	I	237	ILE	6.0
1	M	155	ILE	6.0
1	C	407	ARG	6.0
1	D	33	LEU	6.0
1	D	413	VAL	6.0
1	E	433	ASN	6.0
1	F	223	GLY	6.0
1	H	237	ILE	6.0
1	J	418	GLU	6.0
1	L	234	ILE	6.0
1	E	184	ILE	6.0
1	D	54	SER	6.0
1	H	143	GLY	6.0
1	E	67	ILE	6.0
1	J	272	ILE	6.0
1	K	264	ILE	6.0
1	F	245	GLU	6.0
1	A	137	THR	6.0
1	C	326	SER	6.0
1	E	335	VAL	6.0
1	F	357	VAL	6.0
1	G	416	THR	6.0
1	K	22	THR	6.0
1	J	155	ILE	6.0
1	E	159	LEU	6.0
1	C	238	THR	6.0
1	M	238	THR	6.0
1	C	338	HIS	6.0
1	B	409	GLY	6.0
1	F	201	ASP	6.0
1	B	54	SER	6.0
1	I	109	ARG	6.0

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Mol	Chain	Res	Type	RSRZ
1	M	360	GLY	6.0
1	B	271	VAL	6.0
1	E	357	VAL	6.0
1	G	63	PHE	6.0
1	K	412	THR	6.0
1	G	295	VAL	6.0
1	I	234	ILE	6.0
1	L	207	THR	6.0
1	J	223	GLY	6.0
1	K	409	GLY	6.0
1	L	253	HIS	6.0
1	M	109	ARG	6.0
1	H	334	ALA	6.0
1	B	37	THR	6.0
1	B	298	THR	6.0
1	H	255	LEU	6.0
1	L	364	THR	6.0
1	C	84	GLN	6.0
1	J	203	PRO	6.0
1	L	184	ILE	6.0
1	F	152	ASN	6.0
1	L	132	SER	6.0
1	L	172	SER	6.0
1	I	284	THR	6.0
1	F	19	LEU	6.0
1	C	363	VAL	6.0
1	E	238	THR	6.0
1	F	37	THR	6.0
1	F	18	LEU	6.0
1	G	118	TYR	6.0
1	K	119	ALA	6.0
1	G	335	VAL	6.0
1	D	402	LEU	6.0
1	K	154	LYS	6.0
1	L	381	LYS	6.0
1	A	315	SER	6.0
1	E	404	GLU	6.0
1	A	124	ILE	6.0
1	H	374	ILE	6.0
1	I	267	ASP	6.0
1	L	149	ALA	6.0
1	A	213	ASP	6.0

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Mol	Chain	Res	Type	RSRZ
1	C	255	LEU	6.0
1	K	272	ILE	6.0
1	M	420	THR	6.0
1	J	81	LYS	6.0
1	J	422	PHE	6.0
1	F	106	LEU	6.0
1	B	115	GLY	5.9
1	K	361	SER	6.0
1	L	100	ARG	5.9
1	L	411	LYS	5.9
1	C	75	GLN	5.9
1	I	421	ASP	5.9
1	K	242	VAL	5.9
1	G	53	GLY	5.9
1	G	328	SER	5.9
1	H	163	GLY	5.9
1	J	41	GLU	5.9
1	K	427	MET	5.9
1	G	197	CYS	5.9
1	H	45	TYR	5.9
1	M	383	LEU	5.9
1	A	386	GLU	5.9
1	F	265	GLY	5.9
1	M	62	GLY	5.9
1	A	282	LEU	5.9
1	C	215	GLN	5.9
1	D	50	GLY	5.9
1	F	179	ARG	5.9
1	J	108	VAL	5.9
1	K	25	PRO	5.9
1	A	49	VAL	5.9
1	D	190	ASP	5.9
1	G	135	GLU	5.9
1	L	372	GLU	5.9
1	B	102	VAL	5.9
1	D	357	VAL	5.9
1	L	90	GLN	5.9
1	D	78	GLY	5.9
1	L	285	GLY	5.9
1	A	361	SER	5.9
1	D	47	LEU	5.9
1	L	226	THR	5.9

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Mol	Chain	Res	Type	RSRZ
1	L	239	SER	5.9
1	I	276	VAL	5.9
1	K	71	HIS	5.9
1	D	219	GLN	5.9
1	H	39	ARG	5.9
1	L	15	ILE	5.9
1	D	122	GLY	5.9
1	J	32	THR	5.9
1	K	123	THR	5.9
1	K	326	SER	5.9
1	K	341	ASN	5.9
1	D	17	SER	5.9
1	D	313	VAL	5.9
1	H	182	ASP	5.9
1	H	313	VAL	5.9
1	H	360	GLY	5.9
1	G	128	THR	5.9
1	M	26	ALA	5.9
1	M	66	SER	5.9
1	E	60	PHE	5.9
1	B	148	THR	5.9
1	G	160	VAL	5.9
1	M	300	GLU	5.9
1	M	77	ASN	5.9
1	E	117	VAL	5.9
1	G	221	GLN	5.9
1	M	353	ALA	5.9
1	B	109	ARG	5.9
1	D	280	ASN	5.9
1	J	367	GLY	5.9
1	D	68	VAL	5.9
1	A	143	GLY	5.9
1	B	282	LEU	5.9
1	F	115	GLY	5.9
1	J	143	GLY	5.9
1	A	247	VAL	5.9
1	E	100	ARG	5.9
1	F	128	THR	5.9
1	G	42	THR	5.9
1	D	289	LEU	5.8
1	M	433	ASN	5.8
1	M	366	ALA	5.8

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Mol	Chain	Res	Type	RSRZ
1	A	107	THR	5.8
1	F	342	TYR	5.8
1	B	62	GLY	5.8
1	E	324	GLN	5.8
1	E	395	MET	5.8
1	L	114	PRO	5.8
1	D	151	ILE	5.8
1	B	267	ASP	5.8
1	K	26	ALA	5.8
1	M	201	ASP	5.8
1	I	266	PHE	5.8
1	D	309	LYS	5.8
1	I	378	GLU	5.8
1	K	203	PRO	5.8
1	J	166	VAL	5.8
1	L	138	ASP	5.8
1	E	165	THR	5.8
1	J	298	THR	5.8
1	A	312	ILE	5.8
1	B	289	LEU	5.8
1	F	91	ASN	5.8
1	H	266	PHE	5.8
1	I	335	VAL	5.8
1	G	184	ILE	5.8
1	B	103	SER	5.8
1	C	234	ILE	5.8
1	A	79	ASN	5.8
1	H	270	THR	5.8
1	E	377	PRO	5.8
1	I	406	ASP	5.8
1	J	22	THR	5.8
1	J	46	ASN	5.8
1	D	191	PRO	5.8
1	J	87	LEU	5.8
1	B	111	SER	5.8
1	B	312	ILE	5.8
1	C	92	LEU	5.8
1	M	133	LEU	5.8
1	B	191	PRO	5.8
1	F	331	GLY	5.8
1	K	345	ALA	5.8
1	K	392	PRO	5.8

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Mol	Chain	Res	Type	RSRZ
1	L	306	THR	5.8
1	G	409	GLY	5.8
1	A	330	ARG	5.8
1	D	66	SER	5.8
1	G	169	LEU	5.8
1	B	284	THR	5.8
1	G	20	MET	5.8
1	A	363	VAL	5.8
1	C	259	VAL	5.8
1	E	194	VAL	5.8
1	G	76	GLY	5.8
1	G	131	GLY	5.8
1	D	259	VAL	5.8
1	L	349	VAL	5.8
1	M	259	VAL	5.8
1	A	148	THR	5.8
1	F	133	LEU	5.8
1	B	285	GLY	5.8
1	J	423	ARG	5.8
1	F	49	VAL	5.8
1	E	37	THR	5.8
1	E	120	LEU	5.8
1	G	279	ASN	5.8
1	I	287	ASP	5.8
1	L	86	LEU	5.8
1	G	46	ASN	5.7
1	G	109	ARG	5.7
1	A	409	GLY	5.7
1	L	78	GLY	5.7
1	H	354	TYR	5.7
1	C	152	ASN	5.7
1	F	69	GLY	5.7
1	K	93	PRO	5.7
1	F	427	MET	5.7
1	G	95	SER	5.7
1	L	340	GLY	5.7
1	B	310	LEU	5.7
1	I	379	LEU	5.7
1	H	62	GLY	5.7
1	M	157	ASN	5.7
1	B	144	LEU	5.7
1	D	355	GLU	5.7

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Mol	Chain	Res	Type	RSRZ
1	E	38	LEU	5.7
1	K	378	GLU	5.7
1	E	95	SER	5.7
1	H	63	PHE	5.7
1	C	107	THR	5.7
1	J	70	ALA	5.7
1	L	169	LEU	5.7
1	M	321	ALA	5.7
1	J	170	PRO	5.7
1	M	304	PRO	5.7
1	M	144	LEU	5.7
1	I	422	PHE	5.7
1	D	13	PRO	5.7
1	G	410	ILE	5.7
1	J	233	ASN	5.7
1	F	283	THR	5.7
1	I	65	GLY	5.7
1	G	101	LEU	5.7
1	J	168	SER	5.7
1	D	71	HIS	5.7
1	E	70	ALA	5.7
1	F	360	GLY	5.7
1	K	128	THR	5.7
1	C	33	LEU	5.7
1	D	169	LEU	5.7
1	G	373	LEU	5.7
1	I	105	SER	5.7
1	A	60	PHE	5.7
1	C	249	ARG	5.7
1	E	157	ASN	5.7
1	H	155	ILE	5.7
1	I	186	ALA	5.7
1	K	30	ASP	5.7
1	E	196	THR	5.7
1	B	243	GLY	5.7
1	B	254	GLY	5.7
1	F	107	THR	5.7
1	J	429	VAL	5.7
1	L	392	PRO	5.7
1	M	424	GLU	5.7
1	C	179	ARG	5.7
1	E	327	TRP	5.7

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Mol	Chain	Res	Type	RSRZ
1	D	110	SER	5.7
1	K	86	LEU	5.7
1	C	54	SER	5.7
1	A	26	ALA	5.7
1	G	256	VAL	5.7
1	I	193	MET	5.7
1	I	256	VAL	5.7
1	K	161	GLY	5.7
1	E	34	GLU	5.7
1	B	240	LEU	5.7
1	E	441	ALA	5.7
1	H	224	GLY	5.7
1	L	334	ALA	5.7
1	H	19	LEU	5.7
1	D	102	VAL	5.7
1	K	411	LYS	5.7
1	L	212	ASP	5.6
1	D	210	ALA	5.6
1	G	62	GLY	5.6
1	A	313	VAL	5.6
1	B	203	PRO	5.6
1	M	21	PRO	5.6
1	C	364	THR	5.6
1	D	52	THR	5.6
1	F	74	LEU	5.6
1	E	416	THR	5.6
1	K	238	THR	5.6
1	A	21	PRO	5.6
1	C	245	GLU	5.6
1	H	139	VAL	5.6
1	C	254	GLY	5.6
1	C	29	PRO	5.6
1	G	357	VAL	5.6
1	C	393	GLY	5.6
1	L	163	GLY	5.6
1	M	419	TYR	5.6
1	J	278	ALA	5.6
1	L	331	GLY	5.6
1	B	384	VAL	5.6
1	D	263	LEU	5.6
1	A	428	GLU	5.6
1	E	40	SER	5.6

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Mol	Chain	Res	Type	RSRZ
1	H	301	ILE	5.6
1	E	189	LEU	5.6
1	E	233	ASN	5.6
1	K	289	LEU	5.6
1	J	386	GLU	5.6
1	M	242	VAL	5.6
1	I	203	PRO	5.6
1	B	179	ARG	5.6
1	G	254	GLY	5.6
1	E	186	ALA	5.6
1	G	54	SER	5.6
1	H	89	ALA	5.6
1	E	96	TYR	5.6
1	F	330	ARG	5.6
1	H	41	GLU	5.6
1	K	363	VAL	5.6
1	K	406	ASP	5.6
1	B	227	ILE	5.6
1	C	312	ILE	5.6
1	F	67	ILE	5.6
1	F	334	ALA	5.6
1	F	404	GLU	5.6
1	I	244	GLY	5.6
1	F	216	PHE	5.6
1	L	64	PRO	5.6
1	M	356	ARG	5.6
1	H	172	SER	5.6
1	K	265	GLY	5.6
1	C	315	SER	5.6
1	K	105	SER	5.6
1	D	108	VAL	5.6
1	G	372	GLU	5.6
1	G	430	ALA	5.6
1	G	414	TRP	5.6
1	I	59	PHE	5.6
1	H	330	ARG	5.6
1	H	59	PHE	5.6
1	C	406	ASP	5.6
1	D	95	SER	5.6
1	K	301	ILE	5.6
1	F	423	ARG	5.6
1	B	266	PHE	5.6

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Mol	Chain	Res	Type	RSRZ
1	B	427	MET	5.6
1	K	284	THR	5.6
1	E	341	ASN	5.6
1	E	392	PRO	5.6
1	I	138	ASP	5.6
1	L	160	VAL	5.6
1	B	388	GLY	5.6
1	F	359	THR	5.6
1	G	356	ARG	5.6
1	H	202	ARG	5.6
1	M	28	ILE	5.5
1	C	121	ASN	5.5
1	D	46	ASN	5.5
1	J	342	TYR	5.5
1	L	68	VAL	5.5
1	D	156	GLY	5.5
1	K	281	GLY	5.5
1	D	225	VAL	5.5
1	J	387	TYR	5.5
1	E	287	ASP	5.5
1	G	319	GLY	5.5
1	A	18	LEU	5.5
1	J	414	TRP	5.5
1	B	316	LYS	5.5
1	A	248	PHE	5.5
1	M	338	HIS	5.5
1	D	434	SER	5.5
1	H	204	ARG	5.5
1	L	277	ALA	5.5
1	M	323	ASP	5.5
1	H	242	VAL	5.5
1	B	106	LEU	5.5
1	F	322	GLY	5.5
1	G	396	ASN	5.5
1	I	322	GLY	5.5
1	J	360	GLY	5.5
1	M	402	LEU	5.5
1	E	198	ASP	5.5
1	G	94	ALA	5.5
1	H	262	TYR	5.5
1	F	38	LEU	5.5
1	B	349	VAL	5.5

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Mol	Chain	Res	Type	RSRZ
1	M	407	ARG	5.5
1	A	123	THR	5.5
1	C	371	PHE	5.5
1	E	151	ILE	5.5
1	E	254	GLY	5.5
1	L	324	GLN	5.5
1	F	129	PHE	5.5
1	H	406	ASP	5.5
1	L	397	TYR	5.5
1	A	385	THR	5.5
1	G	413	VAL	5.5
1	L	94	ALA	5.5
1	D	120	LEU	5.5
1	B	344	GLY	5.5
1	D	311	GLU	5.5
1	F	88	THR	5.5
1	F	401	ILE	5.5
1	J	321	ALA	5.5
1	D	121	ASN	5.5
1	I	123	THR	5.5
1	K	377	PRO	5.5
1	C	365	VAL	5.5
1	D	65	GLY	5.5
1	D	242	VAL	5.5
1	G	156	GLY	5.5
1	K	90	GLN	5.5
1	K	292	PHE	5.5
1	F	99	CYS	5.5
1	D	25	PRO	5.5
1	G	41	GLU	5.5
1	L	367	GLY	5.5
1	B	394	ALA	5.5
1	C	143	GLY	5.5
1	L	348	PRO	5.5
1	C	438	ILE	5.5
1	E	36	HIS	5.5
1	B	180	LEU	5.5
1	E	160	VAL	5.5
1	G	108	VAL	5.5
1	H	377	PRO	5.5
1	L	216	PHE	5.5
1	F	434	SER	5.5

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Mol	Chain	Res	Type	RSRZ
1	G	241	SER	5.5
1	M	326	SER	5.5
1	C	205	VAL	5.5
1	E	367	GLY	5.5
1	H	111	SER	5.5
1	H	279	ASN	5.5
1	H	87	LEU	5.5
1	B	69	GLY	5.5
1	F	426	PHE	5.5
1	H	257	LEU	5.5
1	H	259	VAL	5.5
1	H	422	PHE	5.5
1	K	168	SER	5.5
1	A	25	PRO	5.5
1	D	304	PRO	5.5
1	B	311	GLU	5.5
1	J	211	ALA	5.5
1	D	79	ASN	5.5
1	C	69	GLY	5.4
1	C	224	GLY	5.4
1	A	292	PHE	5.4
1	A	419	TYR	5.4
1	G	299	ASN	5.4
1	H	405	ARG	5.4
1	A	332	SER	5.4
1	E	434	SER	5.4
1	J	296	ILE	5.4
1	I	118	TYR	5.4
1	I	194	VAL	5.4
1	B	234	ILE	5.4
1	E	288	ASN	5.4
1	H	157	ASN	5.4
1	L	407	ARG	5.4
1	B	395	MET	5.4
1	G	29	PRO	5.4
1	C	357	VAL	5.4
1	C	347	ARG	5.4
1	E	328	SER	5.4
1	G	289	LEU	5.4
1	I	21	PRO	5.4
1	A	201	ASP	5.4
1	E	300	GLU	5.4

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Mol	Chain	Res	Type	RSRZ
1	A	223	GLY	5.4
1	B	370	ASN	5.4
1	D	318	GLY	5.4
1	G	397	TYR	5.4
1	D	36	HIS	5.4
1	C	284	THR	5.4
1	D	170	PRO	5.4
1	D	368	VAL	5.4
1	G	395	MET	5.4
1	A	267	ASP	5.4
1	E	212	ASP	5.4
1	B	309	LYS	5.4
1	C	148	THR	5.4
1	A	334	ALA	5.4
1	E	402	LEU	5.4
1	L	416	THR	5.4
1	F	184	ILE	5.4
1	F	348	PRO	5.4
1	G	290	MET	5.4
1	G	14	PHE	5.4
1	K	62	GLY	5.4
1	K	367	GLY	5.4
1	C	37	THR	5.4
1	M	123	THR	5.4
1	G	18	LEU	5.4
1	J	118	TYR	5.4
1	L	118	TYR	5.4
1	A	397	TYR	5.4
1	D	163	GLY	5.4
1	J	264	ILE	5.4
1	F	370	ASN	5.4
1	A	323	ASP	5.4
1	A	73	THR	5.4
1	F	256	VAL	5.4
1	J	252	VAL	5.4
1	C	127	VAL	5.4
1	C	302	THR	5.4
1	C	308	ILE	5.4
1	L	67	ILE	5.4
1	B	380	ALA	5.4
1	E	429	VAL	5.4
1	D	287	ASP	5.4

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Mol	Chain	Res	Type	RSRZ
1	J	198	ASP	5.4
1	K	254	GLY	5.4
1	I	34	GLU	5.4
1	A	203	PRO	5.4
1	F	363	VAL	5.3
1	E	259	VAL	5.3
1	L	112	THR	5.3
1	F	414	TRP	5.3
1	J	121	ASN	5.3
1	L	264	ILE	5.3
1	E	354	TYR	5.3
1	K	192	LYS	5.3
1	F	157	ASN	5.3
1	C	133	LEU	5.3
1	F	14	PHE	5.3
1	F	242	VAL	5.3
1	L	120	LEU	5.3
1	I	243	GLY	5.3
1	I	254	GLY	5.3
1	D	320	GLN	5.3
1	A	153	ASP	5.3
1	F	263	LEU	5.3
1	D	127	VAL	5.3
1	G	431	ASP	5.3
1	M	168	SER	5.3
1	C	424	GLU	5.3
1	K	47	LEU	5.3
1	C	87	LEU	5.3
1	G	229	LEU	5.3
1	B	77	ASN	5.3
1	J	216	PHE	5.3
1	L	204	ARG	5.3
1	G	200	SER	5.3
1	A	178	VAL	5.3
1	B	252	VAL	5.3
1	H	230	PHE	5.3
1	J	416	THR	5.3
1	C	116	GLY	5.3
1	G	402	LEU	5.3
1	J	263	LEU	5.3
1	B	356	ARG	5.3
1	I	399	LYS	5.3

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Mol	Chain	Res	Type	RSRZ
1	L	178	VAL	5.3
1	K	162	GLU	5.3
1	D	377	PRO	5.3
1	J	247	VAL	5.3
1	B	292	PHE	5.3
1	K	276	VAL	5.3
1	L	30	ASP	5.3
1	C	57	ILE	5.3
1	M	33	LEU	5.3
1	C	361	SER	5.3
1	L	91	ASN	5.3
1	A	272	ILE	5.3
1	D	291	PRO	5.3
1	L	102	VAL	5.3
1	M	397	TYR	5.3
1	K	379	LEU	5.3
1	E	219	GLN	5.3
1	M	219	GLN	5.3
1	F	11	ILE	5.3
1	C	153	ASP	5.3
1	G	89	ALA	5.3
1	B	268	GLY	5.3
1	H	53	GLY	5.3
1	L	433	ASN	5.3
1	B	153	ASP	5.3
1	C	426	PHE	5.3
1	D	417	ARG	5.3
1	G	348	PRO	5.3
1	G	359	THR	5.3
1	K	314	THR	5.3
1	C	300	GLU	5.2
1	H	281	GLY	5.2
1	B	300	GLU	5.2
1	B	32	THR	5.2
1	A	353	ALA	5.2
1	A	169	LEU	5.2
1	B	50	GLY	5.2
1	F	264	ILE	5.2
1	K	359	THR	5.2
1	J	371	PHE	5.2
1	L	428	GLU	5.2
1	E	68	VAL	5.2

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Mol	Chain	Res	Type	RSRZ
1	F	204	ARG	5.2
1	F	268	GLY	5.2
1	H	246	LEU	5.2
1	M	167	LEU	5.2
1	G	84	GLN	5.2
1	M	425	TYR	5.2
1	H	123	THR	5.2
1	L	117	VAL	5.2
1	L	270	THR	5.2
1	L	313	VAL	5.2
1	K	397	TYR	5.2
1	C	280	ASN	5.2
1	A	417	ARG	5.2
1	E	137	THR	5.2
1	L	73	THR	5.2
1	A	246	LEU	5.2
1	C	192	LYS	5.2
1	A	180	LEU	5.2
1	M	81	LYS	5.2
1	L	279	ASN	5.2
1	B	270	THR	5.2
1	G	45	TYR	5.2
1	C	158	VAL	5.2
1	C	283	THR	5.2
1	F	251	SER	5.2
1	K	79	ASN	5.2
1	K	268	GLY	5.2
1	J	399	LYS	5.2
1	M	96	TYR	5.2
1	B	155	ILE	5.2
1	E	237	ILE	5.2
1	F	305	ILE	5.2
1	E	379	LEU	5.2
1	F	140	SER	5.2
1	J	312	ILE	5.2
1	B	87	LEU	5.2
1	E	221	GLN	5.2
1	G	367	GLY	5.2
1	G	419	TYR	5.2
1	H	325	MET	5.2
1	E	107	THR	5.2
1	B	186	ALA	5.2

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Mol	Chain	Res	Type	RSRZ
1	E	18	LEU	5.2
1	E	170	PRO	5.2
1	D	75	GLN	5.2
1	J	157	ASN	5.2
1	F	36	HIS	5.2
1	I	400	LEU	5.2
1	M	211	ALA	5.2
1	D	113	LEU	5.2
1	E	250	THR	5.2
1	C	204	ARG	5.2
1	E	26	ALA	5.2
1	C	222	PRO	5.2
1	G	111	SER	5.1
1	G	346	LEU	5.2
1	M	265	GLY	5.1
1	M	105	SER	5.1
1	F	55	GLY	5.1
1	F	289	LEU	5.1
1	M	339	GLY	5.1
1	C	139	VAL	5.1
1	D	404	GLU	5.1
1	E	226	THR	5.1
1	B	237	ILE	5.1
1	D	351	LEU	5.1
1	G	15	ILE	5.1
1	C	420	THR	5.1
1	K	81	LYS	5.1
1	G	33	LEU	5.1
1	I	101	LEU	5.1
1	M	190	ASP	5.1
1	G	363	VAL	5.1
1	J	28	ILE	5.1
1	J	289	LEU	5.1
1	I	45	TYR	5.1
1	J	396	ASN	5.1
1	L	162	GLU	5.1
1	M	368	VAL	5.1
1	F	182	ASP	5.1
1	J	48	THR	5.1
1	M	120	LEU	5.1
1	C	419	TYR	5.1
1	E	243	GLY	5.1

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Mol	Chain	Res	Type	RSRZ
1	L	406	ASP	5.1
1	G	424	GLU	5.1
1	M	262	TYR	5.1
1	B	15	ILE	5.1
1	I	16	ARG	5.1
1	M	234	ILE	5.1
1	A	184	ILE	5.1
1	H	272	ILE	5.1
1	H	401	ILE	5.1
1	E	179	ARG	5.1
1	E	180	LEU	5.1
1	E	97	ASN	5.1
1	M	172	SER	5.1
1	C	144	LEU	5.1
1	F	188	GLY	5.1
1	L	301	ILE	5.1
1	A	264	ILE	5.1
1	G	403	SER	5.1
1	H	104	ARG	5.1
1	H	251	SER	5.1
1	G	425	TYR	5.1
1	E	435	PRO	5.1
1	M	131	GLY	5.1
1	I	411	LYS	5.1
1	I	149	ALA	5.1
1	I	370	ASN	5.1
1	M	243	GLY	5.1
1	M	316	LYS	5.1
1	D	200	SER	5.0
1	F	286	THR	5.0
1	K	89	ALA	5.0
1	E	182	ASP	5.0
1	H	98	TYR	5.0
1	J	80	TYR	5.0
1	M	399	LYS	5.0
1	G	360	GLY	5.0
1	H	161	GLY	5.0
1	F	319	GLY	5.0
1	I	71	HIS	5.0
1	F	343	PRO	5.0
1	A	173	TYR	5.0
1	E	389	ARG	5.0

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Mol	Chain	Res	Type	RSRZ
1	E	425	TYR	5.0
1	K	410	ILE	5.0
1	J	428	GLU	5.0
1	F	171	THR	5.0
1	M	171	THR	5.0
1	D	215	GLN	5.0
1	E	187	ILE	5.0
1	F	430	ALA	5.0
1	L	79	ASN	5.0
1	C	177	TYR	5.0
1	E	89	ALA	5.0
1	G	177	TYR	5.0
1	K	342	TYR	5.0
1	K	383	LEU	5.0
1	L	33	LEU	5.0
1	M	256	VAL	5.0
1	A	114	PRO	5.0
1	G	36	HIS	5.0
1	G	50	GLY	5.0
1	A	423	ARG	5.0
1	C	304	PRO	5.0
1	G	159	LEU	5.0
1	E	409	GLY	5.0
1	J	180	LEU	5.0
1	F	169	LEU	5.0
1	K	285	GLY	5.0
1	L	69	GLY	5.0
1	L	143	GLY	5.0
1	G	22	THR	5.0
1	I	412	THR	5.0
1	L	284	THR	5.0
1	D	109	ARG	5.0
1	B	127	VAL	5.0
1	I	139	VAL	5.0
1	C	398	THR	5.0
1	E	394	ALA	5.0
1	K	215	GLN	5.0
1	L	52	THR	5.0
1	M	387	TYR	5.0
1	C	289	LEU	5.0
1	I	33	LEU	5.0
1	I	263	LEU	5.0

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Mol	Chain	Res	Type	RSRZ
1	I	301	ILE	5.0
1	D	412	THR	5.0
1	H	185	PRO	5.0
1	C	47	LEU	5.0
1	C	282	LEU	5.0
1	B	231	SER	5.0
1	L	65	GLY	5.0
1	H	404	GLU	5.0
1	K	216	PHE	5.0
1	A	375	PRO	5.0
1	G	412	THR	5.0
1	C	34	GLU	5.0
1	H	426	PHE	5.0
1	J	351	LEU	5.0
1	L	422	PHE	5.0
1	M	255	LEU	5.0
1	G	404	GLU	5.0
1	J	346	LEU	5.0
1	J	348	PRO	5.0
1	D	398	THR	4.9
1	E	128	THR	4.9
1	D	224	GLY	4.9
1	M	98	TYR	4.9
1	K	235	ASP	4.9
1	J	92	LEU	4.9
1	L	74	LEU	4.9
1	M	41	GLU	4.9
1	M	272	ILE	4.9
1	B	13	PRO	4.9
1	J	230	PHE	4.9
1	J	324	GLN	4.9
1	L	427	MET	4.9
1	H	307	SER	4.9
1	K	239	SER	4.9
1	K	275	ALA	4.9
1	M	381	LYS	4.9
1	I	115	GLY	4.9
1	A	430	ALA	4.9
1	H	366	ALA	4.9
1	E	421	ASP	4.9
1	K	120	LEU	4.9
1	M	257	LEU	4.9

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Mol	Chain	Res	Type	RSRZ
1	F	155	ILE	4.9
1	L	205	VAL	4.9
1	A	357	VAL	4.9
1	M	388	GLY	4.9
1	L	403	SER	4.9
1	C	401	ILE	4.9
1	D	188	GLY	4.9
1	M	53	GLY	4.9
1	A	168	SER	4.9
1	C	28	ILE	4.9
1	G	342	TYR	4.9
1	A	154	LYS	4.9
1	J	432	LEU	4.9
1	I	241	SER	4.9
1	L	425	TYR	4.9
1	M	244	GLY	4.9
1	E	98	TYR	4.9
1	J	158	VAL	4.9
1	H	145	MET	4.9
1	M	119	ALA	4.9
1	M	113	LEU	4.9
1	C	314	THR	4.9
1	K	170	PRO	4.9
1	M	232	ALA	4.9
1	K	223	GLY	4.9
1	E	355	GLU	4.9
1	B	58	VAL	4.9
1	E	342	TYR	4.9
1	D	288	ASN	4.9
1	F	189	LEU	4.9
1	H	248	PHE	4.9
1	A	102	VAL	4.9
1	F	378	GLU	4.9
1	J	421	ASP	4.9
1	I	332	SER	4.9
1	M	330	ARG	4.9
1	D	300	GLU	4.9
1	B	248	PHE	4.9
1	F	153	ASP	4.9
1	A	97	ASN	4.9
1	C	383	LEU	4.9
1	E	439	ALA	4.9

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Mol	Chain	Res	Type	RSRZ
1	A	88	THR	4.9
1	C	266	PHE	4.9
1	D	336	THR	4.9
1	G	344	GLY	4.9
1	J	267	ASP	4.9
1	L	337	ILE	4.9
1	E	86	LEU	4.9
1	K	129	PHE	4.9
1	A	410	ILE	4.9
1	I	249	ARG	4.9
1	H	198	ASP	4.9
1	L	20	MET	4.9
1	M	68	VAL	4.9
1	M	333	LEU	4.9
1	D	352	VAL	4.8
1	F	168	SER	4.8
1	A	74	LEU	4.8
1	E	257	LEU	4.8
1	K	67	ILE	4.8
1	D	369	SER	4.8
1	M	291	PRO	4.8
1	C	288	ASN	4.8
1	I	120	LEU	4.8
1	D	270	THR	4.8
1	F	365	VAL	4.8
1	H	403	SER	4.8
1	J	196	THR	4.8
1	G	401	ILE	4.8
1	I	35	LYS	4.8
1	B	88	THR	4.8
1	H	210	ALA	4.8
1	M	84	GLN	4.8
1	K	241	SER	4.8
1	A	198	ASP	4.8
1	G	127	VAL	4.8
1	F	160	VAL	4.8
1	J	273	THR	4.8
1	L	230	PHE	4.8
1	K	256	VAL	4.8
1	C	356	ARG	4.8
1	L	254	GLY	4.8
1	D	56	LEU	4.8

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Mol	Chain	Res	Type	RSRZ
1	F	187	ILE	4.8
1	A	84	GLN	4.8
1	F	8	THR	4.8
1	G	366	ALA	4.8
1	G	157	ASN	4.8
1	L	386	GLU	4.8
1	B	169	LEU	4.8
1	C	168	SER	4.8
1	L	267	ASP	4.8
1	I	385	THR	4.8
1	K	226	THR	4.8
1	I	20	MET	4.8
1	K	290	MET	4.8
1	K	382	ASN	4.8
1	L	309	LYS	4.8
1	L	379	LEU	4.8
1	D	93	PRO	4.8
1	G	285	GLY	4.8
1	I	53	GLY	4.8
1	J	138	ASP	4.8
1	E	253	HIS	4.8
1	L	383	LEU	4.8
1	M	362	VAL	4.8
1	M	170	PRO	4.8
1	A	56	LEU	4.8
1	D	87	LEU	4.8
1	D	277	ALA	4.8
1	G	185	PRO	4.8
1	I	69	GLY	4.8
1	I	215	GLN	4.8
1	G	301	ILE	4.8
1	E	267	ASP	4.8
1	M	369	SER	4.8
1	B	124	ILE	4.8
1	D	63	PHE	4.7
1	L	60	PHE	4.7
1	D	220	TYR	4.7
1	E	222	PRO	4.7
1	F	225	VAL	4.7
1	H	166	VAL	4.7
1	A	411	LYS	4.7
1	C	36	HIS	4.7

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Mol	Chain	Res	Type	RSRZ
1	D	40	SER	4.7
1	I	251	SER	4.7
1	H	234	ILE	4.7
1	F	347	ARG	4.7
1	M	423	ARG	4.7
1	I	314	THR	4.7
1	D	319	GLY	4.7
1	H	121	ASN	4.7
1	E	201	ASP	4.7
1	B	72	TYR	4.7
1	K	50	GLY	4.7
1	E	370	ASN	4.7
1	G	394	ALA	4.7
1	I	255	LEU	4.7
1	E	21	PRO	4.7
1	L	250	THR	4.7
1	M	325	MET	4.7
1	L	437	LYS	4.7
1	C	413	VAL	4.7
1	F	339	GLY	4.7
1	B	204	ARG	4.7
1	D	154	LYS	4.7
1	I	169	LEU	4.7
1	L	263	LEU	4.7
1	D	365	VAL	4.7
1	I	197	CYS	4.7
1	D	292	PHE	4.7
1	J	364	THR	4.7
1	B	46	ASN	4.7
1	G	433	ASN	4.7
1	B	165	THR	4.7
1	D	310	LEU	4.7
1	F	367	GLY	4.7
1	F	377	PRO	4.7
1	M	18	LEU	4.7
1	E	94	ALA	4.7
1	H	197	CYS	4.7
1	A	175	LEU	4.7
1	B	47	LEU	4.7
1	D	35	LYS	4.7
1	E	39	ARG	4.7
1	L	81	LYS	4.7

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Mol	Chain	Res	Type	RSRZ
1	J	328	SER	4.7
1	F	141	TYR	4.7
1	M	310	LEU	4.7
1	B	201	ASP	4.7
1	K	206	TYR	4.7
1	A	179	ARG	4.7
1	H	164	VAL	4.7
1	I	325	MET	4.7
1	M	406	ASP	4.7
1	B	173	TYR	4.7
1	B	21	PRO	4.7
1	H	76	GLY	4.7
1	D	204	ARG	4.7
1	H	244	GLY	4.7
1	H	80	TYR	4.7
1	A	199	SER	4.7
1	B	342	TYR	4.7
1	E	393	GLY	4.7
1	H	413	VAL	4.7
1	E	195	ALA	4.7
1	H	97	ASN	4.7
1	M	385	THR	4.7
1	A	50	GLY	4.7
1	M	331	GLY	4.7
1	E	149	ALA	4.7
1	G	66	SER	4.7
1	J	310	LEU	4.7
1	H	220	TYR	4.7
1	B	348	PRO	4.6
1	J	69	GLY	4.7
1	E	118	TYR	4.6
1	E	214	TYR	4.6
1	E	311	GLU	4.6
1	A	364	THR	4.6
1	H	383	LEU	4.6
1	K	46	ASN	4.6
1	M	264	ILE	4.6
1	J	425	TYR	4.6
1	E	99	CYS	4.6
1	M	159	LEU	4.6
1	M	386	GLU	4.6
1	I	148	THR	4.6

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Mol	Chain	Res	Type	RSRZ
1	J	154	LYS	4.6
1	B	92	LEU	4.6
1	C	182	ASP	4.6
1	M	104	ARG	4.6
1	B	358	ALA	4.6
1	C	439	ALA	4.6
1	I	413	VAL	4.6
1	B	112	THR	4.6
1	G	107	THR	4.6
1	M	73	THR	4.6
1	L	173	TYR	4.6
1	L	180	LEU	4.6
1	D	53	GLY	4.6
1	E	85	MET	4.6
1	L	405	ARG	4.6
1	J	372	GLU	4.6
1	L	278	ALA	4.6
1	D	103	SER	4.6
1	F	175	LEU	4.6
1	H	250	THR	4.6
1	L	189	LEU	4.6
1	K	100	ARG	4.6
1	G	343	PRO	4.6
1	H	106	LEU	4.6
1	M	37	THR	4.6
1	E	340	GLY	4.6
1	G	437	LYS	4.6
1	M	372	GLU	4.6
1	L	206	TYR	4.6
1	H	162	GLU	4.6
1	A	158	VAL	4.6
1	A	202	ARG	4.6
1	D	107	THR	4.6
1	G	137	THR	4.6
1	J	363	VAL	4.6
1	L	75	GLN	4.6
1	F	114	PRO	4.6
1	K	56	LEU	4.6
1	K	273	THR	4.6
1	C	307	SER	4.6
1	F	282	LEU	4.6
1	F	405	ARG	4.6

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Mol	Chain	Res	Type	RSRZ
1	G	199	SER	4.6
1	I	28	ILE	4.6
1	I	355	GLU	4.6
1	J	164	VAL	4.6
1	A	433	ASN	4.6
1	B	434	SER	4.6
1	E	332	SER	4.6
1	E	80	TYR	4.6
1	G	426	PHE	4.6
1	D	186	ALA	4.6
1	F	34	GLU	4.6
1	E	304	PRO	4.6
1	M	97	ASN	4.6
1	C	56	LEU	4.6
1	E	161	GLY	4.6
1	H	423	ARG	4.6
1	J	345	ALA	4.6
1	L	116	GLY	4.6
1	M	40	SER	4.6
1	A	429	VAL	4.5
1	I	39	ARG	4.6
1	I	330	ARG	4.6
1	A	266	PHE	4.5
1	A	222	PRO	4.5
1	M	314	THR	4.5
1	C	429	VAL	4.5
1	G	139	VAL	4.5
1	G	347	ARG	4.5
1	K	234	ILE	4.5
1	B	343	PRO	4.5
1	I	416	THR	4.5
1	C	346	LEU	4.5
1	B	264	ILE	4.5
1	J	39	ARG	4.5
1	J	424	GLU	4.5
1	I	331	GLY	4.5
1	F	121	ASN	4.5
1	K	101	LEU	4.5
1	B	230	PHE	4.5
1	D	48	THR	4.5
1	J	57	ILE	4.5
1	C	98	TYR	4.5

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Mol	Chain	Res	Type	RSRZ
1	L	210	ALA	4.5
1	K	57	ILE	4.5
1	B	113	LEU	4.5
1	F	262	TYR	4.5
1	C	164	VAL	4.5
1	H	120	LEU	4.5
1	C	114	PRO	4.5
1	K	274	ARG	4.5
1	H	169	LEU	4.5
1	K	224	GLY	4.5
1	C	227	ILE	4.5
1	A	81	LYS	4.5
1	H	170	PRO	4.5
1	A	263	LEU	4.5
1	A	212	ASP	4.5
1	B	363	VAL	4.5
1	B	189	LEU	4.5
1	D	278	ALA	4.5
1	F	4	LEU	4.5
1	G	121	ASN	4.5
1	J	410	ILE	4.5
1	K	313	VAL	4.5
1	J	105	SER	4.5
1	B	34	GLU	4.5
1	I	38	LEU	4.5
1	C	382	ASN	4.5
1	C	66	SER	4.5
1	D	436	LEU	4.5
1	M	217	SER	4.5
1	B	355	GLU	4.5
1	C	214	TYR	4.5
1	G	259	VAL	4.5
1	B	324	GLN	4.5
1	J	91	ASN	4.5
1	D	14	PHE	4.5
1	C	334	ALA	4.5
1	F	234	ILE	4.5
1	K	53	GLY	4.5
1	B	441	ALA	4.5
1	M	184	ILE	4.5
1	E	380	ALA	4.5
1	F	78	GLY	4.5

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Mol	Chain	Res	Type	RSRZ
1	H	427	MET	4.5
1	K	214	TYR	4.5
1	E	92	LEU	4.5
1	K	346	LEU	4.5
1	A	96	TYR	4.5
1	I	386	GLU	4.5
1	E	372	GLU	4.5
1	E	387	TYR	4.5
1	I	95	SER	4.5
1	I	96	TYR	4.5
1	C	411	LYS	4.4
1	H	171	THR	4.4
1	A	434	SER	4.4
1	H	402	LEU	4.4
1	A	328	SER	4.4
1	D	43	SER	4.4
1	L	76	GLY	4.4
1	F	346	LEU	4.4
1	G	300	GLU	4.4
1	A	344	GLY	4.4
1	G	92	LEU	4.4
1	H	113	LEU	4.4
1	C	100	ARG	4.4
1	D	362	VAL	4.4
1	B	405	ARG	4.4
1	D	272	ILE	4.4
1	J	59	PHE	4.4
1	A	283	THR	4.4
1	F	33	LEU	4.4
1	H	90	GLN	4.4
1	M	39	ARG	4.4
1	B	185	PRO	4.4
1	L	262	TYR	4.4
1	A	127	VAL	4.4
1	A	362	VAL	4.4
1	C	351	LEU	4.4
1	J	322	GLY	4.4
1	K	386	GLU	4.4
1	E	158	VAL	4.4
1	G	87	LEU	4.4
1	H	331	GLY	4.4
1	J	279	ASN	4.4

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Mol	Chain	Res	Type	RSRZ
1	G	238	THR	4.4
1	C	349	VAL	4.4
1	D	106	LEU	4.4
1	C	42	THR	4.4
1	F	397	TYR	4.4
1	D	90	GLN	4.4
1	J	100	ARG	4.4
1	K	356	ARG	4.4
1	D	98	TYR	4.4
1	M	354	TYR	4.4
1	H	312	ILE	4.4
1	H	347	ARG	4.4
1	I	311	GLU	4.4
1	I	319	GLY	4.4
1	K	263	LEU	4.4
1	L	93	PRO	4.4
1	D	232	ALA	4.4
1	B	410	ILE	4.4
1	H	305	ILE	4.4
1	G	261	ILE	4.3
1	G	411	LYS	4.3
1	B	413	VAL	4.3
1	J	404	GLU	4.3
1	K	49	VAL	4.3
1	K	211	ALA	4.3
1	K	418	GLU	4.3
1	A	373	LEU	4.3
1	K	99	CYS	4.3
1	K	159	LEU	4.3
1	B	26	ALA	4.3
1	E	129	PHE	4.3
1	G	228	THR	4.3
1	I	161	GLY	4.3
1	I	222	PRO	4.3
1	E	162	GLU	4.3
1	F	125	ASN	4.3
1	L	363	VAL	4.3
1	J	33	LEU	4.3
1	H	340	GLY	4.3
1	C	320	GLN	4.3
1	K	160	VAL	4.3
1	C	380	ALA	4.3

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Mol	Chain	Res	Type	RSRZ
1	F	144	LEU	4.3
1	H	211	ALA	4.3
1	H	416	THR	4.3
1	K	169	LEU	4.3
1	L	268	GLY	4.3
1	F	211	ALA	4.3
1	J	255	LEU	4.3
1	L	355	GLU	4.3
1	M	404	GLU	4.3
1	H	167	LEU	4.3
1	L	328	SER	4.3
1	H	125	ASN	4.3
1	H	245	GLU	4.3
1	A	435	PRO	4.3
1	K	332	SER	4.3
1	L	105	SER	4.3
1	C	79	ASN	4.3
1	L	171	THR	4.3
1	J	115	GLY	4.3
1	L	119	ALA	4.3
1	H	355	GLU	4.3
1	F	25	PRO	4.3
1	I	262	TYR	4.3
1	J	427	MET	4.3
1	E	283	THR	4.3
1	E	310	LEU	4.3
1	J	125	ASN	4.3
1	L	360	GLY	4.3
1	B	345	ALA	4.3
1	J	356	ARG	4.3
1	J	417	ARG	4.3
1	B	335	VAL	4.3
1	J	27	SER	4.3
1	J	303	GLN	4.3
1	K	83	ASP	4.3
1	C	129	PHE	4.3
1	B	49	VAL	4.3
1	C	132	SER	4.3
1	C	149	ALA	4.3
1	D	26	ALA	4.3
1	H	289	LEU	4.3
1	I	94	ALA	4.3

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Mol	Chain	Res	Type	RSRZ
1	A	285	GLY	4.3
1	B	131	GLY	4.3
1	D	81	LYS	4.3
1	J	197	CYS	4.3
1	D	406	ASP	4.3
1	G	383	LEU	4.3
1	F	7	GLN	4.3
1	I	88	THR	4.3
1	K	113	LEU	4.3
1	B	256	VAL	4.3
1	F	109	ARG	4.3
1	I	349	VAL	4.3
1	H	189	LEU	4.3
1	I	99	CYS	4.3
1	M	254	GLY	4.3
1	H	414	TRP	4.3
1	C	155	ILE	4.3
1	L	398	THR	4.3
1	D	328	SER	4.3
1	M	100	ARG	4.2
1	A	310	LEU	4.2
1	D	172	SER	4.2
1	D	148	THR	4.2
1	J	165	THR	4.2
1	D	254	GLY	4.2
1	J	259	VAL	4.2
1	E	351	LEU	4.2
1	I	418	GLU	4.2
1	B	235	ASP	4.2
1	D	364	THR	4.2
1	H	137	THR	4.2
1	D	430	ALA	4.2
1	M	345	ALA	4.2
1	C	228	THR	4.2
1	G	408	LEU	4.2
1	B	304	PRO	4.2
1	C	102	VAL	4.2
1	I	423	ARG	4.2
1	D	370	ASN	4.2
1	E	347	ARG	4.2
1	E	123	THR	4.2
1	G	230	PHE	4.2

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Mol	Chain	Res	Type	RSRZ
1	K	34	GLU	4.2
1	L	417	ARG	4.2
1	E	266	PHE	4.2
1	C	67	ILE	4.2
1	H	275	ALA	4.2
1	I	242	VAL	4.2
1	I	106	LEU	4.2
1	J	190	ASP	4.2
1	D	332	SER	4.2
1	C	189	LEU	4.2
1	I	380	ALA	4.2
1	C	279	ASN	4.2
1	B	149	ALA	4.2
1	B	402	LEU	4.2
1	F	292	PHE	4.2
1	F	429	VAL	4.2
1	E	289	LEU	4.2
1	I	289	LEU	4.2
1	D	424	GLU	4.2
1	E	428	GLU	4.2
1	A	394	ALA	4.2
1	E	306	THR	4.2
1	I	245	GLU	4.2
1	B	429	VAL	4.2
1	K	426	PHE	4.2
1	J	430	ALA	4.2
1	C	352	VAL	4.2
1	M	29	PRO	4.2
1	I	221	GLN	4.2
1	A	304	PRO	4.2
1	F	398	THR	4.2
1	K	283	THR	4.2
1	C	41	GLU	4.2
1	G	427	MET	4.2
1	K	127	VAL	4.2
1	F	158	VAL	4.2
1	M	108	VAL	4.2
1	A	309	LYS	4.2
1	B	218	SER	4.2
1	A	171	THR	4.1
1	J	280	ASN	4.1
1	K	193	MET	4.1

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Mol	Chain	Res	Type	RSRZ
1	M	380	ALA	4.1
1	M	394	ALA	4.1
1	B	22	THR	4.1
1	J	260	THR	4.1
1	G	72	TYR	4.1
1	J	74	LEU	4.1
1	B	332	SER	4.1
1	H	109	ARG	4.1
1	A	347	ARG	4.1
1	C	345	ALA	4.1
1	E	417	ARG	4.1
1	H	21	PRO	4.1
1	A	35	LYS	4.1
1	C	188	GLY	4.1
1	E	76	GLY	4.1
1	I	113	LEU	4.1
1	I	124	ILE	4.1
1	J	265	GLY	4.1
1	B	246	LEU	4.1
1	G	220	TYR	4.1
1	A	68	VAL	4.1
1	C	53	GLY	4.1
1	C	244	GLY	4.1
1	C	344	GLY	4.1
1	D	393	GLY	4.1
1	L	243	GLY	4.1
1	I	102	VAL	4.1
1	E	115	GLY	4.1
1	L	332	SER	4.1
1	D	20	MET	4.1
1	A	92	LEU	4.1
1	D	269	THR	4.1
1	H	428	GLU	4.1
1	C	441	ALA	4.1
1	I	371	PHE	4.1
1	K	319	GLY	4.1
1	M	390	PHE	4.1
1	E	106	LEU	4.1
1	H	37	THR	4.1
1	C	436	LEU	4.1
1	G	304	PRO	4.1
1	G	243	GLY	4.1

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Mol	Chain	Res	Type	RSRZ
1	H	268	GLY	4.1
1	H	127	VAL	4.1
1	I	342	TYR	4.1
1	B	288	ASN	4.1
1	J	361	SER	4.1
1	D	34	GLU	4.1
1	I	407	ARG	4.1
1	G	429	VAL	4.1
1	J	98	TYR	4.1
1	K	387	TYR	4.1
1	B	121	ASN	4.1
1	I	246	LEU	4.1
1	A	301	ILE	4.1
1	C	265	GLY	4.1
1	C	309	LYS	4.1
1	G	294	LEU	4.1
1	B	426	PHE	4.1
1	K	124	ILE	4.1
1	B	162	GLU	4.1
1	E	42	THR	4.1
1	G	269	THR	4.1
1	G	298	THR	4.1
1	F	431	ASP	4.1
1	K	40	SER	4.1
1	G	272	ILE	4.1
1	D	399	LYS	4.1
1	H	292	PHE	4.1
1	C	40	SER	4.0
1	I	403	SER	4.0
1	L	259	VAL	4.0
1	E	323	ASP	4.0
1	G	189	LEU	4.0
1	G	273	THR	4.0
1	K	91	ASN	4.0
1	A	380	ALA	4.0
1	C	119	ALA	4.0
1	H	274	ARG	4.0
1	L	80	TYR	4.0
1	D	250	THR	4.0
1	M	398	THR	4.0
1	A	67	ILE	4.0
1	B	172	SER	4.0

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Mol	Chain	Res	Type	RSRZ
1	D	409	GLY	4.0
1	F	224	GLY	4.0
1	K	380	ALA	4.0
1	L	426	PHE	4.0
1	M	261	ILE	4.0
1	M	241	SER	4.0
1	M	317	SER	4.0
1	L	335	VAL	4.0
1	D	238	THR	4.0
1	L	46	ASN	4.0
1	K	78	GLY	4.0
1	G	113	LEU	4.0
1	M	169	LEU	4.0
1	E	313	VAL	4.0
1	L	108	VAL	4.0
1	B	154	LYS	4.0
1	H	180	LEU	4.0
1	K	109	ARG	4.0
1	C	432	LEU	4.0
1	F	26	ALA	4.0
1	G	415	PRO	4.0
1	A	291	PRO	4.0
1	F	108	VAL	4.0
1	F	237	ILE	4.0
1	I	133	LEU	4.0
1	E	364	THR	4.0
1	G	262	TYR	4.0
1	H	362	VAL	4.0
1	C	170	PRO	4.0
1	H	258	GLY	4.0
1	H	263	LEU	4.0
1	H	328	SER	4.0
1	F	139	VAL	4.0
1	J	271	VAL	4.0
1	M	349	VAL	4.0
1	A	393	GLY	4.0
1	J	358	ALA	4.0
1	C	16	ARG	4.0
1	M	27	SER	4.0
1	M	228	THR	4.0
1	C	18	LEU	4.0
1	C	169	LEU	4.0

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Mol	Chain	Res	Type	RSRZ
1	L	17	SER	4.0
1	A	16	ARG	4.0
1	E	365	VAL	4.0
1	M	352	VAL	3.9
1	F	284	THR	3.9
1	C	258	GLY	3.9
1	D	407	ARG	3.9
1	D	97	ASN	3.9
1	A	356	ARG	3.9
1	K	271	VAL	3.9
1	B	321	ALA	3.9
1	D	145	MET	3.9
1	A	111	SER	3.9
1	A	258	GLY	3.9
1	F	366	ALA	3.9
1	B	308	ILE	3.9
1	C	51	ASP	3.9
1	J	184	ILE	3.9
1	K	207	THR	3.9
1	D	261	ILE	3.9
1	G	28	ILE	3.9
1	B	359	THR	3.9
1	F	5	GLN	3.9
1	F	64	PRO	3.9
1	B	56	LEU	3.9
1	E	127	VAL	3.9
1	G	166	VAL	3.9
1	M	237	ILE	3.9
1	E	88	THR	3.9
1	E	205	VAL	3.9
1	I	79	ASN	3.9
1	I	361	SER	3.9
1	I	401	ILE	3.9
1	J	379	LEU	3.9
1	B	307	SER	3.9
1	B	33	LEU	3.9
1	B	190	ASP	3.9
1	K	258	GLY	3.9
1	C	325	MET	3.9
1	M	260	THR	3.9
1	B	229	LEU	3.9
1	K	17	SER	3.9

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Mol	Chain	Res	Type	RSRZ
1	J	405	ARG	3.9
1	A	37	THR	3.9
1	B	290	MET	3.9
1	F	420	THR	3.9
1	G	382	ASN	3.9
1	M	348	PRO	3.9
1	F	68	VAL	3.9
1	M	405	ARG	3.9
1	J	284	THR	3.9
1	K	260	THR	3.9
1	E	401	ILE	3.9
1	I	180	LEU	3.9
1	I	80	TYR	3.9
1	L	115	GLY	3.9
1	E	399	LYS	3.9
1	H	249	ARG	3.9
1	I	171	THR	3.9
1	B	25	PRO	3.9
1	D	401	ILE	3.9
1	F	230	PHE	3.9
1	B	228	THR	3.8
1	E	430	ALA	3.8
1	H	283	THR	3.8
1	A	53	GLY	3.8
1	A	286	THR	3.8
1	I	82	PHE	3.8
1	C	200	SER	3.8
1	C	271	VAL	3.8
1	F	215	GLN	3.8
1	I	363	VAL	3.8
1	K	172	SER	3.8
1	K	389	ARG	3.8
1	L	39	ARG	3.8
1	M	92	LEU	3.8
1	K	88	THR	3.8
1	I	92	LEU	3.8
1	F	92	LEU	3.8
1	K	402	LEU	3.8
1	E	93	PRO	3.8
1	G	264	ILE	3.8
1	J	15	ILE	3.8
1	A	36	HIS	3.8

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Mol	Chain	Res	Type	RSRZ
1	D	335	VAL	3.8
1	E	339	GLY	3.8
1	J	403	SER	3.8
1	I	318	GLY	3.8
1	F	247	VAL	3.8
1	H	168	SER	3.8
1	L	54	SER	3.8
1	L	145	MET	3.8
1	B	438	ILE	3.8
1	F	220	TYR	3.8
1	J	311	GLU	3.8
1	K	247	VAL	3.8
1	F	17	SER	3.8
1	L	336	THR	3.8
1	B	57	ILE	3.8
1	H	154	LYS	3.8
1	C	17	SER	3.8
1	A	308	ILE	3.8
1	J	102	VAL	3.8
1	F	309	LYS	3.8
1	M	389	ARG	3.8
1	A	106	LEU	3.8
1	H	322	GLY	3.8
1	C	264	ILE	3.8
1	B	143	GLY	3.8
1	A	190	ASP	3.8
1	B	381	LYS	3.8
1	B	421	ASP	3.8
1	K	92	LEU	3.8
1	M	365	VAL	3.8
1	M	426	PHE	3.8
1	H	254	GLY	3.8
1	K	158	VAL	3.8
1	H	165	THR	3.8
1	I	117	VAL	3.7
1	D	230	PHE	3.7
1	F	209	THR	3.7
1	M	395	MET	3.7
1	M	408	LEU	3.7
1	B	398	THR	3.7
1	F	273	THR	3.7
1	K	404	GLU	3.7

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Mol	Chain	Res	Type	RSRZ
1	B	71	HIS	3.7
1	A	306	THR	3.7
1	D	203	PRO	3.7
1	I	365	VAL	3.7
1	B	63	PHE	3.7
1	J	169	LEU	3.7
1	D	307	SER	3.7
1	E	307	SER	3.7
1	H	25	PRO	3.7
1	I	172	SER	3.7
1	A	372	GLU	3.7
1	I	37	THR	3.7
1	D	312	ILE	3.7
1	L	98	TYR	3.7
1	C	339	GLY	3.7
1	A	305	ILE	3.7
1	B	45	TYR	3.7
1	B	86	LEU	3.7
1	C	210	ALA	3.7
1	D	237	ILE	3.7
1	J	305	ILE	3.7
1	B	104	ARG	3.7
1	J	26	ALA	3.7
1	J	113	LEU	3.7
1	K	381	LYS	3.7
1	J	163	GLY	3.7
1	A	343	PRO	3.7
1	B	170	PRO	3.7
1	E	17	SER	3.7
1	B	437	LYS	3.7
1	C	178	VAL	3.7
1	C	428	GLU	3.7
1	M	80	TYR	3.7
1	H	77	ASN	3.7
1	H	229	LEU	3.7
1	K	401	ILE	3.7
1	M	49	VAL	3.7
1	D	433	ASN	3.7
1	H	304	PRO	3.7
1	M	229	LEU	3.7
1	M	379	LEU	3.7
1	A	43	SER	3.7

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Mol	Chain	Res	Type	RSRZ
1	H	173	TYR	3.7
1	L	14	PHE	3.7
1	F	126	ALA	3.7
1	B	297	PRO	3.7
1	H	349	VAL	3.7
1	C	272	ILE	3.7
1	E	101	LEU	3.7
1	E	172	SER	3.7
1	D	185	PRO	3.6
1	G	190	ASP	3.6
1	H	122	GLY	3.6
1	L	168	SER	3.6
1	L	276	VAL	3.6
1	A	336	THR	3.6
1	G	136	LEU	3.6
1	K	423	ARG	3.6
1	G	227	ILE	3.6
1	K	97	ASN	3.6
1	B	197	CYS	3.6
1	H	94	ALA	3.6
1	B	36	HIS	3.6
1	E	330	ARG	3.6
1	F	203	PRO	3.6
1	I	408	LEU	3.6
1	K	417	ARG	3.6
1	F	94	ALA	3.6
1	K	198	ASP	3.6
1	L	382	ASN	3.6
1	C	80	TYR	3.6
1	I	356	ARG	3.6
1	B	328	SER	3.6
1	I	93	PRO	3.6
1	C	263	LEU	3.6
1	G	303	GLN	3.6
1	I	304	PRO	3.6
1	L	35	LYS	3.6
1	M	86	LEU	3.6
1	G	17	SER	3.6
1	K	98	TYR	3.6
1	I	97	ASN	3.6
1	K	405	ARG	3.6
1	E	408	LEU	3.6

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Mol	Chain	Res	Type	RSRZ
1	I	108	VAL	3.6
1	L	368	VAL	3.6
1	A	40	SER	3.6
1	A	234	ILE	3.6
1	L	361	SER	3.6
1	H	424	GLU	3.6
1	K	309	LYS	3.6
1	A	99	CYS	3.6
1	D	96	TYR	3.6
1	J	301	ILE	3.6
1	F	70	ALA	3.6
1	K	291	PRO	3.6
1	M	56	LEU	3.6
1	M	329	ALA	3.6
1	C	409	GLY	3.6
1	D	273	THR	3.6
1	E	247	VAL	3.6
1	A	333	LEU	3.6
1	A	109	ARG	3.6
1	K	286	THR	3.6
1	B	301	ILE	3.6
1	H	358	ALA	3.6
1	I	328	SER	3.6
1	M	132	SER	3.6
1	B	194	VAL	3.6
1	G	278	ALA	3.6
1	C	180	LEU	3.6
1	A	399	LYS	3.6
1	D	201	ASP	3.6
1	K	312	ILE	3.5
1	F	52	THR	3.5
1	I	307	SER	3.5
1	L	107	THR	3.5
1	A	268	GLY	3.5
1	I	76	GLY	3.5
1	D	73	THR	3.5
1	E	242	VAL	3.5
1	M	278	ALA	3.5
1	B	214	TYR	3.5
1	F	118	TYR	3.5
1	C	237	ILE	3.5
1	C	301	ILE	3.5

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Mol	Chain	Res	Type	RSRZ
1	E	16	ARG	3.5
1	D	171	THR	3.5
1	B	96	TYR	3.5
1	K	262	TYR	3.5
1	J	281	GLY	3.5
1	M	35	LYS	3.5
1	K	14	PHE	3.5
1	L	346	LEU	3.5
1	J	334	ALA	3.5
1	C	273	THR	3.5
1	C	203	PRO	3.5
1	E	154	LYS	3.5
1	F	306	THR	3.5
1	G	102	VAL	3.5
1	J	117	VAL	3.5
1	B	382	ASN	3.5
1	A	172	SER	3.5
1	B	211	ALA	3.5
1	C	172	SER	3.5
1	F	285	GLY	3.5
1	L	307	SER	3.5
1	M	230	PHE	3.5
1	K	408	LEU	3.5
1	F	336	THR	3.5
1	I	36	HIS	3.5
1	D	334	ALA	3.5
1	G	158	VAL	3.5
1	K	307	SER	3.5
1	M	271	VAL	3.5
1	F	20	MET	3.5
1	D	371	PHE	3.5
1	K	228	THR	3.5
1	H	425	TYR	3.5
1	J	354	TYR	3.5
1	I	295	VAL	3.5
1	D	205	VAL	3.5
1	E	363	VAL	3.5
1	F	383	LEU	3.5
1	I	271	VAL	3.5
1	J	357	VAL	3.5
1	G	245	GLU	3.5
1	G	417	ARG	3.5

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Mol	Chain	Res	Type	RSRZ
1	D	339	GLY	3.4
1	E	331	GLY	3.4
1	L	400	LEU	3.4
1	E	255	LEU	3.4
1	F	98	TYR	3.4
1	K	106	LEU	3.4
1	L	257	LEU	3.4
1	D	227	ILE	3.4
1	C	333	LEU	3.4
1	D	257	LEU	3.4
1	F	122	GLY	3.4
1	L	283	THR	3.4
1	C	368	VAL	3.4
1	D	92	LEU	3.4
1	E	438	ILE	3.4
1	J	401	ILE	3.4
1	K	187	ILE	3.4
1	M	434	SER	3.4
1	A	259	VAL	3.4
1	E	245	GLU	3.4
1	M	337	ILE	3.4
1	C	97	ASN	3.4
1	L	242	VAL	3.4
1	F	86	LEU	3.4
1	A	271	VAL	3.4
1	B	262	TYR	3.4
1	F	238	THR	3.4
1	C	427	MET	3.4
1	F	119	ALA	3.4
1	M	225	VAL	3.4
1	C	381	LYS	3.4
1	L	92	LEU	3.4
1	D	202	ARG	3.4
1	A	424	GLU	3.4
1	E	27	SER	3.4
1	H	407	ARG	3.4
1	A	98	TYR	3.4
1	K	225	VAL	3.4
1	H	310	LEU	3.4
1	F	274	ARG	3.4
1	F	362	VAL	3.4
1	G	330	ARG	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	367	GLY	3.4
1	G	59	PHE	3.4
1	L	260	THR	3.4
1	A	329	ALA	3.4
1	B	161	GLY	3.4
1	C	50	GLY	3.4
1	A	244	GLY	3.4
1	B	17	SER	3.4
1	D	425	TYR	3.4
1	I	170	PRO	3.4
1	C	399	LYS	3.4
1	J	295	VAL	3.4
1	K	349	VAL	3.4
1	F	428	GLU	3.4
1	D	74	LEU	3.4
1	L	16	ARG	3.4
1	C	440	GLY	3.4
1	A	108	VAL	3.4
1	M	221	GLN	3.4
1	H	368	VAL	3.4
1	D	330	ARG	3.4
1	A	89	ALA	3.4
1	D	251	SER	3.4
1	L	429	VAL	3.3
1	C	410	ILE	3.3
1	C	243	GLY	3.3
1	H	193	MET	3.3
1	D	359	THR	3.3
1	A	346	LEU	3.3
1	E	215	GLN	3.3
1	F	412	THR	3.3
1	L	404	GLU	3.3
1	D	348	PRO	3.3
1	K	87	LEU	3.3
1	F	399	LYS	3.3
1	B	306	THR	3.3
1	K	68	VAL	3.3
1	F	344	GLY	3.3
1	D	419	TYR	3.3
1	E	124	ILE	3.3
1	C	247	VAL	3.3
1	D	429	VAL	3.3

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Mol	Chain	Res	Type	RSRZ
1	H	277	ALA	3.3
1	L	58	VAL	3.3
1	E	113	LEU	3.3
1	G	271	VAL	3.3
1	I	387	TYR	3.3
1	D	21	PRO	3.3
1	I	306	THR	3.3
1	K	173	TYR	3.3
1	J	349	VAL	3.3
1	K	80	TYR	3.3
1	K	189	LEU	3.3
1	M	74	LEU	3.3
1	E	292	PHE	3.3
1	K	122	GLY	3.3
1	F	349	VAL	3.3
1	B	346	LEU	3.3
1	M	403	SER	3.3
1	C	55	GLY	3.2
1	D	349	VAL	3.2
1	L	111	SER	3.2
1	M	312	ILE	3.2
1	I	290	MET	3.2
1	J	171	THR	3.2
1	D	211	ALA	3.2
1	F	21	PRO	3.2
1	K	388	GLY	3.2
1	L	161	GLY	3.2
1	A	82	PHE	3.2
1	J	162	GLU	3.2
1	E	74	LEU	3.2
1	J	84	GLN	3.2
1	G	82	PHE	3.2
1	K	149	ALA	3.2
1	L	21	PRO	3.2
1	L	408	LEU	3.2
1	E	352	VAL	3.2
1	K	230	PHE	3.2
1	M	401	ILE	3.2
1	K	58	VAL	3.2
1	L	106	LEU	3.2
1	F	202	ARG	3.2
1	M	336	THR	3.2

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Mol	Chain	Res	Type	RSRZ
1	M	347	ARG	3.2
1	J	434	SER	3.2
1	G	56	LEU	3.2
1	F	54	SER	3.2
1	I	17	SER	3.2
1	H	319	GLY	3.2
1	L	282	LEU	3.2
1	A	59	PHE	3.2
1	B	242	VAL	3.2
1	E	248	PHE	3.2
1	M	308	ILE	3.2
1	J	256	VAL	3.2
1	K	229	LEU	3.2
1	G	79	ASN	3.2
1	A	87	LEU	3.2
1	H	144	LEU	3.2
1	C	58	VAL	3.2
1	H	365	VAL	3.2
1	D	246	LEU	3.2
1	J	126	ALA	3.2
1	D	244	GLY	3.2
1	L	339	GLY	3.2
1	B	160	VAL	3.2
1	D	283	THR	3.2
1	F	63	PHE	3.2
1	G	258	GLY	3.2
1	G	100	ARG	3.2
1	E	271	VAL	3.1
1	F	127	VAL	3.1
1	A	34	GLU	3.1
1	J	344	GLY	3.1
1	B	44	THR	3.1
1	I	168	SER	3.1
1	B	433	ASN	3.1
1	I	214	TYR	3.1
1	B	322	GLY	3.1
1	E	249	ARG	3.1
1	B	120	LEU	3.1
1	H	114	PRO	3.1
1	H	228	THR	3.1
1	E	422	PHE	3.1
1	C	101	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
1	M	204	ARG	3.1
1	B	40	SER	3.1
1	E	437	LYS	3.1
1	F	408	LEU	3.1
1	H	203	PRO	3.1
1	I	404	GLU	3.1
1	J	380	ALA	3.1
1	F	161	GLY	3.1
1	E	75	GLN	3.1
1	A	69	GLY	3.1
1	E	440	GLY	3.1
1	A	402	LEU	3.1
1	E	199	SER	3.1
1	G	291	PRO	3.1
1	M	85	MET	3.1
1	L	359	THR	3.1
1	F	308	ILE	3.1
1	G	119	ALA	3.1
1	B	98	TYR	3.1
1	D	262	TYR	3.1
1	B	244	GLY	3.1
1	J	161	GLY	3.1
1	A	228	THR	3.1
1	C	262	TYR	3.1
1	C	400	LEU	3.1
1	F	159	LEU	3.1
1	J	73	THR	3.1
1	G	21	PRO	3.1
1	K	61	PRO	3.1
1	I	110	SER	3.1
1	K	331	GLY	3.1
1	K	344	GLY	3.1
1	K	398	THR	3.1
1	I	345	ALA	3.1
1	J	120	LEU	3.1
1	J	343	PRO	3.1
1	C	233	ASN	3.0
1	A	349	VAL	3.0
1	I	258	GLY	3.0
1	D	94	ALA	3.0
1	G	349	VAL	3.0
1	H	216	PHE	3.0

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Mol	Chain	Res	Type	RSRZ
1	H	75	GLN	3.0
1	C	343	PRO	3.0
1	B	305	ILE	3.0
1	F	272	ILE	3.0
1	H	290	MET	3.0
1	I	57	ILE	3.0
1	A	211	ALA	3.0
1	F	355	GLU	3.0
1	H	70	ALA	3.0
1	B	436	LEU	3.0
1	D	354	TYR	3.0
1	J	56	LEU	3.0
1	C	394	ALA	3.0
1	D	345	ALA	3.0
1	K	362	VAL	3.0
1	D	405	ARG	3.0
1	J	331	GLY	3.0
1	G	399	LYS	3.0
1	C	120	LEU	3.0
1	C	269	THR	3.0
1	G	75	GLN	3.0
1	E	290	MET	3.0
1	M	99	CYS	3.0
1	B	399	LYS	3.0
1	C	108	VAL	3.0
1	I	107	THR	3.0
1	D	394	ALA	3.0
1	E	119	ALA	3.0
1	H	74	LEU	3.0
1	J	38	LEU	3.0
1	A	149	ALA	3.0
1	D	343	PRO	3.0
1	L	49	VAL	3.0
1	M	158	VAL	3.0
1	D	346	LEU	3.0
1	J	426	PHE	3.0
1	K	329	ALA	3.0
1	D	100	ARG	3.0
1	G	428	GLU	3.0
1	C	246	LEU	3.0
1	L	36	HIS	3.0
1	M	129	PHE	3.0

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Mol	Chain	Res	Type	RSRZ
1	J	400	LEU	3.0
1	H	306	THR	2.9
1	M	358	ALA	2.9
1	F	425	TYR	2.9
1	I	425	TYR	2.9
1	M	309	LYS	2.9
1	G	106	LEU	2.9
1	B	296	ILE	2.9
1	F	271	VAL	2.9
1	J	257	LEU	2.9
1	K	171	THR	2.9
1	L	220	TYR	2.9
1	C	74	LEU	2.9
1	C	310	LEU	2.9
1	J	333	LEU	2.9
1	F	172	SER	2.9
1	B	400	LEU	2.9
1	J	383	LEU	2.9
1	C	68	VAL	2.9
1	G	123	THR	2.9
1	H	271	VAL	2.9
1	E	204	ARG	2.9
1	K	202	ARG	2.9
1	L	99	CYS	2.9
1	B	263	LEU	2.9
1	A	189	LEU	2.9
1	J	106	LEU	2.9
1	J	114	PRO	2.9
1	A	368	VAL	2.9
1	B	347	ARG	2.9
1	M	371	PHE	2.9
1	I	344	GLY	2.9
1	F	143	GLY	2.9
1	E	349	VAL	2.8
1	B	41	GLU	2.8
1	C	15	ILE	2.8
1	K	308	ILE	2.8
1	E	14	PHE	2.8
1	J	382	ASN	2.8
1	K	419	TYR	2.8
1	G	114	PRO	2.8
1	G	371	PHE	2.8

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Mol	Chain	Res	Type	RSRZ
1	K	39	ARG	2.8
1	F	310	LEU	2.8
1	F	307	SER	2.8
1	M	248	PHE	2.8
1	C	113	LEU	2.8
1	B	435	PRO	2.8
1	E	263	LEU	2.8
1	I	426	PHE	2.8
1	L	248	PHE	2.8
1	C	242	VAL	2.8
1	F	97	ASN	2.8
1	H	339	GLY	2.8
1	A	85	MET	2.8
1	M	428	GLU	2.8
1	J	304	PRO	2.8
1	F	432	LEU	2.8
1	J	308	ILE	2.8
1	K	343	PRO	2.8
1	L	59	PHE	2.8
1	L	271	VAL	2.8
1	B	38	LEU	2.8
1	D	382	ASN	2.8
1	E	256	VAL	2.8
1	F	345	ALA	2.8
1	H	343	PRO	2.8
1	K	246	LEU	2.8
1	G	80	TYR	2.8
1	H	78	GLY	2.8
1	G	364	THR	2.8
1	M	16	ARG	2.8
1	M	416	THR	2.8
1	D	231	SER	2.8
1	M	313	VAL	2.8
1	D	124	ILE	2.8
1	C	268	GLY	2.8
1	H	329	ALA	2.8
1	A	139	VAL	2.8
1	A	390	PHE	2.8
1	B	371	PHE	2.8
1	C	202	ARG	2.8
1	F	258	GLY	2.8
1	H	408	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
1	I	114	PRO	2.8
1	C	328	SER	2.7
1	G	263	LEU	2.7
1	M	311	GLU	2.7
1	D	256	VAL	2.7
1	F	335	VAL	2.7
1	I	360	GLY	2.7
1	I	308	ILE	2.7
1	I	381	LYS	2.7
1	J	134	SER	2.7
1	K	259	VAL	2.7
1	J	248	PHE	2.7
1	J	306	THR	2.7
1	G	305	ILE	2.7
1	C	154	LYS	2.7
1	J	14	PHE	2.7
1	L	387	TYR	2.7
1	J	99	CYS	2.7
1	L	97	ASN	2.7
1	K	21	PRO	2.7
1	G	306	THR	2.7
1	H	359	THR	2.7
1	M	263	LEU	2.7
1	A	204	ARG	2.7
1	D	255	LEU	2.7
1	E	358	ALA	2.7
1	F	371	PHE	2.7
1	M	67	ILE	2.7
1	L	394	ALA	2.7
1	J	359	THR	2.7
1	K	416	THR	2.7
1	B	217	SER	2.7
1	F	411	LYS	2.7
1	I	247	VAL	2.7
1	L	113	LEU	2.7
1	M	240	LEU	2.7
1	D	72	TYR	2.7
1	G	182	ASP	2.7
1	K	422	PHE	2.7
1	G	34	GLU	2.7
1	A	382	ASN	2.7
1	D	305	ILE	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	138	ASP	2.7
1	L	202	ARG	2.7
1	H	371	PHE	2.6
1	M	59	PHE	2.6
1	A	70	ALA	2.6
1	C	332	SER	2.6
1	E	220	TYR	2.6
1	I	98	TYR	2.6
1	K	188	GLY	2.6
1	B	329	ALA	2.6
1	F	329	ALA	2.6
1	D	58	VAL	2.6
1	M	344	GLY	2.6
1	L	72	TYR	2.6
1	K	60	PHE	2.6
1	D	64	PRO	2.6
1	E	109	ARG	2.6
1	K	306	THR	2.6
1	D	216	PHE	2.6
1	J	362	VAL	2.6
1	I	264	ILE	2.6
1	F	124	ILE	2.6
1	D	427	MET	2.6
1	H	264	ILE	2.6
1	I	347	ARG	2.6
1	D	104	ARG	2.6
1	E	291	PRO	2.6
1	G	48	THR	2.6
1	E	329	ALA	2.6
1	J	332	SER	2.6
1	J	127	VAL	2.6
1	H	278	ALA	2.6
1	K	248	PHE	2.6
1	C	331	GLY	2.6
1	G	120	LEU	2.6
1	E	202	ARG	2.6
1	L	333	LEU	2.5
1	G	99	CYS	2.5
1	L	124	ILE	2.5
1	H	344	GLY	2.5
1	A	284	THR	2.5
1	G	58	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	405	ARG	2.5
1	B	287	ASP	2.5
1	E	114	PRO	2.5
1	J	85	MET	2.5
1	D	363	VAL	2.5
1	E	87	LEU	2.5
1	F	257	LEU	2.5
1	E	382	ASN	2.5
1	F	246	LEU	2.5
1	J	53	GLY	2.5
1	A	307	SER	2.5
1	D	99	CYS	2.5
1	L	228	THR	2.5
1	J	234	ILE	2.5
1	H	333	LEU	2.5
1	K	400	LEU	2.5
1	L	393	GLY	2.5
1	L	432	LEU	2.5
1	B	39	ARG	2.5
1	G	55	GLY	2.5
1	E	203	PRO	2.5
1	G	308	ILE	2.5
1	E	305	ILE	2.5
1	H	352	VAL	2.5
1	K	357	VAL	2.5
1	J	21	PRO	2.5
1	E	246	LEU	2.5
1	A	39	ARG	2.5
1	J	16	ARG	2.5
1	B	408	LEU	2.5
1	A	17	SER	2.5
1	D	400	LEU	2.5
1	K	267	ASP	2.5
1	B	75	GLN	2.5
1	D	115	GLY	2.5
1	C	89	ALA	2.4
1	J	97	ASN	2.4
1	C	336	THR	2.4
1	D	347	ARG	2.4
1	F	59	PHE	2.4
1	J	329	ALA	2.4
1	B	383	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	403	SER	2.4
1	D	420	THR	2.4
1	D	381	LYS	2.4
1	F	332	SER	2.4
1	K	74	LEU	2.4
1	J	49	VAL	2.4
1	L	258	GLY	2.4
1	E	260	THR	2.4
1	B	97	ASN	2.4
1	F	120	LEU	2.4
1	G	39	ARG	2.4
1	J	394	ALA	2.4
1	M	343	PRO	2.4
1	H	332	SER	2.4
1	K	174	ASP	2.4
1	I	202	ARG	2.4
1	D	329	ALA	2.4
1	D	344	GLY	2.4
1	E	264	ILE	2.4
1	I	424	GLU	2.4
1	J	243	GLY	2.4
1	K	428	GLU	2.4
1	L	244	GLY	2.4
1	E	345	ALA	2.4
1	C	38	LEU	2.4
1	H	345	ALA	2.4
1	B	202	ARG	2.3
1	G	40	SER	2.3
1	D	55	GLY	2.3
1	A	38	LEU	2.3
1	J	262	TYR	2.3
1	A	265	GLY	2.3
1	C	362	VAL	2.3
1	F	400	LEU	2.3
1	A	401	ILE	2.3
1	F	384	VAL	2.3
1	L	347	ARG	2.3
1	E	108	VAL	2.3
1	H	227	ILE	2.3
1	E	359	THR	2.3
1	M	359	THR	2.3
1	H	291	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
1	K	84	GLN	2.3
1	B	171	THR	2.3
1	B	362	VAL	2.3
1	M	17	SER	2.3
1	F	87	LEU	2.3
1	D	114	PRO	2.3
1	G	35	LYS	2.3
1	D	383	LEU	2.3
1	K	310	LEU	2.3
1	A	205	VAL	2.3
1	A	220	TYR	2.3
1	D	380	ALA	2.3
1	G	242	VAL	2.3
1	M	307	SER	2.3
1	D	49	VAL	2.3
1	G	333	LEU	2.2
1	B	397	TYR	2.2
1	E	368	VAL	2.2
1	B	366	ALA	2.2
1	F	210	ALA	2.2
1	H	284	THR	2.2
1	A	400	LEU	2.2
1	A	408	LEU	2.2
1	F	123	THR	2.2
1	D	264	ILE	2.2
1	L	89	ALA	2.2
1	C	305	ILE	2.2
1	J	228	THR	2.2
1	G	122	GLY	2.2
1	D	432	LEU	2.2
1	F	56	LEU	2.2
1	K	311	GLU	2.2
1	J	335	VAL	2.2
1	J	17	SER	2.2
1	E	277	ALA	2.2
1	F	244	GLY	2.2
1	M	70	ALA	2.2
1	B	365	VAL	2.2
1	K	220	TYR	2.2
1	K	16	ARG	2.2
1	L	345	ALA	2.2
1	B	257	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	I	310	LEU	2.2
1	I	334	ALA	2.2
1	L	211	ALA	2.1
1	C	408	LEU	2.1
1	H	57	ILE	2.1
1	J	292	PHE	2.1
1	C	256	VAL	2.1
1	D	245	GLU	2.1
1	I	49	VAL	2.1
1	J	242	VAL	2.1
1	A	371	PHE	2.1
1	H	17	SER	2.1
1	G	292	PHE	2.1
1	I	127	VAL	2.1
1	B	14	PHE	2.1
1	C	292	PHE	2.1
1	E	57	ILE	2.1
1	E	171	THR	2.1
1	K	55	GLY	2.1
1	L	356	ARG	2.1
1	M	346	LEU	2.1
1	E	333	LEU	2.1
1	E	383	LEU	2.1
1	G	257	LEU	2.1
1	H	16	ARG	2.1
1	J	229	LEU	2.1
1	M	328	SER	2.1
1	C	267	ASP	2.1
1	M	400	LEU	2.1
1	L	292	PHE	2.1
1	L	203	PRO	2.1
1	B	245	GLU	2.1
1	E	322	GLY	2.1
1	G	268	GLY	2.1
1	M	36	HIS	2.1
1	D	422	PHE	2.1
1	L	127	VAL	2.0
1	M	418	GLU	2.0
1	G	49	VAL	2.0
1	M	38	LEU	2.0
1	J	381	LYS	2.0
1	I	70	ALA	2.0

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Mol	Chain	Res	Type	RSRZ
1	M	124	ILE	2.0
1	E	278	ALA	2.0
1	F	333	LEU	2.0
1	C	99	CYS	2.0
1	I	362	VAL	2.0
1	E	261	ILE	2.0
1	F	96	TYR	2.0
1	G	387	TYR	2.0
1	H	311	GLU	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.