



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:49 AM GMT

PDB ID : 2BSE  
Title : STRUCTURE OF LACTOCOCCAL BACTERIOPHAGE P2 RECEPTOR  
BINDING PROTEIN IN COMPLEX WITH A LLAMA VHH DOMAIN  
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billau, C.  
Deposited on : 2005-05-20  
Resolution : 2.70 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

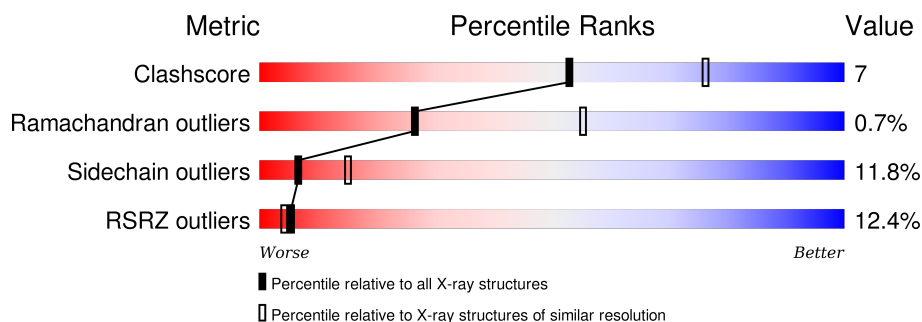
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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	264	<div> <div></div> <div> <div></div> <div>34%</div> <div>6%</div> <div>59%</div> </div> </div>
1	B	264	<div> <div></div> <div> <div></div> <div>34%</div> <div>6%</div> <div>59%</div> </div> </div>
1	C	264	<div> <div></div> <div> <div></div> <div>34%</div> <div>6%</div> <div>59%</div> </div> </div>
2	D	123	<div> <div>13%</div> <div> <div></div> <div>65%</div> <div>28%</div> <div>6%</div> </div> </div>
2	E	123	<div> <div>27%</div> <div> <div></div> <div>74%</div> <div>21%</div> <div></div> </div> </div>
2	F	123	<div> <div>20%</div> <div> <div></div> <div>64%</div> <div>32%</div> <div></div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5311 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 RECEPTOR BINDING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	107	Total	C	N	O	S	4	0	0
			832	530	149	152	1			
1	B	107	Total	C	N	O	S	4	0	0
			832	530	149	152	1			
1	C	107	Total	C	N	O	S	4	0	0
			832	530	149	152	1			

- Molecule 2 is a protein called LLAMA IMMUNOGLOBULIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	122	Total	C	N	O	S	0	0	0
			938	581	165	186	6			
2	E	122	Total	C	N	O	S	0	0	0
			938	581	165	186	6			
2	F	122	Total	C	N	O	S	0	0	0
			938	581	165	186	6			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	1	Total	O	0	0
			1	1		



- Molecule 1: RECEPTOR BINDING PROTEIN





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	74.76 Å 83.94 Å 137.79 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.70 19.99 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.0 (15.00-2.70) 99.0 (19.99-2.70)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.31 (at 2.71 Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, $R_{free}$	0.251 , 0.294 0.243 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	52.5	Xtriage
Anisotropy	0.491	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 28.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 24156 reflections	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	5311	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.50% 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

### 5.1 Standard geometry

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).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.34	0/853	0.66	2/1161 (0.2%)
1	B	0.33	0/853	0.66	1/1161 (0.1%)
1	C	0.35	0/853	0.66	1/1161 (0.1%)
2	D	0.36	0/956	0.70	4/1289 (0.3%)
2	E	0.33	0/956	0.65	3/1289 (0.2%)
2	F	0.32	0/956	0.66	3/1289 (0.2%)
All	All	0.34	0/5427	0.67	14/7350 (0.2%)

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	73	ASP	CB-CG-OD2	5.89	123.60	118.30
2	D	56	ASP	CB-CG-OD2	5.78	123.50	118.30
1	B	209	ASP	CB-CG-OD2	5.76	123.49	118.30
2	F	111	ASP	CB-CG-OD2	5.74	123.47	118.30
1	C	209	ASP	CB-CG-OD2	5.54	123.29	118.30
2	E	111	ASP	CB-CG-OD2	5.42	123.18	118.30
2	E	73	ASP	CB-CG-OD2	5.37	123.13	118.30
2	F	56	ASP	CB-CG-OD2	5.32	123.09	118.30
2	E	62	ASP	CB-CG-OD2	5.16	122.94	118.30
1	A	209	ASP	CB-CG-OD2	5.15	122.94	118.30
2	F	73	ASP	CB-CG-OD2	5.15	122.93	118.30
2	D	62	ASP	CB-CG-OD2	5.13	122.92	118.30
1	A	249	ASP	CB-CG-OD2	5.08	122.87	118.30
2	D	111	ASP	CB-CG-OD2	5.00	122.80	118.30

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts ⓘ

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	832	0	819	9	0
1	B	832	0	819	11	0
1	C	832	0	819	14	0
2	D	938	0	891	13	0
2	E	938	0	891	11	0
2	F	938	0	891	19	0
3	D	1	0	0	0	0
All	All	5311	0	5130	69	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 7.

All (69) 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)
2:F:108:GLU:HG3	2:F:109:LEU:N	1.54	1.18
2:F:108:GLU:CG	2:F:109:LEU:H	1.64	1.08
1:C:199:LYS:H	1:C:247:ASN:ND2	1.64	0.94
2:F:108:GLU:HG3	2:F:109:LEU:H	0.76	0.91
1:C:198:GLN:HA	1:C:247:ASN:HD22	1.42	0.83
2:F:91:THR:HG22	2:F:121:VAL:H	1.45	0.82
2:E:91:THR:HG22	2:E:121:VAL:H	1.47	0.80
1:B:198:GLN:HA	1:B:247:ASN:OD1	1.83	0.78
1:A:244:TRP:HE1	2:E:31:ASN:HD21	1.39	0.69
1:A:223:HIS:ND1	1:C:232:HIS:HD2	1.91	0.69
2:D:88:PRO:O	2:D:91:THR:HG22	1.95	0.66
1:C:198:GLN:CA	1:C:247:ASN:HD22	2.12	0.63
1:C:199:LYS:N	1:C:247:ASN:ND2	2.44	0.61
2:D:37:PHE:CE1	2:D:47:LEU:HD23	2.38	0.59
2:F:20:LEU:HD12	2:F:81:LEU:HD23	1.85	0.59
1:A:232:HIS:HD2	1:B:223:HIS:ND1	2.02	0.58
1:B:198:GLN:CA	1:B:247:ASN:OD1	2.51	0.56
1:C:199:LYS:H	1:C:247:ASN:HD21	1.52	0.56
2:E:36:TRP:HZ3	2:E:79:VAL:HG12	1.71	0.55
1:B:199:LYS:N	1:B:247:ASN:OD1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:72:ARG:HH21	2:D:74:SER:HA	1.72	0.54
2:F:108:GLU:CG	2:F:109:LEU:N	2.38	0.54
2:D:20:LEU:HD12	2:D:81:LEU:HD23	1.90	0.53
1:B:244:TRP:HE1	2:D:31:ASN:HD21	1.58	0.52
2:E:99:ARG:HB3	2:E:110:TYR:CD2	2.45	0.52
1:C:199:LYS:H	1:C:247:ASN:HD22	1.53	0.51
2:F:99:ARG:HB3	2:F:110:TYR:HA	1.92	0.50
2:F:51:LEU:HD12	2:F:58:THR:HG22	1.93	0.50
1:A:223:HIS:ND1	1:C:232:HIS:CD2	2.76	0.50
2:F:49:VAL:HG11	2:F:81:LEU:HD13	1.94	0.50
1:C:244:TRP:HE1	2:F:31:ASN:HD21	1.58	0.50
1:C:172:ASN:HD21	1:C:204:SER:H	1.60	0.49
1:C:210:ARG:HA	1:C:213:ARG:HD2	1.95	0.49
2:F:107:ARG:N	2:F:107:ARG:HD3	2.29	0.48
2:E:23:THR:HG22	2:E:78:THR:HG23	1.95	0.47
2:F:34:MET:HG3	2:F:53:PHE:CE1	2.49	0.47
1:B:177:GLN:OE1	1:B:189:ARG:NH1	2.48	0.47
2:E:64:VAL:HA	2:E:67:ARG:HH11	1.79	0.46
2:E:91:THR:HG22	2:E:121:VAL:N	2.25	0.46
1:B:229:THR:HB	1:C:228:ASP:HB2	1.98	0.46
2:F:23:THR:HG22	2:F:78:THR:HG23	1.97	0.46
2:D:11:LEU:HG	2:D:120:THR:HB	1.97	0.45
2:D:67:ARG:NH2	2:D:90:ASP:OD2	2.50	0.45
1:A:173:GLY:HA3	1:A:193:SER:O	2.16	0.45
2:D:36:TRP:CZ3	2:D:79:VAL:HG12	2.52	0.44
1:A:198:GLN:HA	1:A:247:ASN:OD1	2.17	0.44
2:F:18:LEU:HD23	2:F:119:VAL:HG13	2.00	0.44
2:E:14:ALA:HB2	2:E:123:SER:HA	2.00	0.44
2:E:40:LEU:HB2	2:E:43:LYS:HB2	1.99	0.44
2:F:37:PHE:CE1	2:F:47:LEU:HD23	2.52	0.44
2:F:20:LEU:HB2	2:F:81:LEU:HB3	2.00	0.43
2:D:12:VAL:HB	2:D:18:LEU:HD13	2.00	0.43
1:B:186:VAL:O	1:B:260:SER:HA	2.19	0.42
1:C:199:LYS:N	1:C:247:ASN:HD22	2.13	0.42
1:A:232:HIS:CD2	1:B:223:HIS:ND1	2.85	0.42
2:E:36:TRP:CZ3	2:E:79:VAL:HG12	2.53	0.42
1:B:187:ILE:HG12	1:B:260:SER:HB3	2.00	0.42
1:C:195:SER:HB3	1:C:252:PRO:HA	2.01	0.41
2:D:45:PRO:HG2	2:D:107:ARG:HH22	1.85	0.41
2:F:39:GLN:HG3	2:F:45:PRO:HG3	2.02	0.41
1:A:209:ASP:HB3	1:A:211:PRO:HD2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:53:PHE:CE2	2:D:72:ARG:HD2	2.56	0.41
2:F:106:ASN:HA	2:F:107:ARG:HH11	1.86	0.41
1:A:210:ARG:HA	1:A:213:ARG:HD2	2.02	0.41
2:D:38:ARG:HD2	2:D:94:TYR:OH	2.21	0.41
2:E:108:GLU:CG	2:E:109:LEU:N	2.83	0.41
2:D:97:ALA:HB1	2:D:110:TYR:CD2	2.57	0.40
2:F:36:TRP:CZ3	2:F:79:VAL:HG12	2.55	0.40
1:B:173:GLY:HA3	1:B:193:SER:O	2.21	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	105/264 (40%)	102 (97%)	3 (3%)	0	100	100
1	B	105/264 (40%)	102 (97%)	3 (3%)	0	100	100
1	C	105/264 (40%)	102 (97%)	3 (3%)	0	100	100
2	D	120/123 (98%)	114 (95%)	5 (4%)	1 (1%)	24	51
2	E	120/123 (98%)	114 (95%)	3 (2%)	3 (2%)	7	18
2	F	120/123 (98%)	113 (94%)	6 (5%)	1 (1%)	24	51
All	All	675/1161 (58%)	647 (96%)	23 (3%)	5 (1%)	26	55

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	74	SER
2	E	108	GLU
2	F	74	SER
2	E	41	ALA
2	E	74	SER

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	90/228 (40%)	83 (92%)	7 (8%)	16	35
1	B	90/228 (40%)	84 (93%)	6 (7%)	20	44
1	C	90/228 (40%)	86 (96%)	4 (4%)	35	65
2	D	99/100 (99%)	79 (80%)	20 (20%)	1	4
2	E	99/100 (99%)	86 (87%)	13 (13%)	5	12
2	F	99/100 (99%)	82 (83%)	17 (17%)	2	6
All	All	567/984 (58%)	500 (88%)	67 (12%)	6	15

All (67) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	159	ILE
1	A	165	THR
1	A	177	GLN
1	A	199	LYS
1	A	209	ASP
1	A	210	ARG
1	A	228	ASP
1	B	161	VAL
1	B	165	THR
1	B	177	GLN
1	B	197	ILE
1	B	199	LYS
1	B	228	ASP
1	C	158	SER
1	C	165	THR
1	C	177	GLN
1	C	199	LYS
2	D	11	LEU
2	D	17	SER
2	D	19	ARG
2	D	23	THR
2	D	27	ARG

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Mol	Chain	Res	Type
2	D	38	ARG
2	D	43	LYS
2	D	49	VAL
2	D	52	ASN
2	D	65	LYS
2	D	73	ASP
2	D	77	ASN
2	D	79	VAL
2	D	86	LEU
2	D	91	THR
2	D	107	ARG
2	D	109	LEU
2	D	117	THR
2	D	122	SER
2	D	123	SER
2	E	27	ARG
2	E	38	ARG
2	E	43	LYS
2	E	47	LEU
2	E	52	ASN
2	E	63	SER
2	E	65	LYS
2	E	73	ASP
2	E	74	SER
2	E	77	ASN
2	E	106	ASN
2	E	109	LEU
2	E	117	THR
2	F	11	LEU
2	F	26	ARG
2	F	27	ARG
2	F	34	MET
2	F	43	LYS
2	F	52	ASN
2	F	65	LYS
2	F	73	ASP
2	F	77	ASN
2	F	89	GLU
2	F	93	ILE
2	F	105	SER
2	F	107	ARG
2	F	108	GLU

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Mol	Chain	Res	Type
2	F	115	GLN
2	F	117	THR
2	F	123	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	172	ASN
1	A	175	GLN
1	A	177	GLN
1	A	232	HIS
1	A	236	ASN
1	B	164	GLN
1	B	172	ASN
1	B	175	GLN
1	B	183	ASN
1	B	232	HIS
1	B	236	ASN
1	C	172	ASN
1	C	177	GLN
1	C	183	ASN
1	C	232	HIS
1	C	236	ASN
1	C	247	ASN
2	D	31	ASN
2	D	52	ASN
2	D	106	ASN
2	E	31	ASN
2	E	52	ASN
2	E	106	ASN
2	F	31	ASN
2	F	52	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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 [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

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	107/264 (40%)	-0.01	3 (2%) 56 57	13, 20, 31, 41	1 (0%)
1	B	107/264 (40%)	-0.11	4 (3%) 45 45	14, 20, 31, 41	1 (0%)
1	C	107/264 (40%)	-0.15	4 (3%) 45 45	14, 20, 31, 41	1 (0%)
2	D	122/123 (99%)	0.77	16 (13%) 5 4	19, 26, 34, 38	0
2	E	122/123 (99%)	1.44	33 (27%) 1 1	20, 26, 33, 37	0
2	F	122/123 (99%)	1.09	25 (20%) 1 1	20, 26, 34, 37	0
All	All	687/1161 (59%)	0.54	85 (12%) 5 4	13, 23, 34, 41	3 (0%)

All (85) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	2	VAL	10.2
2	E	41	ALA	8.6
2	D	42	GLY	8.5
2	D	75	GLY	7.7
2	D	123	SER	7.4
2	E	39	GLN	7.3
2	E	42	GLY	7.0
2	F	123	SER	7.0
2	E	76	LYS	6.9
2	F	75	GLY	5.5
2	D	74	SER	5.3
2	E	75	GLY	5.3
2	F	2	VAL	5.1
2	F	109	LEU	5.0
2	E	114	GLY	5.0
2	F	76	LYS	4.9
1	C	160	ASP	4.7
2	D	109	LEU	4.6
2	F	74	SER	4.5

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Mol	Chain	Res	Type	RSRZ
2	F	41	ALA	4.4
2	F	42	GLY	4.3
1	B	160	ASP	4.3
2	F	44	GLU	4.0
2	E	35	GLY	4.0
2	E	9	GLY	4.0
2	E	45	PRO	4.0
2	F	108	GLU	3.9
2	E	73	ASP	3.6
2	D	44	GLU	3.5
2	E	26	ARG	3.5
2	F	73	ASP	3.4
2	E	36	TRP	3.4
2	E	66	GLY	3.4
1	B	158	SER	3.4
2	E	28	THR	3.3
2	F	35	GLY	3.2
2	E	49	VAL	3.2
2	E	74	SER	3.1
2	F	13	GLN	3.1
2	F	107	ARG	3.1
2	E	17	SER	3.0
2	E	44	GLU	3.0
2	D	41	ALA	3.0
1	C	158	SER	2.9
2	F	106	ASN	2.9
2	D	35	GLY	2.9
2	E	10	GLY	2.8
2	D	76	LYS	2.8
2	F	36	TRP	2.8
1	A	160	ASP	2.8
2	F	43	LYS	2.7
2	E	40	LEU	2.7
1	A	158	SER	2.7
2	D	108	GLU	2.6
2	E	115	GLN	2.6
2	E	33	CYS	2.6
2	D	13	GLN	2.5
1	C	159	ILE	2.5
2	F	122	SER	2.4
2	D	43	LYS	2.4
1	B	175	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
2	E	50	ALA	2.4
2	F	116	GLY	2.4
2	E	65	LYS	2.3
1	B	159	ILE	2.3
2	F	115	GLN	2.3
2	F	96	CYS	2.3
2	E	94	TYR	2.3
1	A	198	GLN	2.2
2	E	111	ASP	2.2
2	E	62	ASP	2.2
2	F	8	GLY	2.2
2	D	62	ASP	2.2
2	E	95	TYR	2.1
1	C	215	ALA	2.1
2	F	120	THR	2.1
2	F	50	ALA	2.1
2	E	87	LYS	2.1
2	D	50	ALA	2.1
2	D	49	VAL	2.1
2	E	34	MET	2.1
2	F	46	GLU	2.1
2	E	19	ARG	2.0
2	D	97	ALA	2.0
2	E	96	CYS	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.