



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:46 PM GMT

PDB ID : 4JHA  
Title : Crystal Structure of RSV-Neutralizing Human Antibody D25  
Authors : Mclellan, J.S.; Chen, M.; Leung, S.; Graepel, K.W.; Du, X.; Yang, Y.; Zhou, T.; Baxa, U.; Yasuda, E.; Beaumont, T.; Kumar, A.; Modjarrad, K.; Zheng, Z.; Zhao, M.; Xia, N.; Kwong, P.D.; Graham, B.S.  
Deposited on : 2013-03-04  
Resolution : 1.60 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.

---

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

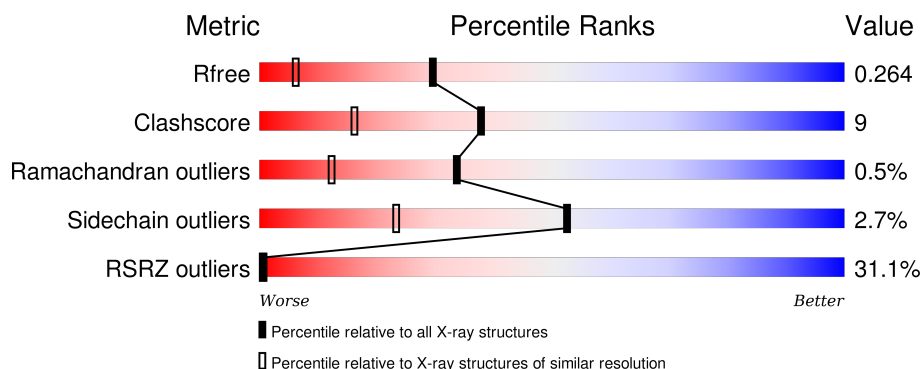
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.60 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))
$R_{free}$	91344	2475 (1.60-1.60)
Clashscore	102246	2732 (1.60-1.60)
Ramachandran outliers	100387	2654 (1.60-1.60)
Sidechain outliers	100360	2653 (1.60-1.60)
RSRZ outliers	91569	2479 (1.60-1.60)

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	H	231	<div> <div>26%</div> <div>83%</div> <div>13%</div> <div>..</div> </div>
2	L	214	<div> <div>35%</div> <div>75%</div> <div>22%</div> <div>..</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3575 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 D25 antigen-binding fragment heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	226	Total	C	N	O	S	0	1	0
			1686	1069	279	330	8			

- Molecule 2 is a protein called D25 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	211	Total	C	N	O	S	0	0	0
			1619	1014	269	331	5			

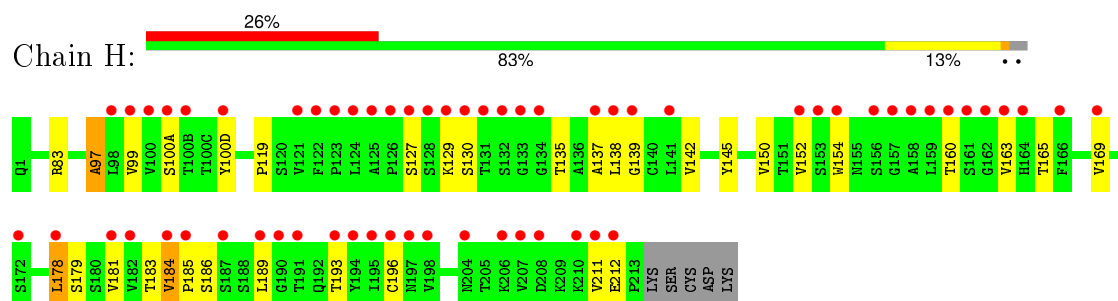
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	H	141	Total	O	0	0
			141	141		
3	L	129	Total	O	0	0
			129	129		

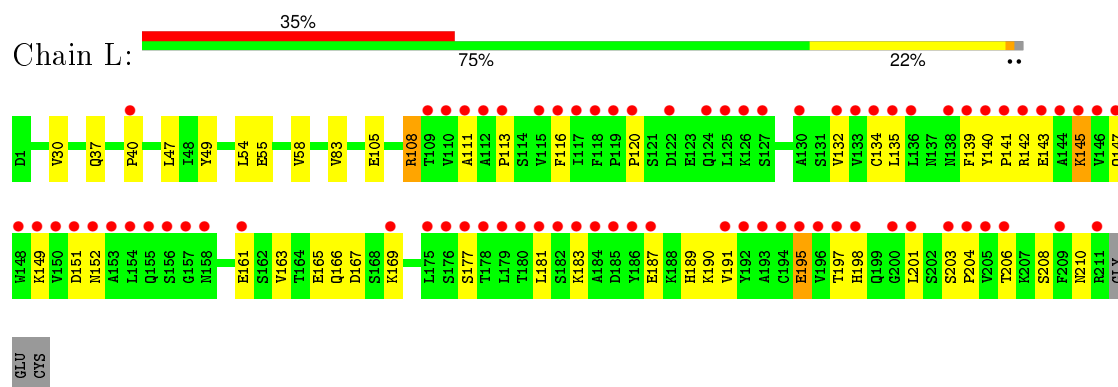
### 3 Residue-property plots [i](#)

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: D25 antigen-binding fragment heavy chain



- Molecule 2: D25 light chain



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	108.72Å 108.72Å 139.91Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	35.40 – 1.60 35.40 – 1.60	Depositor EDS
% Data completeness (in resolution range)	98.1 (35.40-1.60) 98.1 (35.40-1.60)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.98 (at 1.60Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.8.1_1168)	Depositor
R, $R_{free}$	0.240 , 0.255 0.250 , 0.264	Depositor DCC
$R_{free}$ test set	3211 reflections (5.34%)	DCC
Wilson B-factor (Å <sup>2</sup> )	23.3	Xtriage
Anisotropy	0.396	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 59.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 63432 reflections (0.002%)	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	3575	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 5.11% 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).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	H	0.38	0/1732	0.61	1/2371 (0.0%)
2	L	0.35	0/1652	0.57	0/2247
All	All	0.37	0/3384	0.59	1/4618 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	178	LEU	CA-CB-CG	5.50	127.96	115.30

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	H	1686	0	1666	22	0
2	L	1619	0	1579	40	1
3	H	141	0	0	8	0
3	L	129	0	0	13	0
All	All	3575	0	3245	60	1

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 9.

All (60) 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:L:147:GLN:O	3:L:418:HOH:O	1.82	0.97
2:L:147:GLN:HG2	3:L:418:HOH:O	1.63	0.96
2:L:161:GLU:O	3:L:408:HOH:O	1.89	0.90
1:H:179:SER:OG	3:H:412:HOH:O	1.91	0.87
2:L:203:SER:OG	3:L:420:HOH:O	1.96	0.82
2:L:183:LYS:NZ	3:L:378:HOH:O	2.15	0.79
2:L:120:PRO:HD3	2:L:132:VAL:HG22	1.65	0.77
2:L:187:GLU:OE1	3:L:427:HOH:O	2.05	0.74
1:H:100(A):SER:HB3	1:H:100(D):TYR:HD2	1.49	0.74
2:L:167:ASP:OD1	2:L:169:LYS:HG2	1.89	0.72
2:L:149:LYS:NZ	2:L:152:ASN:O	2.22	0.67
2:L:151:ASP:HA	2:L:191:VAL:HG13	1.79	0.62
1:H:138:LEU:HD13	1:H:211:VAL:HG21	1.81	0.62
2:L:151:ASP:OD2	2:L:189:HIS:ND1	2.33	0.61
2:L:105:GLU:HG3	3:L:388:HOH:O	1.99	0.61
2:L:37:GLN:HB2	2:L:47:LEU:HD11	1.83	0.60
1:H:163:VAL:HG13	3:H:435:HOH:O	2.00	0.60
1:H:181:VAL:HG11	2:L:135:LEU:HD22	1.82	0.59
1:H:100(A):SER:HB3	1:H:100(D):TYR:CD2	2.36	0.58
1:H:165:THR:N	3:H:434:HOH:O	2.03	0.57
2:L:116:PHE:HD2	2:L:135:LEU:HD23	1.70	0.56
1:H:142:VAL:HG11	1:H:150:VAL:HG11	1.90	0.53
2:L:198:HIS:CD2	3:L:415:HOH:O	2.61	0.53
2:L:113:PRO:HB3	2:L:139:PHE:CD2	2.45	0.52
1:H:139:GLY:HA2	1:H:154:TRP:CH2	2.46	0.51
1:H:119:PRO:HB3	1:H:145:TYR:HB3	1.92	0.51
2:L:140:TYR:HA	3:L:407:HOH:O	2.11	0.51
1:H:184:VAL:HG22	1:H:185:PRO:HD2	1.92	0.51
1:H:137:ALA:HB2	1:H:183:THR:HG22	1.92	0.51
1:H:160:THR:O	1:H:163:VAL:HG22	2.11	0.51
1:H:137:ALA:N	3:H:433:HOH:O	2.44	0.51
1:H:129:LYS:HE2	2:L:208:SER:O	2.10	0.51
2:L:55:GLU:O	2:L:58:VAL:HG22	2.11	0.51
1:H:186:SER:HA	1:H:189:LEU:HD13	1.92	0.50
1:H:152:VAL:HG22	3:H:432:HOH:O	2.11	0.50
1:H:196:CYS:N	3:H:431:HOH:O	2.45	0.49
2:L:140:TYR:CG	2:L:141:PRO:HA	2.47	0.49
2:L:142:ARG:NH2	2:L:163:VAL:HG11	2.28	0.49
2:L:83:VAL:HG11	2:L:166:GLN:HB3	1.95	0.48
1:H:169:VAL:HA	3:H:364:HOH:O	2.14	0.48
2:L:198:HIS:H	2:L:201:LEU:HD11	1.78	0.48
1:H:97:ALA:C	1:H:99:VAL:H	2.17	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:108:ARG:HH12	2:L:111:ALA:HB2	1.79	0.47
2:L:55:GLU:HG2	3:L:387:HOH:O	2.15	0.46
1:H:127:SER:N	1:H:130:SER:OG	2.42	0.45
2:L:140:TYR:CD1	2:L:141:PRO:HA	2.51	0.45
2:L:142:ARG:CZ	2:L:163:VAL:HG21	2.47	0.44
2:L:40:PRO:HB3	2:L:165:GLU:HG3	1.99	0.43
2:L:195:GLU:HA	2:L:206:THR:HA	2.00	0.43
2:L:165:GLU:OE1	3:L:395:HOH:O	2.21	0.42
2:L:197:THR:HG22	2:L:204:PRO:HB3	2.00	0.42
2:L:134:CYS:HB3	2:L:177:SER:OG	2.20	0.42
2:L:190:LYS:NZ	2:L:210:ASN:CG	2.73	0.42
2:L:190:LYS:NZ	2:L:210:ASN:HB3	2.35	0.41
2:L:190:LYS:HZ3	2:L:210:ASN:CG	2.23	0.41
2:L:145:LYS:HB2	3:L:390:HOH:O	2.21	0.41
1:H:196:CYS:HB3	3:H:431:HOH:O	2.20	0.41
2:L:108:ARG:HB3	3:L:322:HOH:O	2.20	0.41
2:L:54:LEU:HG	2:L:58:VAL:CG2	2.51	0.41
2:L:143:GLU:OE1	2:L:143:GLU:N	2.49	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:49:TYR:OH	2:L:204:PRO:O[8_565]	2.01	0.19

## 5.3 Torsion angles [i](#)

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

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	H	225/231 (97%)	217 (96%)	7 (3%)	1 (0%)	39	17
2	L	209/214 (98%)	202 (97%)	6 (3%)	1 (0%)	34	12

Continued on next page...



*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	434/445 (98%)	419 (96%)	13 (3%)	2 (0%)	34 12

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	97	ALA
2	L	30	VAL

### 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	H	192/196 (98%)	186 (97%)	6 (3%)	47 19
2	L	186/188 (99%)	182 (98%)	4 (2%)	60 31
All	All	378/384 (98%)	368 (97%)	10 (3%)	52 25

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	83	ARG
1	H	135	THR
1	H	178	LEU
1	H	184	VAL
1	H	193	THR
1	H	212	GLU
2	L	108	ARG
2	L	145	LYS
2	L	181	LEU
2	L	195	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 [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	H	226/231 (97%)	1.34	61 (26%) <b>1</b> <b>1</b>	17, 32, 135, 157	0
2	L	211/214 (98%)	1.67	75 (35%) <b>0</b> <b>0</b>	18, 50, 94, 102	0
All	All	437/445 (98%)	1.50	136 (31%) <b>1</b> <b>0</b>	17, 42, 115, 157	0

All (136) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	100	VAL	10.5
2	L	116	PHE	9.5
1	H	138	LEU	9.2
2	L	153	ALA	9.2
1	H	191	THR	8.9
2	L	196	VAL	8.3
1	H	190	GLY	8.2
2	L	200	GLY	7.7
2	L	193	ALA	7.7
2	L	186	TYR	7.6
1	H	126	PRO	7.6
1	H	195	ILE	7.4
1	H	161	SER	7.3
2	L	146	VAL	7.3
1	H	128	SER	7.3
2	L	142	ARG	7.2
2	L	134	CYS	7.1
1	H	157	GLY	7.0
1	H	181	VAL	6.9
1	H	158	ALA	6.9
1	H	124	LEU	6.7
1	H	211	VAL	6.6
1	H	163	VAL	6.5
1	H	131	THR	6.4

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
2	L	194	CYS	6.2
2	L	184	ALA	6.2
2	L	127	SER	6.0
1	H	166	PHE	5.8
1	H	132	SER	5.8
2	L	152	ASN	5.7
1	H	206	LYS	5.7
2	L	117	ILE	5.6
2	L	181	LEU	5.6
2	L	147	GLN	5.5
1	H	99	VAL	5.5
1	H	133	GLY	5.3
2	L	126	LYS	5.3
2	L	175	LEU	5.3
1	H	197	ASN	5.3
1	H	134	GLY	5.3
1	H	122	PHE	5.2
1	H	137	ALA	5.1
2	L	133	VAL	5.0
1	H	98	LEU	4.8
1	H	125	ALA	4.7
2	L	197	THR	4.7
2	L	136	LEU	4.7
2	L	192	TYR	4.4
1	H	198	VAL	4.4
2	L	205	VAL	4.3
2	L	157	GLY	4.3
1	H	160	THR	4.3
1	H	193	THR	4.3
1	H	172	SER	4.3
1	H	178	LEU	4.3
1	H	204	ASN	4.3
1	H	152	VAL	4.2
2	L	118	PHE	4.2
1	H	129	LYS	4.2
1	H	187	SER	4.2
2	L	179	LEU	4.2
2	L	122	ASP	4.2
2	L	148	TRP	4.1
2	L	115	VAL	4.1
2	L	198	HIS	4.0
1	H	156	SER	4.0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
2	L	178	THR	4.0
1	H	212	GLU	4.0
2	L	169	LYS	4.0
2	L	183	LYS	3.9
2	L	151	ASP	3.9
1	H	182	VAL	3.9
2	L	120	PRO	3.9
2	L	143	GLU	3.9
1	H	154	TRP	3.8
2	L	119	PRO	3.8
2	L	201	LEU	3.8
2	L	155	GLN	3.8
2	L	132	VAL	3.7
2	L	191	VAL	3.7
2	L	138	ASN	3.7
2	L	158	ASN	3.6
2	L	139	PHE	3.6
1	H	127	SER	3.5
1	H	189	LEU	3.5
2	L	206	THR	3.5
2	L	150	VAL	3.5
2	L	113	PRO	3.5
1	H	184	VAL	3.4
1	H	123	PRO	3.4
2	L	187	GLU	3.3
2	L	130	ALA	3.3
2	L	109	THR	3.3
2	L	144	ALA	3.3
2	L	182	SER	3.3
2	L	111	ALA	3.2
1	H	153	SER	3.2
2	L	125	LEU	3.2
1	H	194	TYR	3.2
2	L	112	ALA	3.2
1	H	185	PRO	3.1
1	H	207	VAL	3.1
2	L	141	PRO	3.1
2	L	176	SER	3.1
2	L	135	LEU	3.0
2	L	149	LYS	2.9
2	L	204	PRO	2.9
2	L	110	VAL	2.9

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
2	L	195	GLU	2.7
2	L	177	SER	2.7
1	H	139	GLY	2.7
1	H	210	LYS	2.7
1	H	130	SER	2.7
1	H	100(A)	SER	2.6
1	H	208	ASP	2.6
1	H	159	LEU	2.6
1	H	100(B)	THR	2.6
1	H	196	CYS	2.6
2	L	156	SER	2.6
2	L	140	TYR	2.5
2	L	209	PHE	2.5
1	H	169	VAL	2.5
2	L	185	ASP	2.5
1	H	164	HIS	2.4
2	L	203	SER	2.4
1	H	141	LEU	2.3
2	L	40	PRO	2.3
2	L	211	ARG	2.2
1	H	100(D)	TYR	2.2
1	H	121	VAL	2.2
2	L	145	LYS	2.1
1	H	162	GLY	2.1
2	L	161	GLU	2.1
2	L	180	THR	2.1
2	L	154	LEU	2.1
2	L	124	GLN	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.