



# Full wwPDB X-ray Structure Validation Report ⓘ

Apr 8, 2014 – 04:12 AM EDT

PDB ID : 3W2D  
Title : Crystal Structure of Staphylococcal Enterotoxin B in complex with a novel neutralization monoclonal antibody Fab fragment  
Authors : Liang, S.Y.; Hu, S.; Dai, J.X.; Guo, Y.J.; Lou, Z.Y.  
Deposited on : 2012-11-28  
Resolution : 3.10 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

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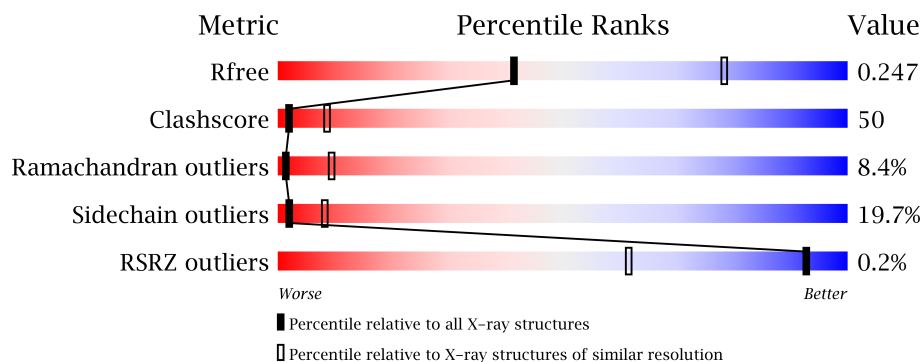
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : **FAILED**  
Xtriage (Phenix) : dev-1439  
EDS : stable22978  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22978

# 1 Overall quality at a glance

The reported resolution of this entry is 3.10 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))
$R_{free}$	66092	1007 (3.18-3.02)
Clashscore	79885	1078 (3.16-3.04)
Ramachandran outliers	78287	1044 (3.16-3.04)
Sidechain outliers	78261	1044 (3.16-3.04)
RSRZ outliers	66119	1008 (3.18-3.02)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	239	
2	L	215	
3	H	223	

## 2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 5393 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Enterotoxin type B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	225	1883	1208	305	360	10	0	0	0

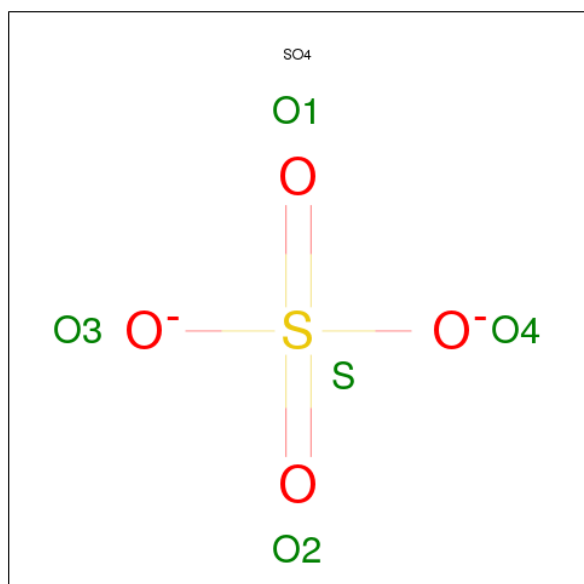
- Molecule 2 is a protein called Monoclonal Antibody 3E2 Fab figment light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	L	215	1647	1023	273	343	8	0	0	0

- Molecule 3 is a protein called Monoclonal Antibody 3E2 Fab figment heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	H	223	1723	1095	284	337	7	0	0	0

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	H	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is water.

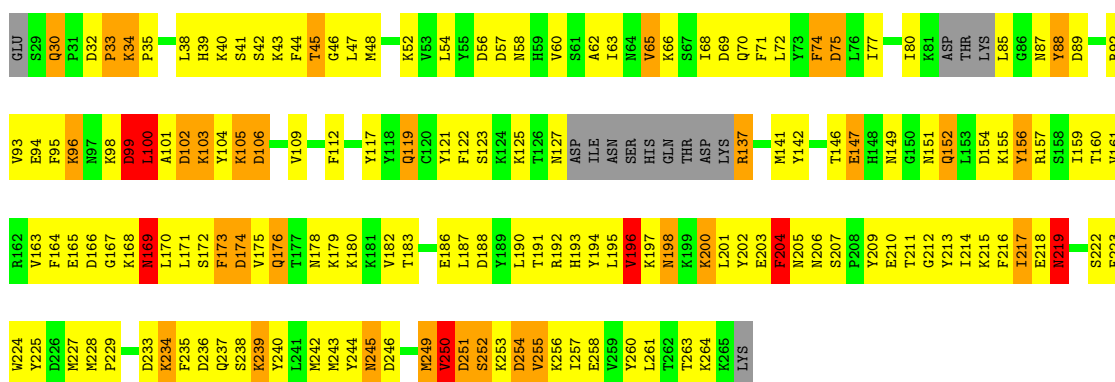
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	40	Total	O	0	0
			40	40		
5	L	47	Total	O	0	0
			47	47		
5	H	48	Total	O	0	0
			48	48		

### 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 ( $RSRZ > 2$ ). 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.

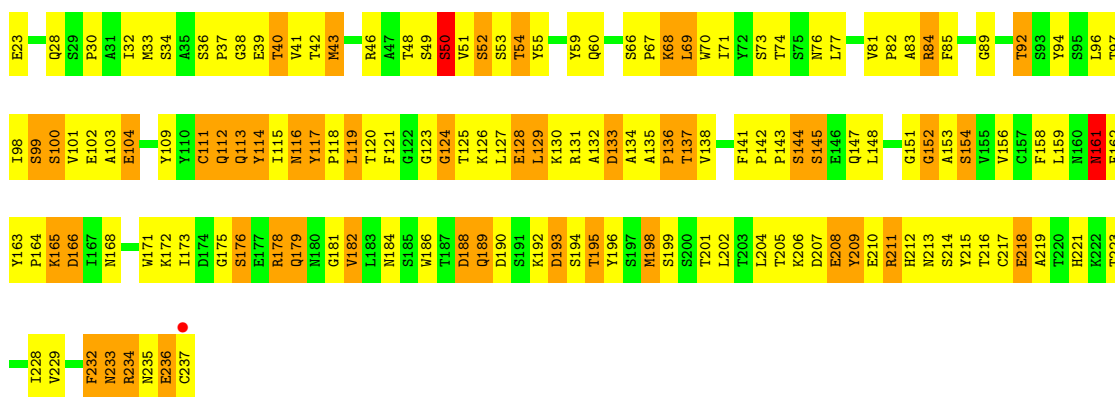
#### • Molecule 1: Enterotoxin type B

Chain A: 



#### • Molecule 2: Monoclonal Antibody 3E2 Fab figment light chain

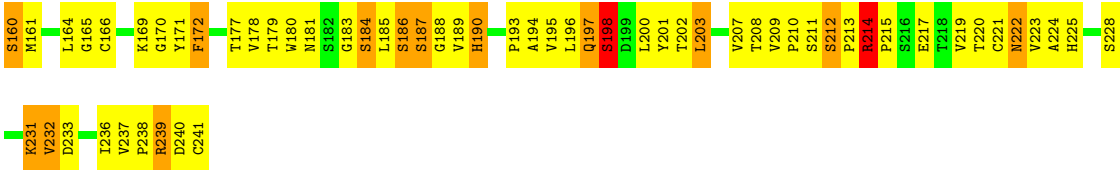
Chain L: 



#### • Molecule 3: Monoclonal Antibody 3E2 Fab figment heavy chain

Chain H: 





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	40.56Å 109.31Å 86.22Å 90.00° 96.08° 90.00°	Depositor
Resolution (Å)	36.44 – 3.10 36.44 – 3.10	Depositor EDS
% Data completeness (in resolution range)	98.8 (36.44-3.10) 92.4 (36.44-3.10)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.13 (at 3.12Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, $R_{free}$	0.196 , 0.261 0.186 , 0.247	Depositor DCC
$R_{free}$ test set	621 reflections (4.91%)	DCC
Wilson B-factor (Å <sup>2</sup> )	41.2	Xtriage
Anisotropy	0.585	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 49.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	1 of 13506 reflections (0.007%)	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	5393	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.53% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	0.57	0/1925	0.71	0/2586
2	L	0.56	0/1685	0.79	0/2292
3	H	0.57	0/1773	0.73	0/2430
All	All	0.57	0/5383	0.74	0/7308

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1883	0	1831	179	0
2	L	1647	0	1564	215	0
3	H	1723	0	1662	141	0
4	H	5	0	0	0	0
5	A	40	0	0	1	0
5	H	48	0	0	2	0
5	L	47	0	0	4	0
All	All	5393	0	5057	518	0



Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 50.

All (518) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:207:SER:O	1:A:264:LYS:NZ	1.85	1.10
2:L:172:LYS:HD2	2:L:216:THR:HG22	1.34	1.08
1:A:234:LYS:HD3	1:A:235:PHE:H	1.19	1.06
3:H:181:ASN:O	3:H:184:SER:OG	1.73	1.04
2:L:55:TYR:CD1	2:L:115:ILE:HD11	1.94	1.01
1:A:99:ASP:O	1:A:101:ALA:N	1.93	1.01
2:L:49:SER:O	2:L:50:SER:HB3	1.59	1.01
2:L:193:ASP:O	2:L:195:THR:N	1.98	0.96
3:H:100:GLN:NE2	3:H:102:ASN:OD1	2.01	0.94
3:H:78:TYR:HE1	3:H:88:ILE:HG13	1.31	0.94
1:A:234:LYS:CD	1:A:235:PHE:H	1.82	0.93
1:A:244:TYR:O	1:A:246:ASP:N	2.02	0.93
2:L:159:LEU:O	2:L:162:PHE:HE1	1.53	0.92
3:H:214:ARG:HD2	3:H:215:PRO:HA	1.51	0.91
2:L:113:GLN:NE2	2:L:114:TYR:O	2.03	0.90
1:A:234:LYS:HD3	1:A:235:PHE:N	1.85	0.90
2:L:113:GLN:HE21	2:L:113:GLN:C	1.74	0.90
2:L:23:GLU:HB2	2:L:118:PRO:HD2	1.51	0.90
1:A:88:TYR:HA	1:A:137:ARG:HB3	1.51	0.89
1:A:72:LEU:HD22	2:L:115:ILE:HG22	1.55	0.88
2:L:213:ASN:O	2:L:233:ASN:HA	1.72	0.88
2:L:211:ARG:HH11	2:L:211:ARG:HB2	1.38	0.87
1:A:156:TYR:HD2	1:A:156:TYR:N	1.74	0.86
1:A:168:LYS:O	1:A:170:LEU:N	2.06	0.86
3:H:160:SER:O	3:H:211:SER:N	2.07	0.86
3:H:213:PRO:O	3:H:214:ARG:HB2	1.74	0.86
2:L:178:ARG:CZ	2:L:178:ARG:HA	2.05	0.86
1:A:176:GLN:OE1	1:A:176:GLN:N	2.09	0.85
2:L:141:PHE:HB2	2:L:156:VAL:HG12	1.58	0.84
2:L:165:LYS:O	2:L:166:ASP:HB2	1.76	0.84
2:L:172:LYS:HE2	2:L:175:GLY:H	1.40	0.84
1:A:88:TYR:HB3	1:A:117:TYR:HE1	1.42	0.83
2:L:172:LYS:NZ	2:L:214:SER:OG	2.11	0.83
1:A:66:LYS:HD2	1:A:106:ASP:HA	1.60	0.83
1:A:179:LYS:O	1:A:252:SER:OG	1.96	0.82
2:L:136:PRO:O	2:L:137:THR:OG1	1.97	0.82
2:L:68:LYS:HB2	2:L:68:LYS:NZ	1.94	0.82
2:L:114:TYR:CZ	2:L:119:LEU:HD12	2.15	0.82
2:L:236:GLU:HB2	3:H:153:GLY:HA2	1.61	0.82

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:H:22:LEU:HD23	3:H:114:CYS:O	1.80	0.81
2:L:39:GLU:O	2:L:101:VAL:HG13	1.80	0.81
1:A:188:ASP:OD1	1:A:214:ILE:HD13	1.81	0.81
1:A:156:TYR:CD2	1:A:156:TYR:N	2.48	0.81
1:A:72:LEU:N	1:A:75:ASP:OD2	2.14	0.80
2:L:53:SER:HB2	2:L:74:THR:HG21	1.64	0.80
3:H:161:MET:HA	3:H:210:PRO:HA	1.62	0.80
2:L:70:TRP:HZ3	2:L:85:PHE:CE2	2.00	0.79
1:A:56:ASP:OD1	1:A:57:ASP:N	2.15	0.79
3:H:157:GLN:HE21	3:H:158:THR:HG23	1.49	0.78
1:A:70:GLN:HG3	1:A:75:ASP:O	1.84	0.77
2:L:172:LYS:HE2	2:L:175:GLY:N	1.98	0.77
2:L:41:VAL:HG12	2:L:42:THR:H	1.48	0.77
1:A:192:ARG:O	1:A:196:VAL:HG22	1.84	0.77
2:L:50:SER:HB2	2:L:92:THR:HG22	1.65	0.77
2:L:33:MET:HG3	2:L:127:LEU:HD12	1.68	0.76
2:L:51:VAL:HG12	2:L:52:SER:O	1.86	0.76
1:A:203:GLU:O	1:A:204:PHE:HB2	1.86	0.75
2:L:208:GLU:OE1	2:L:212:HIS:ND1	2.20	0.74
1:A:154:ASP:H	1:A:155:LYS:HB3	1.53	0.74
2:L:117:TYR:HE1	3:H:77:ASN:HD21	1.36	0.74
2:L:131:ARG:NH1	2:L:132:ALA:O	2.21	0.73
1:A:210:GLU:HG2	1:A:264:LYS:HG2	1.69	0.73
1:A:41:SER:OG	1:A:209:TYR:O	2.03	0.73
2:L:85:PHE:CE1	2:L:98:ILE:HG12	2.24	0.73
1:A:70:GLN:O	1:A:125:LYS:NZ	2.21	0.72
2:L:104:GLU:O	2:L:104:GLU:HG3	1.87	0.72
2:L:211:ARG:NH1	2:L:211:ARG:HB2	2.04	0.71
2:L:113:GLN:NE2	2:L:113:GLN:O	2.24	0.71
2:L:159:LEU:O	2:L:162:PHE:CE1	2.43	0.71
2:L:40:THR:HB	2:L:99:SER:HA	1.71	0.71
1:A:194:TYR:O	1:A:198:ASN:ND2	2.24	0.71
3:H:210:PRO:HB2	3:H:213:PRO:HD2	1.73	0.70
1:A:48:MET:HB3	1:A:204:PHE:H	1.56	0.70
3:H:78:TYR:CE1	3:H:88:ILE:HG13	2.22	0.70
1:A:200:LYS:HD2	1:A:200:LYS:N	2.07	0.70
2:L:55:TYR:HE1	3:H:122:ARG:HB2	1.55	0.69
2:L:46:ARG:HD3	5:L:308:HOH:O	1.92	0.69
3:H:66:TRP:CZ2	3:H:68:GLY:HA2	2.27	0.69
3:H:149:PRO:O	3:H:150:LEU:HD23	1.93	0.69
2:L:84:ARG:NH2	2:L:102:GLU:HB2	2.08	0.68
1:A:45:THR:O	1:A:45:THR:OG1	2.09	0.68

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:H:85:ARG:HB3	3:H:102:ASN:HB2	1.75	0.68
2:L:23:GLU:CB	2:L:118:PRO:HD2	2.23	0.68
2:L:82:PRO:HB2	2:L:84:ARG:HD3	1.74	0.68
2:L:172:LYS:HD2	2:L:216:THR:CG2	2.18	0.68
3:H:196:LEU:HD13	3:H:201:TYR:CE1	2.29	0.68
1:A:210:GLU:HG2	1:A:264:LYS:HA	1.75	0.68
1:A:213:TYR:HA	1:A:227:MET:HG3	1.74	0.68
2:L:55:TYR:CE1	2:L:115:ILE:HD11	2.29	0.67
1:A:154:ASP:N	1:A:155:LYS:HB3	2.09	0.67
2:L:55:TYR:CG	2:L:115:ILE:HD11	2.29	0.67
2:L:193:ASP:OD2	2:L:195:THR:HG22	1.94	0.67
3:H:212:SER:HB2	3:H:213:PRO:HD3	1.76	0.67
1:A:75:ASP:HB3	1:A:92:ARG:HH21	1.59	0.67
2:L:213:ASN:HA	2:L:234:ARG:HH21	1.61	0.66
1:A:187:LEU:HD11	1:A:250:VAL:HG21	1.75	0.66
1:A:154:ASP:HB2	1:A:155:LYS:HB3	1.76	0.66
2:L:131:ARG:HG3	2:L:132:ALA:N	2.10	0.66
2:L:131:ARG:HG3	2:L:132:ALA:O	1.94	0.66
2:L:208:GLU:O	2:L:211:ARG:HD3	1.95	0.66
3:H:50:ASP:HB3	3:H:51:PHE:CE2	2.31	0.66
1:A:100:LEU:H	1:A:100:LEU:HD23	1.59	0.66
3:H:71:ASN:OD1	3:H:72:TYR:N	2.29	0.66
2:L:209:TYR:CD1	2:L:215:TYR:HE2	2.13	0.66
1:A:66:LYS:NZ	1:A:106:ASP:OD2	2.28	0.66
1:A:52:LYS:HB2	1:A:202:TYR:HB3	1.77	0.66
3:H:50:ASP:HB3	3:H:51:PHE:CD2	2.30	0.65
2:L:113:GLN:NE2	2:L:113:GLN:C	2.48	0.65
1:A:102:ASP:O	1:A:103:LYS:C	2.35	0.65
2:L:211:ARG:O	2:L:212:HIS:CD2	2.49	0.65
2:L:54:THR:O	2:L:73:SER:HA	1.96	0.65
1:A:47:LEU:H	1:A:234:LYS:HE2	1.62	0.64
2:L:145:SER:HA	2:L:148:LEU:HD12	1.78	0.64
1:A:34:LYS:H	1:A:35:PRO:CD	2.11	0.64
2:L:206:LYS:C	2:L:208:GLU:H	2.00	0.64
1:A:54:LEU:HD21	1:A:237:GLN:NE2	2.12	0.64
2:L:172:LYS:CD	2:L:216:THR:HG22	2.21	0.64
3:H:231:LYS:HE2	3:H:232:VAL:H	1.60	0.64
1:A:95:PHE:HB3	1:A:100:LEU:HD12	1.79	0.64
1:A:171:LEU:HD23	1:A:172:SER:N	2.13	0.63
3:H:186:SER:O	3:H:188:GLY:N	2.31	0.63
2:L:117:TYR:HE1	3:H:77:ASN:ND2	1.96	0.63
2:L:159:LEU:N	2:L:159:LEU:HD12	2.14	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:L:236:GLU:CB	3:H:153:GLY:HA2	2.29	0.63
3:H:71:ASN:OD1	3:H:73:SER:N	2.29	0.63
2:L:70:TRP:CZ3	2:L:85:PHE:CE2	2.87	0.63
3:H:109:THR:HG23	3:H:136:THR:HA	1.81	0.63
2:L:101:VAL:HG23	2:L:101:VAL:O	1.99	0.62
1:A:62:ALA:HB2	1:A:80:ILE:HD12	1.82	0.62
3:H:66:TRP:HH2	3:H:77:ASN:HD22	1.48	0.62
2:L:209:TYR:HA	2:L:215:TYR:OH	1.99	0.61
1:A:154:ASP:CA	1:A:155:LYS:HB3	2.30	0.61
1:A:101:ALA:O	1:A:105:LYS:HB2	2.01	0.61
1:A:161:VAL:N	1:A:173:PHE:O	2.30	0.61
1:A:39:HIS:O	1:A:211:THR:HG22	2.00	0.61
1:A:217:ILE:HG23	1:A:222:SER:HB3	1.83	0.61
2:L:153:ALA:N	2:L:204:LEU:O	2.30	0.61
1:A:172:SER:O	1:A:173:PHE:HB3	2.01	0.60
2:L:228:ILE:HD12	2:L:228:ILE:H	1.66	0.60
1:A:103:LYS:HD3	1:A:104:TYR:CE1	2.37	0.60
3:H:38:LEU:HD12	3:H:99:LEU:HD23	1.84	0.60
2:L:68:LYS:HZ3	2:L:68:LYS:HB2	1.67	0.60
1:A:33:PRO:HB3	1:A:224:TRP:CZ2	2.36	0.60
1:A:99:ASP:O	1:A:100:LEU:C	2.37	0.60
2:L:119:LEU:HD11	3:H:126:PHE:HZ	1.67	0.60
3:H:145:PRO:HD3	3:H:225:HIS:ND1	2.15	0.60
2:L:159:LEU:HD21	2:L:219:ALA:HB2	1.84	0.59
2:L:164:PRO:HD2	2:L:221:HIS:NE2	2.17	0.59
1:A:213:TYR:CE1	1:A:260:TYR:HB2	2.38	0.59
3:H:177:THR:HG22	3:H:224:ALA:HB3	1.84	0.59
3:H:82:LEU:O	3:H:83:LYS:C	2.41	0.59
2:L:211:ARG:HD3	2:L:211:ARG:H	1.67	0.59
3:H:59:PHE:HB3	3:H:60:PRO:HD2	1.84	0.59
3:H:179:THR:HB	3:H:183:GLY:HA2	1.85	0.59
1:A:165:GLU:HA	1:A:261:LEU:HB2	1.84	0.59
1:A:75:ASP:HB2	1:A:92:ARG:HE	1.67	0.59
2:L:46:ARG:HG2	2:L:46:ARG:HH11	1.67	0.59
1:A:154:ASP:CB	1:A:155:LYS:HB3	2.33	0.58
1:A:161:VAL:HG13	1:A:257:ILE:HG22	1.84	0.58
1:A:191:THR:HG21	1:A:257:ILE:HD13	1.85	0.58
2:L:228:ILE:N	2:L:228:ILE:HD12	2.18	0.58
1:A:157:ARG:HH11	1:A:252:SER:HB2	1.67	0.58
2:L:70:TRP:HZ3	2:L:85:PHE:CD2	2.20	0.58
1:A:56:ASP:CG	1:A:57:ASP:H	2.07	0.58
1:A:66:LYS:HD2	1:A:106:ASP:CA	2.32	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:151:ASN:OD1	1:A:180:LYS:HB2	2.04	0.58
2:L:182:VAL:HA	2:L:201:THR:O	2.03	0.58
3:H:160:SER:HB3	5:H:413:HOH:O	2.03	0.58
2:L:55:TYR:CD2	2:L:115:ILE:HG13	2.39	0.58
1:A:48:MET:N	1:A:204:PHE:O	2.23	0.58
1:A:152:GLN:HE21	1:A:152:GLN:N	2.02	0.57
2:L:69:LEU:O	2:L:70:TRP:CD1	2.57	0.57
2:L:73:SER:O	2:L:74:THR:HG22	2.03	0.57
3:H:160:SER:O	3:H:210:PRO:HA	2.04	0.57
1:A:119:GLN:NE2	1:A:236:ASP:OD1	2.23	0.57
1:A:88:TYR:HB3	1:A:117:TYR:CE1	2.33	0.57
3:H:166:CYS:HB2	3:H:180:TRP:CH2	2.40	0.57
2:L:208:GLU:O	2:L:209:TYR:C	2.43	0.57
1:A:183:THR:O	1:A:186:GLU:HB3	2.05	0.57
3:H:239:ARG:HD3	3:H:239:ARG:N	2.20	0.57
3:H:82:LEU:O	3:H:84:SER:N	2.38	0.57
2:L:119:LEU:HD11	3:H:126:PHE:CZ	2.40	0.56
3:H:171:TYR:O	3:H:172:PHE:HB2	2.05	0.56
1:A:74:PHE:N	1:A:74:PHE:CD2	2.74	0.56
3:H:59:PHE:HB3	3:H:60:PRO:CD	2.35	0.56
2:L:179:GLN:HA	2:L:179:GLN:OE1	2.05	0.56
1:A:98:LYS:NZ	3:H:117:GLU:OE2	2.39	0.56
3:H:186:SER:O	3:H:187:SER:C	2.45	0.55
3:H:42:VAL:HG21	3:H:47:LEU:HD21	1.86	0.55
3:H:52:ALA:HB3	3:H:117:GLU:CD	2.27	0.55
1:A:154:ASP:HB2	1:A:155:LYS:CB	2.36	0.55
2:L:235:ASN:HA	5:L:343:HOH:O	2.06	0.55
1:A:171:LEU:HD23	1:A:172:SER:O	2.06	0.55
3:H:213:PRO:HA	3:H:217:GLU:OE1	2.06	0.55
3:H:66:TRP:HH2	3:H:77:ASN:ND2	2.05	0.55
3:H:106:THR:C	3:H:108:ASP:H	2.09	0.55
3:H:26:GLY:HA3	3:H:38:LEU:HD23	1.87	0.55
3:H:70:ILE:HD11	3:H:74:GLY:HA2	1.88	0.55
1:A:168:LYS:HB2	1:A:170:LEU:HG	1.88	0.55
2:L:172:LYS:HZ1	2:L:214:SER:HG	1.54	0.55
1:A:253:LYS:O	1:A:255:VAL:N	2.37	0.55
2:L:172:LYS:HE2	2:L:175:GLY:CA	2.37	0.55
3:H:240:ASP:O	3:H:241:CYS:HB2	2.08	0.55
2:L:23:GLU:HB2	2:L:118:PRO:CD	2.32	0.55
1:A:69:ASP:HB3	1:A:77:ILE:HD12	1.87	0.54
2:L:172:LYS:C	2:L:172:LYS:HD3	2.28	0.54
3:H:194:ALA:HB2	3:H:203:LEU:HB2	1.89	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:182:VAL:HG13	1:A:250:VAL:HG23	1.90	0.54
2:L:84:ARG:HH22	2:L:102:GLU:HB2	1.71	0.54
3:H:169:LYS:HA	3:H:202:THR:HG23	1.89	0.54
2:L:128:GLU:HB3	2:L:189:GLN:NE2	2.22	0.54
2:L:30:PRO:O	2:L:125:THR:HG23	2.07	0.54
2:L:41:VAL:HG12	2:L:42:THR:N	2.21	0.54
3:H:164:LEU:HD11	3:H:219:VAL:HG11	1.90	0.54
3:H:71:ASN:CG	3:H:72:TYR:N	2.61	0.54
3:H:171:TYR:CZ	3:H:201:TYR:HB2	2.43	0.54
2:L:236:GLU:HG3	3:H:153:GLY:HA2	1.89	0.54
2:L:151:GLY:O	2:L:152:GLY:O	2.25	0.54
2:L:70:TRP:CZ2	2:L:81:VAL:HG12	2.42	0.54
3:H:129:TRP:CD1	3:H:129:TRP:N	2.76	0.54
2:L:135:ALA:HA	2:L:223:THR:OG1	2.08	0.53
2:L:208:GLU:O	2:L:210:GLU:N	2.41	0.53
3:H:71:ASN:C	3:H:71:ASN:OD1	2.47	0.53
2:L:50:SER:CB	2:L:92:THR:HG22	2.37	0.53
2:L:193:ASP:OD2	2:L:195:THR:CG2	2.57	0.53
3:H:141:LYS:HE2	3:H:142:THR:O	2.08	0.53
2:L:158:PHE:C	2:L:159:LEU:HD12	2.29	0.53
2:L:161:ASN:HD22	2:L:195:THR:HG21	1.73	0.53
2:L:53:SER:HB2	2:L:74:THR:CG2	2.36	0.53
1:A:244:TYR:C	1:A:246:ASP:H	2.12	0.53
1:A:60:VAL:O	1:A:112:PHE:HA	2.09	0.53
2:L:129:LEU:CD2	2:L:129:LEU:N	2.71	0.53
1:A:63:ILE:HD12	1:A:63:ILE:N	2.23	0.53
2:L:69:LEU:O	2:L:70:TRP:HD1	1.91	0.52
1:A:165:GLU:C	1:A:167:GLY:H	2.13	0.52
2:L:84:ARG:HH22	2:L:102:GLU:CB	2.21	0.52
2:L:190:ASP:HB2	2:L:193:ASP:OD1	2.08	0.52
2:L:43:MET:HE2	2:L:125:THR:CG2	2.40	0.52
2:L:37:PRO:HA	2:L:101:VAL:O	2.10	0.52
3:H:212:SER:CB	3:H:213:PRO:HD3	2.38	0.52
1:A:202:TYR:OH	1:A:227:MET:O	2.26	0.52
3:H:197:GLN:O	3:H:198:SER:C	2.48	0.52
2:L:103:ALA:HA	2:L:129:LEU:HD11	1.90	0.52
2:L:141:PHE:HB3	2:L:142:PRO:HD2	1.91	0.52
2:L:186:TRP:CD1	2:L:198:MET:HB2	2.45	0.52
1:A:236:ASP:OD2	1:A:239:LYS:HB2	2.10	0.52
2:L:161:ASN:HB3	2:L:195:THR:HG21	1.91	0.52
2:L:171:TRP:CD1	2:L:182:VAL:HG11	2.45	0.51
3:H:222:ASN:HB3	3:H:233:ASP:OD1	2.10	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:H:58:GLN:HG3	3:H:62:ASN:O	2.10	0.51
2:L:123:GLY:O	2:L:124:GLY:O	2.27	0.51
1:A:194:TYR:C	1:A:198:ASN:HD21	2.13	0.51
1:A:44:PHE:CZ	1:A:46:GLY:HA3	2.45	0.51
3:H:179:THR:OG1	3:H:183:GLY:N	2.44	0.51
1:A:42:SER:HB3	1:A:264:LYS:CD	2.40	0.51
1:A:182:VAL:HG13	1:A:250:VAL:CG2	2.41	0.51
3:H:161:MET:HA	3:H:210:PRO:CA	2.36	0.51
3:H:120:TYR:O	3:H:123:ALA:HB3	2.10	0.51
1:A:195:LEU:O	1:A:196:VAL:C	2.50	0.51
1:A:203:GLU:O	1:A:204:PHE:CB	2.56	0.51
2:L:213:ASN:HA	2:L:234:ARG:NH2	2.26	0.51
1:A:100:LEU:N	1:A:100:LEU:HD23	2.25	0.51
1:A:201:LEU:HD21	1:A:227:MET:HE2	1.92	0.51
1:A:39:HIS:HB2	1:A:228:MET:HB2	1.93	0.51
1:A:65:VAL:CG1	5:A:309:HOH:O	2.59	0.51
3:H:169:LYS:HG3	3:H:202:THR:HG23	1.92	0.51
3:H:178:VAL:HG22	3:H:179:THR:N	2.26	0.51
2:L:123:GLY:O	5:L:341:HOH:O	2.19	0.51
2:L:173:ILE:O	2:L:214:SER:O	2.29	0.51
2:L:73:SER:HB2	2:L:76:ASN:OD1	2.11	0.51
1:A:34:LYS:N	1:A:35:PRO:CD	2.73	0.50
3:H:231:LYS:NZ	3:H:233:ASP:OD1	2.44	0.50
1:A:40:LYS:HD2	1:A:43:LYS:HD2	1.93	0.50
3:H:133:THR:O	3:H:133:THR:HG23	2.12	0.50
2:L:51:VAL:HG12	2:L:52:SER:N	2.26	0.50
1:A:242:MET:HG2	1:A:242:MET:O	2.11	0.50
1:A:182:VAL:CG1	1:A:250:VAL:HG23	2.42	0.50
1:A:71:PHE:N	1:A:75:ASP:OD2	2.43	0.50
2:L:181:GLY:O	2:L:202:LEU:HD12	2.12	0.50
1:A:154:ASP:N	1:A:155:LYS:O	2.45	0.50
2:L:195:THR:HG23	2:L:196:TYR:N	2.27	0.50
2:L:159:LEU:N	2:L:159:LEU:CD1	2.74	0.50
1:A:52:LYS:HB2	1:A:202:TYR:CB	2.42	0.50
2:L:28:GLN:HE22	2:L:124:GLY:CA	2.24	0.50
2:L:142:PRO:HG3	2:L:236:GLU:CD	2.33	0.50
1:A:69:ASP:OD1	1:A:70:GLN:N	2.43	0.50
2:L:193:ASP:CG	2:L:195:THR:HG22	2.33	0.50
2:L:209:TYR:CD1	2:L:215:TYR:CE2	2.99	0.50
1:A:57:ASP:HA	1:A:193:HIS:NE2	2.27	0.49
2:L:114:TYR:CZ	2:L:119:LEU:CD1	2.90	0.49
1:A:263:THR:HG22	1:A:264:LYS:N	2.28	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:H:217:GLU:CD	3:H:217:GLU:H	2.15	0.49
1:A:161:VAL:O	1:A:172:SER:HA	2.13	0.49
3:H:161:MET:HG2	3:H:210:PRO:N	2.27	0.49
2:L:142:PRO:HG3	2:L:236:GLU:OE2	2.12	0.49
2:L:166:ASP:OD1	5:L:304:HOH:O	2.18	0.49
2:L:236:GLU:CG	3:H:153:GLY:HA2	2.42	0.49
1:A:234:LYS:CD	1:A:235:PHE:N	2.59	0.49
1:A:187:LEU:CD1	1:A:250:VAL:HG21	2.41	0.49
3:H:111:THR:HG23	3:H:133:THR:H	1.77	0.49
2:L:186:TRP:HE1	2:L:198:MET:CE	2.25	0.49
2:L:209:TYR:CE1	2:L:215:TYR:HE2	2.30	0.49
1:A:88:TYR:CB	1:A:117:TYR:HE1	2.22	0.49
3:H:200:LEU:HD12	3:H:200:LEU:N	2.27	0.49
2:L:163:TYR:CD2	2:L:164:PRO:HA	2.47	0.49
2:L:172:LYS:HB3	2:L:216:THR:HG22	1.95	0.49
2:L:178:ARG:NE	2:L:178:ARG:HA	2.27	0.49
1:A:88:TYR:N	1:A:88:TYR:CD2	2.81	0.49
3:H:105:THR:O	3:H:108:ASP:HB2	2.13	0.49
2:L:143:PRO:O	2:L:144:SER:OG	2.24	0.49
1:A:96:LYS:HD2	1:A:245:ASN:ND2	2.27	0.48
3:H:144:PRO:HG3	3:H:228:SER:HB2	1.94	0.48
3:H:58:GLN:HB2	3:H:64:LEU:CD2	2.43	0.48
2:L:70:TRP:CD2	2:L:81:VAL:HG11	2.48	0.48
1:A:161:VAL:HG21	1:A:191:THR:HG22	1.95	0.48
3:H:195:VAL:HG12	3:H:196:LEU:H	1.77	0.48
3:H:21:GLN:O	3:H:22:LEU:HD12	2.13	0.48
2:L:206:LYS:C	2:L:208:GLU:N	2.66	0.48
2:L:43:MET:HE2	2:L:125:THR:HG21	1.95	0.48
1:A:121:TYR:CG	1:A:122:PHE:N	2.81	0.48
1:A:155:LYS:C	1:A:156:TYR:HD2	2.16	0.48
1:A:188:ASP:OD1	1:A:214:ILE:HG21	2.13	0.48
2:L:172:LYS:HE2	2:L:175:GLY:HA2	1.96	0.48
3:H:169:LYS:HG3	3:H:202:THR:CG2	2.43	0.48
3:H:66:TRP:CE2	3:H:68:GLY:HA2	2.48	0.48
1:A:39:HIS:HB2	1:A:228:MET:CB	2.43	0.48
3:H:161:MET:HB3	3:H:208:THR:HG22	1.95	0.48
1:A:103:LYS:HD3	1:A:104:TYR:CZ	2.49	0.48
3:H:42:VAL:HG21	3:H:47:LEU:CD2	2.43	0.48
2:L:131:ARG:HG2	2:L:163:TYR:CG	2.49	0.48
2:L:193:ASP:O	2:L:193:ASP:CG	2.51	0.48
1:A:87:ASN:O	1:A:137:ARG:HG2	2.14	0.47
1:A:240:TYR:O	1:A:243:MET:HG2	2.14	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:H:161:MET:HG2	3:H:210:PRO:CD	2.43	0.47
2:L:113:GLN:HG3	2:L:120:THR:HB	1.95	0.47
2:L:133:ASP:HB3	2:L:223:THR:HG22	1.96	0.47
2:L:215:TYR:HB2	2:L:232:PHE:CD2	2.49	0.47
1:A:217:ILE:HD12	1:A:217:ILE:N	2.29	0.47
2:L:101:VAL:O	2:L:101:VAL:CG2	2.62	0.47
2:L:145:SER:O	2:L:148:LEU:HB2	2.14	0.47
2:L:41:VAL:O	2:L:97:THR:HG23	2.14	0.47
1:A:195:LEU:N	1:A:195:LEU:HD23	2.29	0.47
2:L:126:LYS:HB2	2:L:126:LYS:HE3	1.70	0.47
1:A:41:SER:CB	1:A:207:SER:HB3	2.45	0.47
1:A:39:HIS:ND1	1:A:228:MET:O	2.33	0.47
3:H:145:PRO:HB3	3:H:171:TYR:HB3	1.97	0.47
1:A:165:GLU:O	1:A:166:ASP:HB3	2.14	0.47
1:A:244:TYR:C	1:A:246:ASP:N	2.68	0.47
3:H:35:SER:HA	3:H:101:LEU:O	2.14	0.47
3:H:171:TYR:CE2	3:H:201:TYR:HB2	2.50	0.47
2:L:60:GLN:HG3	2:L:109:TYR:CE1	2.49	0.47
2:L:43:MET:HG2	2:L:96:LEU:HB3	1.96	0.47
1:A:215:LYS:HE2	1:A:222:SER:HB2	1.96	0.47
2:L:141:PHE:CD2	2:L:156:VAL:HG13	2.49	0.47
2:L:46:ARG:HG2	2:L:46:ARG:NH1	2.29	0.47
3:H:215:PRO:HB3	3:H:238:PRO:HG3	1.97	0.47
2:L:130:LYS:HA	2:L:163:TYR:OH	2.15	0.47
2:L:186:TRP:HE1	2:L:198:MET:HE2	1.80	0.47
1:A:204:PHE:C	1:A:204:PHE:HD2	2.19	0.46
2:L:116:ASN:HD22	2:L:116:ASN:HA	1.52	0.46
2:L:163:TYR:CG	2:L:164:PRO:HA	2.51	0.46
1:A:193:HIS:O	1:A:197:LYS:HG2	2.15	0.46
1:A:251:ASP:O	1:A:255:VAL:HG12	2.16	0.46
3:H:71:ASN:CG	3:H:72:TYR:H	2.17	0.46
2:L:112:GLN:HA	2:L:120:THR:O	2.15	0.46
2:L:68:LYS:HZ2	2:L:68:LYS:HB2	1.78	0.46
3:H:26:GLY:HA3	3:H:38:LEU:CD2	2.44	0.46
1:A:167:GLY:C	1:A:168:LYS:HD3	2.36	0.46
1:A:204:PHE:CD2	1:A:204:PHE:C	2.89	0.46
3:H:209:VAL:CG2	3:H:213:PRO:HB2	2.46	0.46
2:L:152:GLY:HA2	2:L:205:THR:HA	1.98	0.46
2:L:172:LYS:NZ	2:L:173:ILE:O	2.41	0.46
1:A:66:LYS:HE3	1:A:66:LYS:HB3	1.80	0.46
3:H:101:LEU:HG	3:H:104:VAL:HG12	1.97	0.46
2:L:138:VAL:HA	2:L:158:PHE:O	2.16	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:236:ASP:HB3	1:A:239:LYS:HB2	1.98	0.46
2:L:175:GLY:O	2:L:176:SER:C	2.54	0.46
2:L:193:ASP:C	2:L:195:THR:N	2.64	0.46
1:A:52:LYS:HG2	1:A:52:LYS:O	2.15	0.45
1:A:75:ASP:CB	1:A:92:ARG:HE	2.29	0.45
2:L:208:GLU:O	2:L:211:ARG:N	2.42	0.45
1:A:71:PHE:O	2:L:116:ASN:O	2.33	0.45
2:L:67:PRO:O	2:L:68:LYS:HG3	2.16	0.45
2:L:55:TYR:CE1	3:H:122:ARG:HB2	2.44	0.45
2:L:37:PRO:HG3	2:L:129:LEU:HD12	1.97	0.45
2:L:154:SER:HA	2:L:202:LEU:O	2.16	0.45
2:L:119:LEU:HD22	3:H:66:TRP:HB2	1.99	0.45
2:L:115:ILE:HD12	2:L:115:ILE:HG23	1.70	0.45
2:L:84:ARG:NH2	2:L:102:GLU:CB	2.79	0.45
1:A:253:LYS:HG3	1:A:254:ASP:OD1	2.17	0.45
3:H:30:VAL:HG11	3:H:104:VAL:HG21	1.98	0.45
3:H:157:GLN:HG2	3:H:158:THR:N	2.32	0.45
2:L:215:TYR:HB2	2:L:232:PHE:HD2	1.82	0.45
2:L:114:TYR:O	2:L:116:ASN:N	2.46	0.45
2:L:115:ILE:HD13	2:L:115:ILE:N	2.32	0.45
2:L:34:SER:HA	2:L:128:GLU:O	2.17	0.45
2:L:82:PRO:HB2	2:L:84:ARG:CD	2.44	0.45
3:H:32:PRO:O	3:H:33:SER:CB	2.65	0.45
1:A:216:PHE:O	1:A:222:SER:HA	2.17	0.45
1:A:44:PHE:CE1	1:A:235:PHE:HB2	2.52	0.44
3:H:97:PHE:CZ	3:H:114:CYS:HB2	2.52	0.44
2:L:102:GLU:HG2	2:L:103:ALA:H	1.81	0.44
2:L:70:TRP:HZ3	2:L:85:PHE:CZ	2.35	0.44
2:L:28:GLN:NE2	2:L:124:GLY:CA	2.80	0.44
2:L:32:ILE:HG21	2:L:128:GLU:OE2	2.16	0.44
2:L:188:ASP:O	2:L:189:GLN:C	2.56	0.44
2:L:173:ILE:HG23	2:L:215:TYR:CE1	2.52	0.44
3:H:132:GLY:O	3:H:133:THR:HB	2.18	0.44
3:H:237:VAL:HG23	3:H:238:PRO:HD2	1.98	0.44
1:A:137:ARG:NH1	1:A:137:ARG:HA	2.33	0.44
1:A:75:ASP:HB2	1:A:92:ARG:NE	2.31	0.44
2:L:237:CYS:SG	3:H:241:CYS:HA	2.58	0.44
1:A:228:MET:HA	1:A:229:PRO:HD3	1.63	0.44
1:A:74:PHE:H	1:A:74:PHE:HD2	1.66	0.44
3:H:145:PRO:HA	3:H:170:GLY:O	2.18	0.44
3:H:43:THR:C	3:H:45:TYR:H	2.21	0.44
3:H:217:GLU:CD	3:H:217:GLU:N	2.71	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:L:173:ILE:HD11	2:L:179:GLN:CG	2.46	0.44
1:A:38:LEU:HD13	1:A:211:THR:HB	1.99	0.44
2:L:134:ALA:C	2:L:223:THR:HG21	2.38	0.44
1:A:88:TYR:N	1:A:88:TYR:HD2	2.16	0.44
2:L:136:PRO:HA	2:L:162:PHE:HB3	2.00	0.44
1:A:146:THR:HG22	1:A:249:MET:SD	2.58	0.43
1:A:165:GLU:HB3	1:A:170:LEU:HD12	2.00	0.43
1:A:62:ALA:C	1:A:63:ILE:HD12	2.37	0.43
3:H:155:ALA:HA	3:H:157:GLN:CD	2.38	0.43
3:H:197:GLN:HE21	3:H:197:GLN:HB3	1.62	0.43
3:H:188:GLY:O	3:H:207:VAL:HA	2.17	0.43
1:A:152:GLN:HE21	1:A:152:GLN:CA	2.30	0.43
2:L:43:MET:SD	2:L:96:LEU:HD12	2.59	0.43
1:A:165:GLU:O	1:A:167:GLY:N	2.46	0.43
1:A:236:ASP:OD2	1:A:239:LYS:HD3	2.18	0.43
1:A:253:LYS:C	1:A:255:VAL:H	2.19	0.43
3:H:171:TYR:HB2	3:H:225:HIS:CE1	2.54	0.43
3:H:83:LYS:O	3:H:86:ILE:HG22	2.19	0.43
1:A:219:ASN:H	1:A:219:ASN:ND2	2.16	0.43
2:L:48:THR:O	2:L:49:SER:C	2.56	0.43
1:A:72:LEU:CD2	2:L:116:ASN:ND2	2.81	0.43
3:H:212:SER:CB	3:H:213:PRO:CD	2.96	0.43
2:L:28:GLN:OE1	2:L:111:CYS:SG	2.76	0.43
1:A:75:ASP:CB	1:A:92:ARG:HH21	2.29	0.43
2:L:114:TYR:CE2	2:L:119:LEU:HD12	2.53	0.43
1:A:210:GLU:HG2	1:A:264:LYS:CA	2.44	0.43
1:A:96:LYS:HD2	1:A:245:ASN:CG	2.39	0.43
3:H:151:ALA:HB3	3:H:239:ARG:NE	2.34	0.43
3:H:41:THR:HA	3:H:96:GLN:HB3	2.01	0.43
2:L:59:TYR:CD1	2:L:69:LEU:HA	2.53	0.43
3:H:189:VAL:HG12	3:H:190:HIS:N	2.34	0.43
2:L:119:LEU:HD23	2:L:119:LEU:C	2.39	0.42
1:A:154:ASP:H	1:A:155:LYS:CB	2.26	0.42
1:A:159:ILE:O	1:A:174:ASP:HA	2.19	0.42
1:A:212:GLY:HA2	1:A:260:TYR:O	2.19	0.42
2:L:147:GLN:O	2:L:151:GLY:O	2.37	0.42
2:L:141:PHE:HD2	2:L:156:VAL:HG13	1.84	0.42
1:A:186:GLU:O	1:A:190:LEU:HG	2.20	0.42
3:H:143:THR:HA	3:H:144:PRO:HD3	1.88	0.42
2:L:142:PRO:HA	2:L:143:PRO:HD3	1.93	0.42
3:H:169:LYS:CG	3:H:202:THR:HG23	2.49	0.42
3:H:36:LEU:HD11	3:H:38:LEU:HD11	2.01	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:L:171:TRP:CH2	2:L:217:CYS:HB3	2.55	0.42
2:L:161:ASN:N	2:L:196:TYR:O	2.53	0.42
2:L:77:LEU:HB3	2:L:81:VAL:HG23	2.02	0.42
1:A:200:LYS:O	1:A:201:LEU:C	2.57	0.42
1:A:250:VAL:HG23	1:A:251:ASP:H	1.85	0.42
3:H:165:GLY:C	3:H:180:TRP:HH2	2.23	0.42
3:H:177:THR:CG2	3:H:224:ALA:HB3	2.50	0.42
2:L:114:TYR:CE2	2:L:119:LEU:CD1	3.02	0.42
1:A:42:SER:HB3	1:A:264:LYS:HE3	2.01	0.42
3:H:50:ASP:C	3:H:51:PHE:CD2	2.93	0.42
1:A:251:ASP:O	1:A:253:LYS:N	2.53	0.42
3:H:169:LYS:CB	3:H:202:THR:HG23	2.50	0.42
1:A:213:TYR:HB2	1:A:225:TYR:O	2.19	0.41
3:H:161:MET:CA	3:H:210:PRO:HA	2.42	0.41
2:L:55:TYR:CG	2:L:115:ILE:CG1	3.03	0.41
3:H:179:THR:HB	3:H:183:GLY:CA	2.49	0.41
3:H:36:LEU:HD22	3:H:36:LEU:C	2.40	0.41
2:L:112:GLN:HG3	2:L:121:PHE:CE1	2.55	0.41
2:L:89:GLY:HA3	2:L:94:TYR:HA	2.02	0.41
2:L:128:GLU:HB3	2:L:189:GLN:HE21	1.85	0.41
1:A:93:VAL:HG22	1:A:141:MET:HG3	2.01	0.41
3:H:106:THR:C	3:H:108:ASP:N	2.74	0.41
1:A:165:GLU:O	1:A:166:ASP:CB	2.69	0.41
1:A:30:GLN:HG2	1:A:223:PHE:HA	2.03	0.41
1:A:99:ASP:HA	1:A:102:ASP:OD2	2.20	0.41
3:H:197:GLN:HG3	3:H:202:THR:OG1	2.21	0.41
2:L:36:SER:HA	2:L:37:PRO:HD3	1.84	0.41
2:L:52:SER:OG	2:L:54:THR:HG23	2.21	0.41
2:L:82:PRO:O	2:L:84:ARG:N	2.54	0.41
1:A:204:PHE:O	1:A:204:PHE:HD2	2.03	0.41
1:A:34:LYS:H	1:A:35:PRO:HD3	1.85	0.41
2:L:190:ASP:CB	2:L:193:ASP:OD1	2.68	0.41
1:A:142:TYR:HB3	1:A:245:ASN:HA	2.02	0.41
1:A:164:PHE:CE2	1:A:169:ASN:HA	2.55	0.41
3:H:100:GLN:HB2	5:H:405:HOH:O	2.21	0.41
3:H:171:TYR:O	3:H:200:LEU:HA	2.21	0.41
3:H:37:SER:HA	3:H:99:LEU:O	2.20	0.41
2:L:163:TYR:CD2	2:L:164:PRO:CA	3.04	0.41
2:L:168:ASN:O	2:L:219:ALA:HA	2.20	0.41
1:A:41:SER:HB2	1:A:207:SER:CB	2.51	0.41
3:H:223:VAL:CG1	3:H:224:ALA:N	2.84	0.41
2:L:184:ASN:HA	2:L:199:SER:O	2.21	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:56:ASP:HA	1:A:197:LYS:NZ	2.36	0.41
3:H:143:THR:HG22	3:H:171:TYR:HA	2.03	0.41
3:H:97:PHE:HZ	3:H:114:CYS:HB2	1.86	0.40
2:L:117:TYR:HA	2:L:118:PRO:HA	1.66	0.40
2:L:82:PRO:CB	2:L:84:ARG:CD	2.99	0.40
1:A:109:VAL:HG12	1:A:147:GLU:HA	2.02	0.40
1:A:217:ILE:HG22	1:A:218:GLU:O	2.20	0.40
2:L:38:GLY:HA2	2:L:100:SER:OG	2.21	0.40
1:A:99:ASP:HB2	1:A:100:LEU:H	1.62	0.40
3:H:43:THR:O	3:H:45:TYR:N	2.54	0.40
2:L:218:GLU:HB2	2:L:229:VAL:HG12	2.03	0.40
1:A:69:ASP:HB3	1:A:77:ILE:HB	2.04	0.40
1:A:96:LYS:HA	3:H:122:ARG:NH2	2.36	0.40
3:H:196:LEU:HD13	3:H:201:TYR:CZ	2.56	0.40
3:H:40:CYS:O	3:H:96:GLN:HB2	2.21	0.40
3:H:42:VAL:CG2	3:H:47:LEU:HD21	2.51	0.40
2:L:204:LEU:HD23	2:L:208:GLU:CG	2.52	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	219/239 (92%)	158 (72%)	41 (19%)	20 (9%)	1	8
2	L	213/215 (99%)	161 (76%)	30 (14%)	22 (10%)	1	6
3	H	221/223 (99%)	177 (80%)	31 (14%)	13 (6%)	2	17
All	All	653/677 (96%)	496 (76%)	102 (16%)	55 (8%)	1	9

All (55) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	32	ASP
1	A	99	ASP

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Mol	Chain	Res	Type
1	A	100	LEU
1	A	169	ASN
1	A	245	ASN
1	A	251	ASP
1	A	254	ASP
2	L	50	SER
2	L	99	SER
2	L	124	GLY
2	L	136	PRO
2	L	137	THR
2	L	152	GLY
2	L	166	ASP
2	L	193	ASP
2	L	194	SER
3	H	34	GLN
3	H	107	GLU
3	H	154	SER
3	H	172	PHE
3	H	187	SER
1	A	89	ASP
1	A	102	ASP
1	A	103	LYS
1	A	173	PHE
1	A	204	PHE
1	A	252	SER
2	L	83	ALA
2	L	144	SER
2	L	176	SER
2	L	178	ARG
2	L	207	ASP
2	L	208	GLU
2	L	209	TYR
2	L	232	PHE
3	H	33	SER
3	H	133	THR
3	H	198	SER
3	H	214	ARG
1	A	200	LYS
1	A	219	ASN
2	L	119	LEU
2	L	192	LYS
3	H	83	LYS

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Mol	Chain	Res	Type
1	A	33	PRO
2	L	133	ASP
2	L	161	ASN
3	H	157	GLN
1	A	205	ASN
1	A	34	LYS
1	A	196	VAL
2	L	117	TYR
1	A	250	VAL
3	H	44	GLY
3	H	232	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	A	211/225 (94%)	166 (79%)	45 (21%)	1	7
2	L	188/188 (100%)	153 (81%)	35 (19%)	2	9
3	H	195/195 (100%)	158 (81%)	37 (19%)	2	9
All	All	594/608 (98%)	477 (80%)	117 (20%)	2	8

All (117) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	GLN
1	A	45	THR
1	A	58	ASN
1	A	65	VAL
1	A	68	ILE
1	A	74	PHE
1	A	75	ASP
1	A	85	LEU
1	A	88	TYR
1	A	94	GLU
1	A	96	LYS
1	A	99	ASP

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Mol	Chain	Res	Type
1	A	100	LEU
1	A	105	LYS
1	A	106	ASP
1	A	119	GLN
1	A	123	SER
1	A	127	ASN
1	A	137	ARG
1	A	147	GLU
1	A	149	ASN
1	A	152	GLN
1	A	156	TYR
1	A	160	THR
1	A	163	VAL
1	A	169	ASN
1	A	174	ASP
1	A	175	VAL
1	A	176	GLN
1	A	178	ASN
1	A	196	VAL
1	A	198	ASN
1	A	204	PHE
1	A	206	ASN
1	A	217	ILE
1	A	219	ASN
1	A	233	ASP
1	A	234	LYS
1	A	238	SER
1	A	239	LYS
1	A	249	MET
1	A	250	VAL
1	A	255	VAL
1	A	256	LYS
1	A	258	GLU
2	L	40	THR
2	L	43	MET
2	L	50	SER
2	L	52	SER
2	L	54	THR
2	L	66	SER
2	L	68	LYS
2	L	69	LEU
2	L	71	ILE

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Mol	Chain	Res	Type
2	L	84	ARG
2	L	92	THR
2	L	100	SER
2	L	104	GLU
2	L	111	CYS
2	L	112	GLN
2	L	113	GLN
2	L	114	TYR
2	L	116	ASN
2	L	128	GLU
2	L	129	LEU
2	L	145	SER
2	L	154	SER
2	L	161	ASN
2	L	165	LYS
2	L	179	GLN
2	L	182	VAL
2	L	188	ASP
2	L	189	GLN
2	L	195	THR
2	L	198	MET
2	L	211	ARG
2	L	218	GLU
2	L	233	ASN
2	L	234	ARG
2	L	236	GLU
3	H	31	ARG
3	H	36	LEU
3	H	37	SER
3	H	39	THR
3	H	49	SER
3	H	56	ILE
3	H	71	ASN
3	H	72	TYR
3	H	87	SER
3	H	88	ILE
3	H	89	THR
3	H	93	SER
3	H	94	LYS
3	H	99	LEU
3	H	103	SER
3	H	105	THR

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Mol	Chain	Res	Type
3	H	116	ARG
3	H	122	ARG
3	H	131	GLN
3	H	157	GLN
3	H	160	SER
3	H	184	SER
3	H	185	LEU
3	H	186	SER
3	H	190	HIS
3	H	193	PRO
3	H	197	GLN
3	H	198	SER
3	H	203	LEU
3	H	212	SER
3	H	214	ARG
3	H	220	THR
3	H	221	CYS
3	H	222	ASN
3	H	231	LYS
3	H	236	ILE
3	H	239	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	148	HIS
1	A	152	GLN
1	A	198	ASN
1	A	219	ASN
1	A	237	GLN
1	A	245	ASN
2	L	24	ASN
2	L	113	GLN
2	L	116	ASN
2	L	161	ASN
2	L	189	GLN
2	L	233	ASN
3	H	157	GLN
3	H	197	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

Mogul failed to run properly - this section will therefore be empty.

## 5.5 Carbohydrates ⓘ

Mogul failed to run properly - this section will therefore be empty.

## 5.6 Ligand geometry ⓘ

Mogul failed to run properly - this section will therefore be empty.

## 5.7 Other polymers ⓘ

Mogul failed to run properly - this section will therefore be empty.

## 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	225/239 (94%)	-0.12	0 100 100	18, 45, 69, 85	0
2	L	215/215 (100%)	-0.10	1 (0%) 88 39	13, 40, 80, 103	0
3	H	223/223 (100%)	-0.20	0 100 100	13, 32, 96, 117	0
All	All	663/677 (97%)	-0.14	1 (0%) 93 61	13, 40, 84, 117	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	L	237	CYS	2.2

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

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

### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	SO4	H	301	5/5	0.14	-0.87	30,31,38,44	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.