Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 01:34 PM GMT

PDB ID	:	3U36
Title	:	Crystal Structure of PG9 Fab
Authors	:	McLellan, J.S.; Kwong, P.D.
Deposited on	:	2011-10-04
Resolution	:	3.28 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
A user guide is available at
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

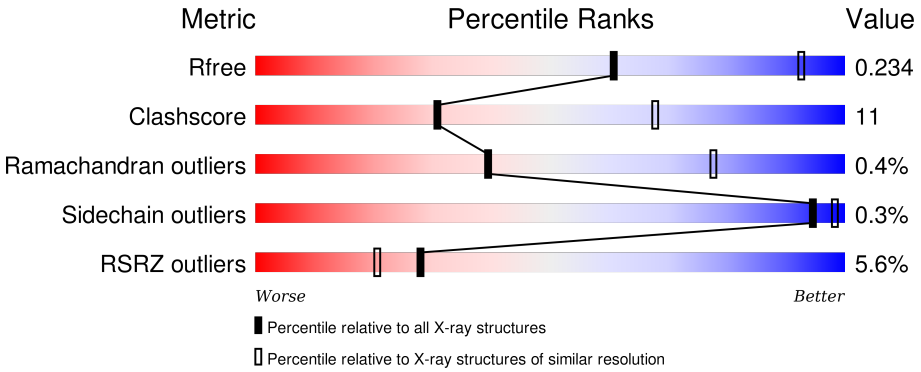
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.28 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	1756 (3.36-3.20)
Clashscore	102246	1941 (3.36-3.20)
Ramachandran outliers	100387	1905 (3.36-3.20)
Sidechain outliers	100360	1903 (3.36-3.20)
RSRZ outliers	91569	1764 (3.36-3.20)

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 >=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 <=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	248	7% 71% 16% 13%
1	C	248	5% 71% 17% 13%
1	E	248	4% 69% 18% 13%
1	H	248	8% 68% 19% 13%
2	B	216	6% 71% 25% • •

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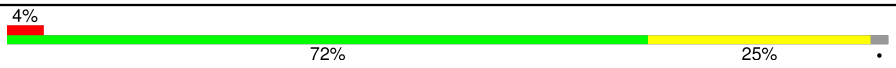
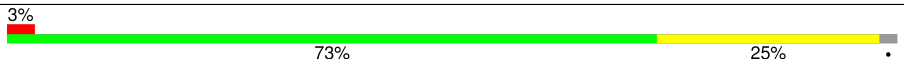
Mol	Chain	Length	Quality of chain
2	D	216	
2	F	216	
2	L	216	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12854 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.

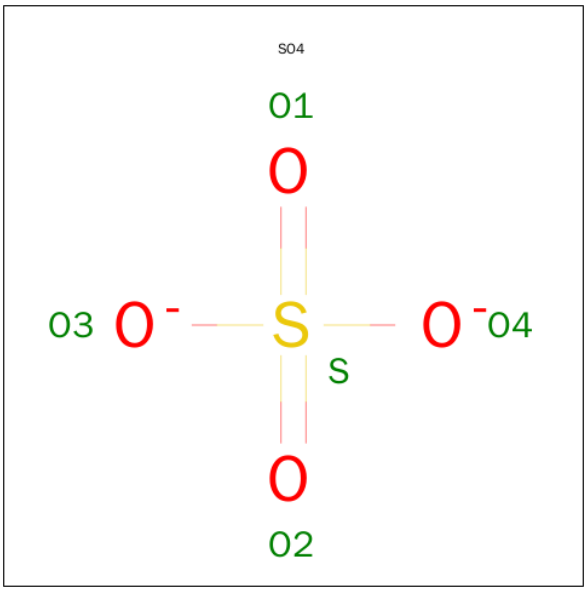
- Molecule 1 is a protein called PG9 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	216	Total	C	N	O	S	0	0	0
			1642	1037	279	319	7			
1	A	216	Total	C	N	O	S	0	0	0
			1642	1037	279	319	7			
1	C	216	Total	C	N	O	S	0	0	0
			1642	1037	279	319	7			
1	E	215	Total	C	N	O	S	0	0	0
			1634	1033	278	316	7			

- Molecule 2 is a protein called PG9 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	211	Total	C	N	O	S	0	0	0
			1566	974	267	321	4			
2	B	211	Total	C	N	O	S	0	0	0
			1566	974	267	321	4			
2	D	211	Total	C	N	O	S	0	0	0
			1566	974	267	321	4			
2	F	211	Total	C	N	O	S	0	0	0
			1566	974	267	321	4			

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



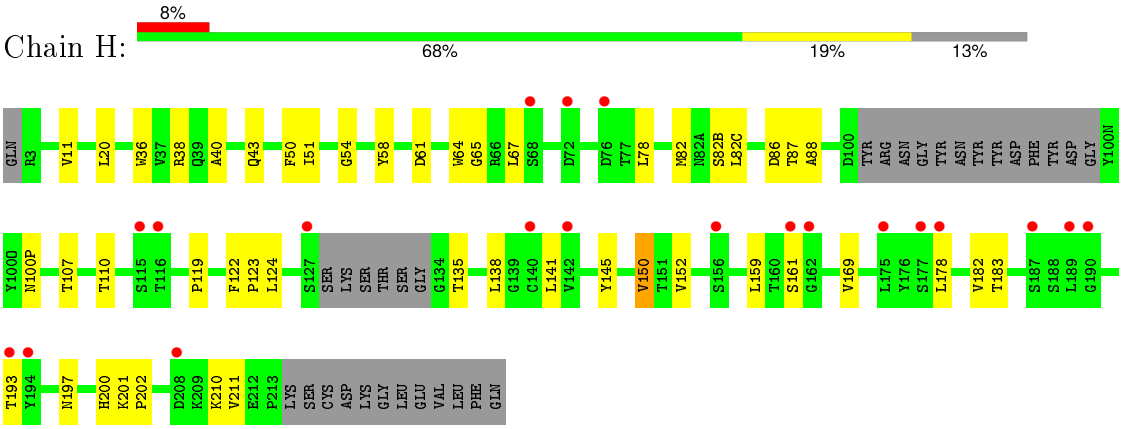
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total O S 5 4 1	0	0
3	L	1	Total O S 5 4 1	0	0
3	D	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	L	1	Total O S 5 4 1	0	0
3	F	1	Total O S 5 4 1	0	0

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 (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.

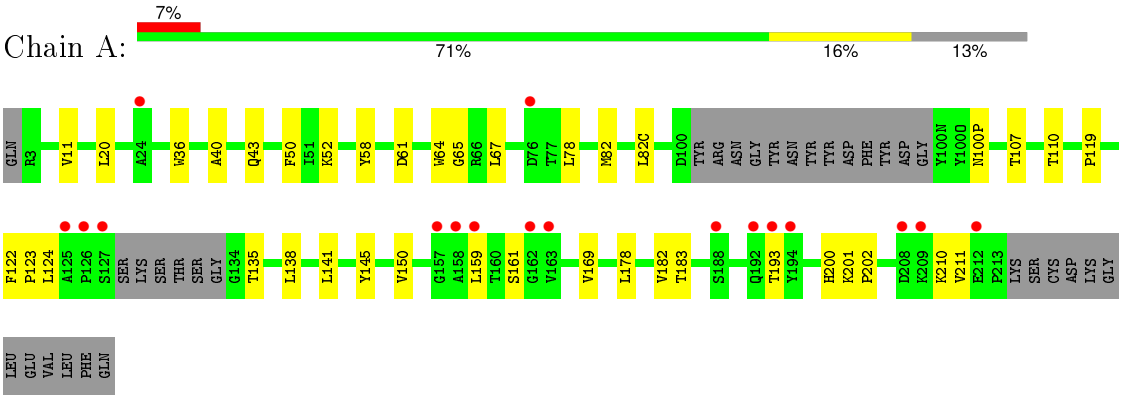
- Molecule 1: PG9 Fab heavy chain

Chain H:



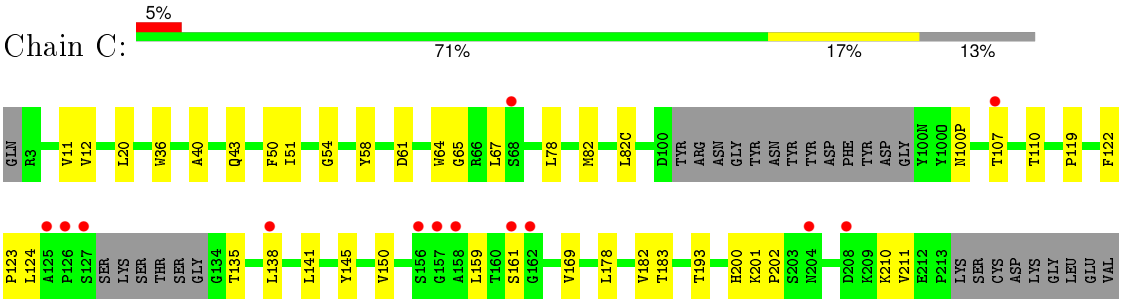
- Molecule 1: PG9 Fab heavy chain

Chain A:

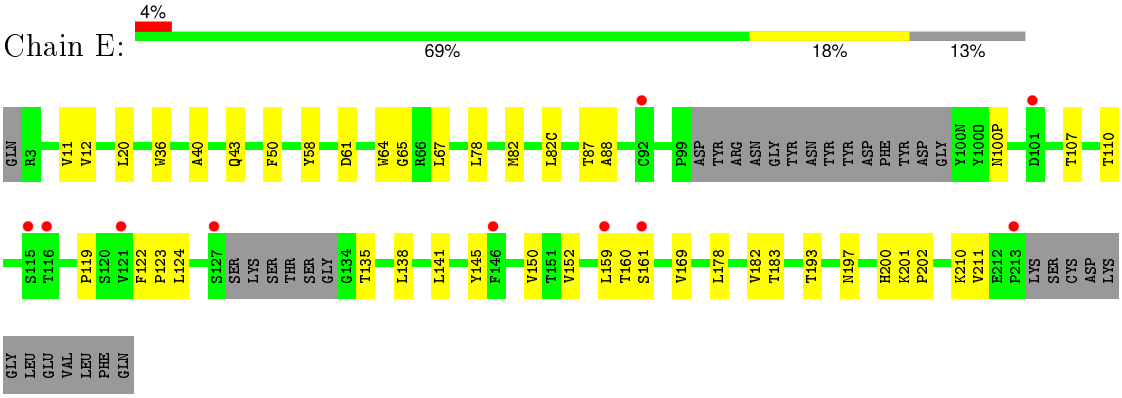


- Molecule 1: PG9 Fab heavy chain

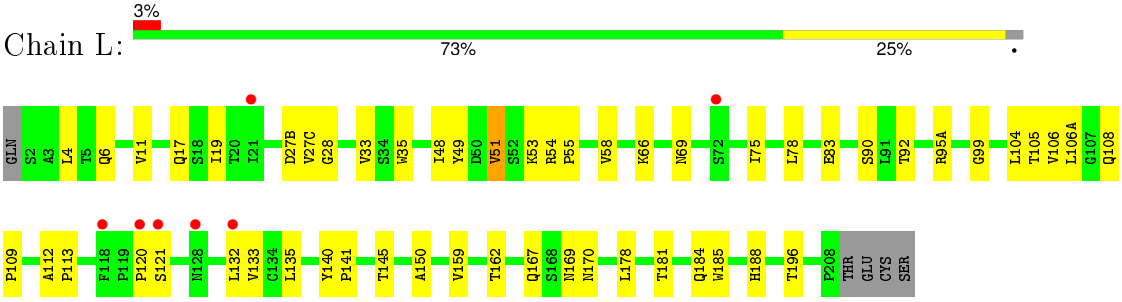
Chain C:



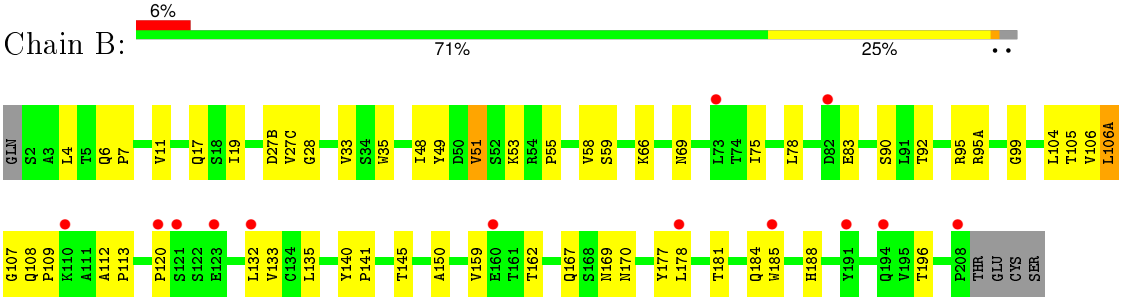
• Molecule 1: PG9 Fab heavy chain



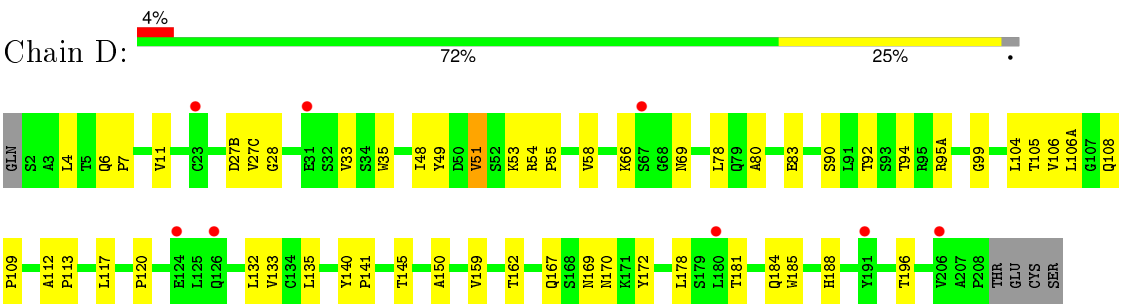
• Molecule 2: PG9 Fab light chain



• Molecule 2: PG9 Fab light chain

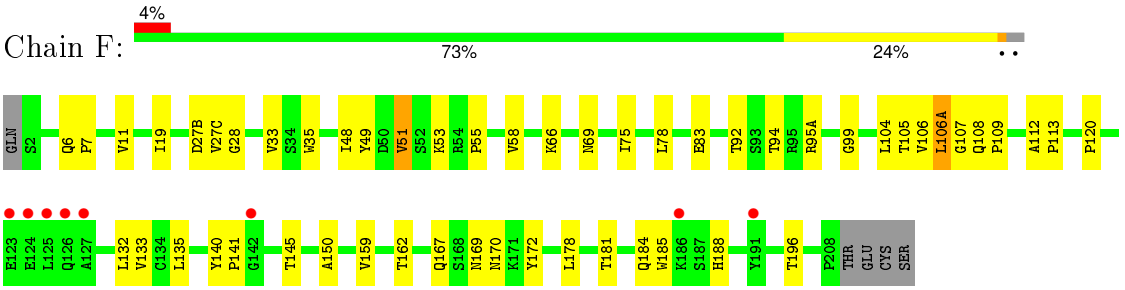


• Molecule 2: PG9 Fab light chain



• Molecule 2: PG9 Fab light chain

Chain F:


4%
73%
24%
GLN S2 Q6 P7 V11 I19 D27B V27C G28 V33 S34 W35 I48 Y49 D50 V51 S52 K53 H54 P55 V58 K66 N69 I75 L78 E83 T92 S93 T94 R95 R95A G99 L104 T105 V106 L106A G107 Q108 P109 A112 P113 P120
E123 E124 L125 Q126 A127 L132 V133 C134 L135 Y140 P141 G142 T145 A150 V159 T162 Q167 S168 N169 N170 K171 Y172 L178 T181 Q184 W185 K186 S187 H188 Y191 T196 P208 THR GLU CYS SER

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	71.59Å 81.04Å 91.69Å 107.23° 90.13° 107.96°	Depositor
Resolution (Å)	38.48 – 3.28 38.48 – 3.28	Depositor EDS
% Data completeness (in resolution range)	87.8 (38.48-3.28) 80.0 (38.48-3.28)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.44 (at 3.25Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, R_{free}	0.214 , 0.249 0.203 , 0.234	Depositor DCC
R_{free} test set	1267 reflections (5.07%)	DCC
Wilson B-factor (Å^2)	83.1	Xtriage
Anisotropy	0.603	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.27 , 66.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.30$	Xtriage
Outliers	0 of 25031 reflections	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	12854	wwPDB-VP
Average B, all atoms (Å^2)	125.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.99% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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

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	0.28	0/1684	0.46	0/2291
1	C	0.27	0/1684	0.45	0/2291
1	E	0.27	0/1676	0.46	0/2280
1	H	0.27	0/1684	0.45	0/2291
2	B	0.29	0/1601	0.54	0/2180
2	D	0.28	0/1601	0.51	0/2180
2	F	0.29	0/1601	0.54	0/2180
2	L	0.29	0/1601	0.51	0/2180
All	All	0.28	0/13132	0.49	0/17873

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	1
2	F	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	106(A)	LEU	Peptide
2	F	106(A)	LEU	Peptide

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	1642	0	1579	31	0
1	C	1642	0	1579	31	0
1	E	1634	0	1575	33	0
1	H	1642	0	1579	35	0
2	B	1566	0	1533	46	0
2	D	1566	0	1533	45	0
2	F	1566	0	1533	41	0
2	L	1566	0	1533	41	0
3	B	10	0	0	1	0
3	D	5	0	0	1	0
3	F	5	0	0	1	0
3	L	10	0	0	0	0
All	All	12854	0	12444	275	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 11.

All (275) 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:E:61:ASP:OD2	2:F:95(A):ARG:NH1	1.88	1.04
1:H:61:ASP:OD2	2:L:95(A):ARG:NH1	1.96	0.99
2:D:94:THR:OG1	3:D:213:SO4:O1	1.81	0.99
2:D:33:VAL:HB	2:D:51:VAL:HG22	1.48	0.95
2:L:33:VAL:HB	2:L:51:VAL:HG22	1.49	0.94
2:F:33:VAL:HB	2:F:51:VAL:HG22	1.51	0.92
2:B:33:VAL:HB	2:B:51:VAL:HG22	1.52	0.90
1:C:61:ASP:OD2	2:D:95(A):ARG:NH1	2.04	0.89
1:E:61:ASP:CG	2:F:95(A):ARG:HH12	1.80	0.85
1:A:11:VAL:HG22	1:A:110:THR:HB	1.68	0.75
1:A:61:ASP:OD2	2:B:95(A):ARG:NH1	2.20	0.75
1:H:11:VAL:HG22	1:H:110:THR:HB	1.67	0.75
2:B:108:GLN:HB2	2:B:109:PRO:HD2	1.67	0.74
1:E:11:VAL:HG22	1:E:110:THR:HB	1.69	0.73
2:L:132:LEU:HD12	2:L:178:LEU:HD23	1.72	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:108:GLN:HB2	2:F:109:PRO:HD2	1.70	0.72
2:L:108:GLN:HB2	2:L:109:PRO:HD2	1.71	0.72
2:D:132:LEU:HD12	2:D:178:LEU:HD23	1.72	0.71
2:D:108:GLN:HB2	2:D:109:PRO:HD2	1.73	0.71
1:A:82:MET:HB3	1:A:82(C):LEU:HD21	1.73	0.70
1:C:82:MET:HB3	1:C:82(C):LEU:HD21	1.74	0.70
1:E:82:MET:HB3	1:E:82(C):LEU:HD21	1.75	0.69
2:L:106(A):LEU:HD22	2:L:140:TYR:HE2	1.57	0.69
2:D:106(A):LEU:HD22	2:D:140:TYR:HE2	1.57	0.68
1:H:82:MET:HB3	1:H:82(C):LEU:HD21	1.75	0.68
2:B:132:LEU:HD12	2:B:178:LEU:HD23	1.74	0.68
1:C:61:ASP:CG	2:D:95(A):ARG:HH12	1.98	0.67
1:H:159:LEU:HD21	1:H:182:VAL:HG21	1.74	0.67
2:B:59:SER:OG	3:B:213:SO4:O3	2.11	0.67
1:C:11:VAL:HG22	1:C:110:THR:HB	1.74	0.67
2:B:145:THR:HB	2:B:196:THR:HB	1.75	0.67
2:F:132:LEU:HD12	2:F:178:LEU:HD23	1.75	0.66
2:D:145:THR:HB	2:D:196:THR:HB	1.76	0.66
1:E:159:LEU:HD21	1:E:182:VAL:HG21	1.78	0.66
2:F:145:THR:HB	2:F:196:THR:HB	1.75	0.66
1:H:61:ASP:CG	2:L:95(A):ARG:HH12	1.98	0.66
2:B:106(A):LEU:HD22	2:B:140:TYR:HE2	1.60	0.66
2:L:145:THR:HB	2:L:196:THR:HB	1.76	0.66
2:F:6:GLN:OE1	2:F:99:GLY:HA3	1.96	0.66
1:C:159:LEU:HD21	1:C:182:VAL:HG21	1.76	0.66
2:F:106(A):LEU:HD22	2:F:140:TYR:HE2	1.60	0.66
1:A:159:LEU:HD21	1:A:182:VAL:HG21	1.78	0.65
2:D:27(B):ASP:HB3	2:D:92:THR:HG22	1.78	0.65
2:L:105:THR:HG22	2:L:106(A):LEU:HD23	1.79	0.65
2:D:35:TRP:HB2	2:D:48:ILE:HB	1.79	0.65
2:B:27(B):ASP:OD1	2:B:27(C):VAL:N	2.30	0.64
2:F:105:THR:HG22	2:F:106(A):LEU:HD23	1.79	0.63
2:B:159:VAL:HG22	2:B:178:LEU:HD13	1.79	0.63
2:B:35:TRP:HB2	2:B:48:ILE:HB	1.80	0.63
2:D:6:GLN:OE1	2:D:99:GLY:HA3	1.98	0.63
2:L:159:VAL:HG22	2:L:178:LEU:HD13	1.81	0.63
1:A:65:GLY:HA2	2:F:170:ASN:OD1	1.98	0.63
2:F:35:TRP:HB2	2:F:48:ILE:HB	1.80	0.62
2:L:35:TRP:HB2	2:L:48:ILE:HB	1.81	0.62
2:F:159:VAL:HG22	2:F:178:LEU:HD13	1.81	0.62
2:B:132:LEU:HD21	2:B:185:TRP:CZ3	2.34	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:27(B):ASP:OD1	2:F:27(C):VAL:N	2.32	0.62
2:D:159:VAL:HG22	2:D:178:LEU:HD13	1.82	0.61
2:L:132:LEU:HD21	2:L:185:TRP:CZ3	2.36	0.61
2:D:105:THR:HG22	2:D:106(A):LEU:HD23	1.83	0.61
2:B:105:THR:HG22	2:B:106(A):LEU:HD23	1.81	0.61
2:F:132:LEU:HD21	2:F:185:TRP:CZ3	2.36	0.61
2:L:27(B):ASP:HB3	2:L:92:THR:HG22	1.83	0.60
2:L:6:GLN:OE1	2:L:99:GLY:HA3	2.00	0.60
2:D:132:LEU:HD21	2:D:185:TRP:CZ3	2.37	0.60
2:F:27(B):ASP:HB3	2:F:92:THR:HG22	1.82	0.60
1:A:52:LYS:NZ	1:E:161:SER:OG	2.35	0.59
2:F:49:TYR:O	2:F:53:LYS:HB2	2.03	0.58
2:B:27(B):ASP:HB3	2:B:92:THR:HG22	1.83	0.58
2:D:49:TYR:O	2:D:53:LYS:HB2	2.04	0.58
2:B:6:GLN:OE1	2:B:99:GLY:HA3	2.03	0.58
1:A:193:THR:HG23	1:A:210:LYS:HE3	1.86	0.57
2:L:27(B):ASP:OD1	2:L:27(C):VAL:N	2.33	0.57
1:H:124:LEU:HD21	1:H:141:LEU:HB2	1.87	0.57
1:A:124:LEU:HD21	1:A:141:LEU:HB2	1.87	0.56
2:D:27(B):ASP:OD1	2:D:27(C):VAL:N	2.33	0.56
1:A:67:LEU:HD22	1:A:82:MET:HA	1.86	0.56
1:A:150:VAL:HG12	1:A:200:HIS:CD2	2.40	0.56
1:C:193:THR:HG23	1:C:210:LYS:HE3	1.87	0.56
1:H:193:THR:HG23	1:H:210:LYS:HE3	1.87	0.56
1:A:20:LEU:HD22	1:A:107:THR:HG21	1.87	0.56
1:E:150:VAL:HG12	1:E:200:HIS:CD2	2.40	0.56
2:B:167:GLN:NE2	2:B:169:ASN:OD1	2.36	0.56
2:L:167:GLN:NE2	2:L:169:ASN:OD1	2.36	0.55
1:E:124:LEU:HD21	1:E:141:LEU:HB2	1.88	0.55
1:H:67:LEU:HD22	1:H:82:MET:HA	1.88	0.55
1:E:193:THR:HG23	1:E:210:LYS:HE3	1.88	0.55
2:B:95:ARG:HD3	1:E:160:THR:HG21	1.87	0.55
1:C:124:LEU:HD21	1:C:141:LEU:HB2	1.88	0.55
2:L:49:TYR:O	2:L:53:LYS:HB2	2.07	0.55
2:D:167:GLN:NE2	2:D:169:ASN:OD1	2.36	0.55
1:A:40:ALA:HB3	1:A:43:GLN:HB2	1.89	0.55
1:E:20:LEU:HD22	1:E:107:THR:HG21	1.89	0.54
1:C:150:VAL:HG12	1:C:200:HIS:CD2	2.41	0.54
1:C:20:LEU:HD22	1:C:107:THR:HG21	1.88	0.54
1:H:150:VAL:HG12	1:H:200:HIS:CD2	2.42	0.54
2:L:150:ALA:HB1	2:L:188:HIS:ND1	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:150:ALA:HB1	2:B:188:HIS:ND1	2.23	0.54
1:E:40:ALA:HB3	1:E:43:GLN:HB2	1.90	0.53
2:F:150:ALA:HB1	2:F:188:HIS:ND1	2.24	0.53
2:D:150:ALA:HB1	2:D:188:HIS:ND1	2.24	0.53
2:F:169:ASN:O	2:F:170:ASN:HB2	2.08	0.53
1:C:67:LEU:HD22	1:C:82:MET:HA	1.91	0.53
1:A:169:VAL:HG12	2:B:162:THR:HG23	1.91	0.53
2:D:169:ASN:O	2:D:170:ASN:HB2	2.09	0.52
1:A:64:TRP:HH2	2:F:172:TYR:CE1	2.28	0.52
1:H:40:ALA:HB3	1:H:43:GLN:HB2	1.92	0.52
2:F:55:PRO:HD2	2:F:58:VAL:HG21	1.91	0.52
2:F:167:GLN:NE2	2:F:169:ASN:OD1	2.37	0.52
1:H:20:LEU:HD22	1:H:107:THR:HG21	1.90	0.52
2:B:95:ARG:HD3	1:E:160:THR:CG2	2.40	0.51
2:D:55:PRO:HD2	2:D:58:VAL:HG21	1.92	0.51
2:F:78:LEU:HD13	2:F:106:VAL:HG22	1.92	0.51
2:L:55:PRO:HD2	2:L:58:VAL:HG21	1.92	0.51
2:B:108:GLN:NE2	2:B:170:ASN:O	2.44	0.51
2:L:108:GLN:NE2	2:L:170:ASN:O	2.42	0.50
2:B:49:TYR:O	2:B:53:LYS:HB2	2.11	0.50
2:D:78:LEU:HD13	2:D:106:VAL:HG22	1.92	0.50
2:F:106(A):LEU:HD22	2:F:140:TYR:CE2	2.45	0.50
1:E:67:LEU:HD23	1:E:67:LEU:N	2.27	0.50
2:B:112:ALA:HB1	2:B:113:PRO:HD2	1.95	0.49
1:A:67:LEU:N	1:A:67:LEU:HD23	2.27	0.49
2:B:105:THR:HG21	2:B:141:PRO:HB3	1.94	0.49
2:B:55:PRO:HD2	2:B:58:VAL:HG21	1.93	0.49
1:H:82(B):SER:HB3	2:D:80:ALA:HB2	1.95	0.49
2:D:108:GLN:NE2	2:D:170:ASN:O	2.45	0.49
1:H:65:GLY:HA2	2:D:170:ASN:OD1	2.12	0.49
1:A:159:LEU:HD12	1:A:161:SER:H	1.77	0.49
2:F:112:ALA:HB1	2:F:113:PRO:HD2	1.95	0.49
2:B:17:GLN:HB2	1:C:12:VAL:HG12	1.94	0.49
1:C:40:ALA:HB3	1:C:43:GLN:HB2	1.95	0.48
2:B:78:LEU:HD13	2:B:106:VAL:HG22	1.94	0.48
2:L:169:ASN:O	2:L:170:ASN:HB2	2.13	0.48
1:E:67:LEU:HD22	1:E:82:MET:HA	1.94	0.48
2:F:105:THR:HG21	2:F:141:PRO:HB3	1.96	0.48
1:A:169:VAL:CG1	2:B:162:THR:HG23	2.44	0.48
2:L:78:LEU:HD13	2:L:106:VAL:HG22	1.95	0.47
1:A:138:LEU:HD13	1:A:211:VAL:HG11	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:159:LEU:HD12	1:C:161:SER:H	1.80	0.47
1:H:159:LEU:HD12	1:H:161:SER:H	1.79	0.47
1:C:67:LEU:HD23	1:C:67:LEU:N	2.30	0.47
2:D:112:ALA:HB1	2:D:113:PRO:HD2	1.97	0.47
1:A:40:ALA:HB3	1:A:43:GLN:CG	2.45	0.47
1:C:200:HIS:CD2	1:C:202:PRO:HD2	2.49	0.47
2:B:17:GLN:HA	1:C:12:VAL:HA	1.96	0.47
2:D:83:GLU:HG3	2:D:104:LEU:O	2.15	0.47
1:H:200:HIS:CD2	1:H:202:PRO:HD2	2.49	0.47
2:L:105:THR:HG21	2:L:141:PRO:HB3	1.97	0.47
2:B:169:ASN:O	2:B:170:ASN:HB2	2.15	0.47
2:F:108:GLN:NE2	2:F:170:ASN:O	2.48	0.47
2:D:11:VAL:HG23	2:D:104:LEU:HD13	1.97	0.47
1:E:40:ALA:HB3	1:E:43:GLN:CG	2.45	0.46
2:L:112:ALA:HB1	2:L:113:PRO:HD2	1.97	0.46
1:H:36:TRP:HE1	1:H:78:LEU:HG	1.79	0.46
2:D:28:GLY:HA3	2:D:69:ASN:OD1	2.15	0.46
2:B:140:TYR:CD2	2:B:140:TYR:C	2.89	0.46
2:D:106(A):LEU:HD22	2:D:140:TYR:CE2	2.45	0.46
1:C:135:THR:CG2	1:C:183:THR:HG23	2.45	0.46
1:C:178:LEU:C	1:C:178:LEU:HD12	2.36	0.46
2:L:104:LEU:HD12	2:L:105:THR:N	2.30	0.46
1:E:201:LYS:HB3	1:E:202:PRO:HD3	1.96	0.46
2:D:27(C):VAL:O	2:D:66:LYS:HD2	2.16	0.46
2:L:106(A):LEU:HD22	2:L:140:TYR:CE2	2.45	0.46
2:B:28:GLY:HA3	2:B:69:ASN:OD1	2.16	0.46
2:F:94:THR:OG1	3:F:213:SO4:O4	2.33	0.46
1:H:67:LEU:HD23	1:H:67:LEU:N	2.31	0.46
1:A:200:HIS:CD2	1:A:202:PRO:HD2	2.50	0.46
2:B:104:LEU:HD12	2:B:105:THR:N	2.31	0.45
1:E:159:LEU:HD12	1:E:161:SER:H	1.81	0.45
2:B:83:GLU:HG3	2:B:104:LEU:O	2.15	0.45
1:E:36:TRP:HE1	1:E:78:LEU:HG	1.81	0.45
1:H:135:THR:CG2	1:H:183:THR:HG23	2.47	0.45
2:D:105:THR:HG21	2:D:141:PRO:HB3	1.99	0.45
1:E:135:THR:CG2	1:E:183:THR:HG23	2.46	0.45
1:A:135:THR:CG2	1:A:183:THR:HG23	2.46	0.45
2:F:6:GLN:HB3	2:F:7:PRO:HD2	1.98	0.45
1:C:201:LYS:HB3	1:C:202:PRO:HD3	1.98	0.45
1:H:40:ALA:HB3	1:H:43:GLN:CG	2.46	0.45
2:L:11:VAL:HG23	2:L:104:LEU:HD13	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:83:GLU:HG3	2:F:104:LEU:O	2.16	0.45
2:F:11:VAL:HG23	2:F:104:LEU:HD13	1.99	0.45
1:A:201:LYS:HB3	1:A:202:PRO:HD3	1.98	0.45
2:D:4:LEU:HD11	2:D:90:SER:HB3	1.99	0.45
2:B:11:VAL:HG23	2:B:104:LEU:HD13	1.99	0.44
2:F:104:LEU:HD12	2:F:105:THR:N	2.32	0.44
1:A:178:LEU:HD12	1:A:178:LEU:C	2.37	0.44
1:H:201:LYS:HB3	1:H:202:PRO:HD3	1.98	0.44
1:E:119:PRO:HB3	1:E:145:TYR:HB3	1.99	0.44
2:L:27(C):VAL:O	2:L:66:LYS:HD2	2.18	0.44
2:F:28:GLY:HA3	2:F:69:ASN:OD1	2.18	0.44
2:D:140:TYR:CD2	2:D:140:TYR:C	2.91	0.44
1:E:200:HIS:CD2	1:E:202:PRO:HD2	2.52	0.44
1:E:178:LEU:HD12	1:E:178:LEU:C	2.37	0.44
1:A:36:TRP:HE1	1:A:78:LEU:HG	1.82	0.44
1:H:119:PRO:HB3	1:H:145:TYR:HB3	1.99	0.44
2:L:133:VAL:HG12	2:L:135:LEU:HG	2.00	0.44
2:B:108:GLN:HB2	2:B:109:PRO:CD	2.43	0.43
2:F:27(C):VAL:O	2:F:66:LYS:HD2	2.18	0.43
1:C:169:VAL:HG12	2:D:162:THR:HG23	2.01	0.43
1:C:119:PRO:HB3	1:C:145:TYR:HB3	1.99	0.43
1:H:138:LEU:HD13	1:H:211:VAL:HG11	2.00	0.43
2:F:133:VAL:HG12	2:F:135:LEU:HG	2.00	0.43
1:E:138:LEU:HD13	1:E:211:VAL:HG11	2.00	0.43
1:H:122:PHE:HA	1:H:123:PRO:HD3	1.82	0.43
2:L:28:GLY:HA3	2:L:69:ASN:OD1	2.18	0.43
2:D:132:LEU:HB2	2:D:178:LEU:HB3	2.00	0.43
2:D:104:LEU:HD12	2:D:105:THR:N	2.33	0.43
1:H:64:TRP:HH2	2:D:172:TYR:CE1	2.36	0.43
1:A:119:PRO:HB3	1:A:145:TYR:HB3	2.00	0.43
2:B:4:LEU:HD11	2:B:90:SER:HB3	2.01	0.43
1:H:178:LEU:C	1:H:178:LEU:HD12	2.38	0.43
1:E:169:VAL:CG1	2:F:162:THR:HG23	2.48	0.43
2:B:133:VAL:HG12	2:B:135:LEU:HG	2.01	0.43
2:L:83:GLU:HG3	2:L:104:LEU:O	2.19	0.42
2:F:140:TYR:CD2	2:F:140:TYR:C	2.92	0.42
2:D:6:GLN:HB3	2:D:7:PRO:HD2	2.00	0.42
1:A:169:VAL:HG11	2:B:177:TYR:CD2	2.54	0.42
1:E:122:PHE:HA	1:E:123:PRO:HD3	1.82	0.42
1:A:122:PHE:HA	1:A:123:PRO:HD3	1.83	0.42
2:F:19:ILE:HD11	2:F:75:ILE:HD12	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:138:LEU:HD13	1:C:211:VAL:HG11	2.01	0.42
1:E:64:TRP:CE3	1:E:65:GLY:N	2.87	0.42
2:L:4:LEU:HD11	2:L:90:SER:HB3	2.01	0.42
1:E:152:VAL:HA	1:E:197:ASN:O	2.19	0.42
2:L:108:GLN:HB2	2:L:109:PRO:CD	2.46	0.42
2:L:140:TYR:C	2:L:140:TYR:CD2	2.92	0.42
2:B:132:LEU:HB2	2:B:178:LEU:HB3	2.00	0.42
2:L:132:LEU:HB2	2:L:178:LEU:HB3	2.01	0.42
1:A:169:VAL:HG11	2:B:177:TYR:HD2	1.85	0.42
2:D:133:VAL:HG12	2:D:135:LEU:HG	2.02	0.42
1:C:135:THR:HG23	1:C:183:THR:HG23	2.02	0.42
1:C:122:PHE:HA	1:C:123:PRO:HD3	1.83	0.42
1:H:64:TRP:HA	1:H:65:GLY:HA2	1.83	0.42
2:B:106(A):LEU:HD22	2:B:140:TYR:CE2	2.47	0.42
1:C:169:VAL:CG1	2:D:162:THR:HG23	2.49	0.42
1:H:87:THR:O	1:H:88:ALA:HB2	2.20	0.41
2:L:54:ARG:HA	2:L:55:PRO:HD3	1.83	0.41
1:A:135:THR:HG23	1:A:183:THR:HG23	2.02	0.41
2:B:181:THR:OG1	2:B:184:GLN:HG3	2.20	0.41
1:E:50:PHE:HD2	1:E:58:TYR:HD2	1.68	0.41
1:H:51:ILE:HD11	1:H:54:GLY:HA2	2.02	0.41
2:F:181:THR:OG1	2:F:184:GLN:HG3	2.20	0.41
1:H:64:TRP:CE3	1:H:65:GLY:N	2.88	0.41
2:L:19:ILE:HD11	2:L:75:ILE:HD12	2.02	0.41
1:H:169:VAL:HG12	2:L:162:THR:HG23	2.02	0.41
1:C:40:ALA:HB3	1:C:43:GLN:CG	2.49	0.41
1:E:135:THR:HG23	1:E:183:THR:HG23	2.03	0.41
2:F:108:GLN:HB2	2:F:109:PRO:CD	2.46	0.41
2:B:6:GLN:HB3	2:B:7:PRO:HD2	2.03	0.41
1:C:36:TRP:HE1	1:C:78:LEU:HG	1.84	0.41
1:C:64:TRP:CE3	1:C:65:GLY:N	2.88	0.41
2:F:120:PRO:HD3	2:F:132:LEU:HD23	2.02	0.41
1:H:50:PHE:HD2	1:H:58:TYR:HD2	1.68	0.41
2:D:54:ARG:HA	2:D:55:PRO:HD3	1.84	0.41
2:D:181:THR:OG1	2:D:184:GLN:HG3	2.20	0.41
2:L:181:THR:OG1	2:L:184:GLN:HG3	2.20	0.41
2:L:120:PRO:HD3	2:L:132:LEU:HD23	2.03	0.41
1:H:64:TRP:CE2	2:D:170:ASN:HA	2.56	0.41
1:E:64:TRP:HA	1:E:65:GLY:HA2	1.85	0.41
2:B:19:ILE:HD11	2:B:75:ILE:HD12	2.02	0.41
1:C:64:TRP:HA	1:C:65:GLY:HA2	1.84	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:87:THR:O	1:E:88:ALA:HB2	2.21	0.40
1:A:50:PHE:HD2	1:A:58:TYR:HD2	1.68	0.40
2:B:120:PRO:HD3	2:B:132:LEU:HD23	2.02	0.40
1:H:38:ARG:NH1	1:H:86:ASP:HA	2.37	0.40
1:C:50:PHE:HD2	1:C:58:TYR:HD2	1.68	0.40
1:H:152:VAL:HA	1:H:197:ASN:O	2.21	0.40
2:B:27(C):VAL:O	2:B:66:LYS:HD2	2.22	0.40
1:H:123:PRO:O	2:L:121:SER:HB3	2.21	0.40
2:L:17:GLN:HA	1:E:12:VAL:HA	2.03	0.40
1:C:51:ILE:HD11	1:C:54:GLY:HA2	2.03	0.40
1:A:64:TRP:HA	1:A:65:GLY:HA2	1.84	0.40
2:D:120:PRO:HD3	2:D:132:LEU:HD23	2.04	0.40
2:F:132:LEU:HB2	2:F:178:LEU:HB3	2.02	0.40
2:D:117:LEU:HD12	2:D:133:VAL:O	2.22	0.40

There are no symmetry-related clashes.

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	A	210/248 (85%)	208 (99%)	2 (1%)	0	100	100
1	C	210/248 (85%)	208 (99%)	2 (1%)	0	100	100
1	E	209/248 (84%)	207 (99%)	2 (1%)	0	100	100
1	H	210/248 (85%)	208 (99%)	2 (1%)	0	100	100
2	B	209/216 (97%)	203 (97%)	4 (2%)	2 (1%)	19	61
2	D	209/216 (97%)	203 (97%)	5 (2%)	1 (0%)	34	74
2	F	209/216 (97%)	202 (97%)	5 (2%)	2 (1%)	19	61
2	L	209/216 (97%)	204 (98%)	4 (2%)	1 (0%)	34	74
All	All	1675/1856 (90%)	1643 (98%)	26 (2%)	6 (0%)	39	78

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	L	51	VAL
2	B	51	VAL
2	D	51	VAL
2	F	51	VAL
2	B	107	GLY
2	F	107	GLY

5.3.2 Protein sidechains (i)

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	182/210 (87%)	181 (100%)	1 (0%)	92 96
1	C	182/210 (87%)	181 (100%)	1 (0%)	92 96
1	E	181/210 (86%)	180 (99%)	1 (1%)	90 96
1	H	182/210 (87%)	180 (99%)	2 (1%)	80 92
2	B	178/183 (97%)	178 (100%)	0	100 100
2	D	178/183 (97%)	178 (100%)	0	100 100
2	F	178/183 (97%)	178 (100%)	0	100 100
2	L	178/183 (97%)	178 (100%)	0	100 100
All	All	1439/1572 (92%)	1434 (100%)	5 (0%)	94 98

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	100(P)	ASN
1	H	150	VAL
1	A	100(P)	ASN
1	C	100(P)	ASN
1	E	100(P)	ASN

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

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

There are no carbohydrates in this entry.

5.6 Ligand geometry

6 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	SO4	B	213	-	4,4,4	0.21	0	6,6,6	0.10	0
3	SO4	B	214	-	4,4,4	0.33	0	6,6,6	0.19	0
3	SO4	D	213	-	4,4,4	0.34	0	6,6,6	0.23	0
3	SO4	F	213	-	4,4,4	0.31	0	6,6,6	0.17	0
3	SO4	L	213	-	4,4,4	0.18	0	6,6,6	0.08	0
3	SO4	L	214	-	4,4,4	0.30	0	6,6,6	0.12	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SO4	B	213	-	-	0/0/0/0	0/0/0/0
3	SO4	B	214	-	-	0/0/0/0	0/0/0/0
3	SO4	D	213	-	-	0/0/0/0	0/0/0/0
3	SO4	F	213	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SO4	L	213	-	-	0/0/0/0	0/0/0/0
3	SO4	L	214	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	213	SO4	1	0
3	D	213	SO4	1	0
3	F	213	SO4	1	0

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^{th} 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^2)	Q<0.9
1	A	216/248 (87%)	0.22	17 (7%)	15	11	74, 124, 198, 227	0
1	C	216/248 (87%)	0.27	13 (6%)	25	18	75, 123, 196, 229	0
1	E	215/248 (86%)	0.13	10 (4%)	35	28	75, 122, 195, 227	0
1	H	216/248 (87%)	0.40	20 (9%)	11	8	73, 122, 196, 228	0
2	B	211/216 (97%)	0.13	13 (6%)	24	18	71, 114, 191, 251	0
2	D	211/216 (97%)	0.11	8 (3%)	44	34	71, 114, 191, 251	0
2	F	211/216 (97%)	-0.01	8 (3%)	44	34	75, 113, 191, 251	0
2	L	211/216 (97%)	0.07	7 (3%)	50	41	69, 113, 190, 251	0
All	All	1707/1856 (91%)	0.17	96 (5%)	28	21	69, 117, 195, 251	0

All (96) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	161	SER	7.4
1	A	158	ALA	7.0
1	A	194	TYR	6.5
1	A	76	ASP	6.2
1	C	161	SER	6.1
1	C	157	GLY	5.6
1	C	127	SER	5.4
2	D	191	TYR	5.4
2	F	124	GLU	4.9
2	B	132	LEU	4.9
2	B	121	SER	4.8
1	C	158	ALA	4.7
1	A	159	LEU	4.4
1	H	208	ASP	4.4
2	F	123	GLU	4.4
1	A	157	GLY	4.3

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Mol	Chain	Res	Type	RSRZ
1	A	208	ASP	4.3
1	H	127	SER	4.3
1	A	193	THR	4.3
2	F	126	GLN	4.2
2	L	132	LEU	4.1
2	D	180	LEU	4.0
1	C	156	SER	3.9
1	A	126	PRO	3.8
2	B	160	GLU	3.8
1	A	162	GLY	3.8
1	H	178	LEU	3.7
1	E	127	SER	3.7
2	L	120	PRO	3.7
1	H	177	SER	3.6
1	A	192	GLN	3.6
1	E	146	PHE	3.6
2	D	126	GLN	3.6
1	H	193	THR	3.5
2	B	178	LEU	3.5
1	E	115	SER	3.5
1	A	127	SER	3.4
2	B	82	ASP	3.4
1	H	142	VAL	3.2
1	A	188	SER	3.2
2	B	191	TYR	3.2
1	C	162	GLY	3.1
1	A	163	VAL	3.1
2	B	73	LEU	3.0
2	F	142	GLY	3.0
1	H	161	SER	3.0
2	B	185	TRP	3.0
1	E	92	CYS	2.9
1	C	208	ASP	2.9
2	D	206	VAL	2.9
2	B	120	PRO	2.8
1	H	76	ASP	2.8
1	E	116	THR	2.7
2	B	110	LYS	2.7
2	F	191	TYR	2.6
1	C	68	SER	2.5
1	A	209	LYS	2.5
1	A	212	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
2	D	23	CYS	2.5
1	H	72	ASP	2.4
1	H	187	SER	2.4
1	E	213	PRO	2.4
2	L	128	ASN	2.4
1	C	138	LEU	2.4
1	H	140	CYS	2.4
1	A	125	ALA	2.4
1	E	121	VAL	2.4
1	H	68	SER	2.3
1	H	175	LEU	2.3
2	B	123	GLU	2.3
2	L	72	SER	2.3
1	H	162	GLY	2.3
2	L	21	ILE	2.3
1	H	194	TYR	2.3
2	D	124	GLU	2.3
2	F	125	LEU	2.3
2	B	208	PRO	2.3
1	H	156	SER	2.3
1	H	189	LEU	2.2
1	C	126	PRO	2.2
1	C	204	ASN	2.2
2	B	194	GLN	2.2
1	E	159	LEU	2.2
2	D	31	GLU	2.2
2	D	67	SER	2.1
1	E	101	ASP	2.1
1	C	125	ALA	2.1
2	L	118	PHE	2.1
1	H	190	GLY	2.1
1	H	116	THR	2.1
2	F	127	ALA	2.1
1	A	24	ALA	2.1
2	L	121	SER	2.1
1	C	107	THR	2.1
2	F	186	LYS	2.0
1	H	115	SER	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)

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^{th} 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	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
3	SO4	F	213	5/5	0.84	0.21	0.81	139,161,167,176	0
3	SO4	L	214	5/5	0.73	0.12	-0.91	174,176,185,192	0
3	SO4	D	213	5/5	0.90	0.18	-1.13	145,165,170,171	0
3	SO4	B	213	5/5	0.95	0.28	-	155,156,166,172	0
3	SO4	L	213	5/5	0.94	0.10	-	132,150,155,156	0
3	SO4	B	214	5/5	0.92	0.13	-	116,155,157,175	0

6.5 Other polymers (i)

There are no such residues in this entry.