



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 07:19 am GMT

PDB ID : 1Q9O  
Title : S45-18 Fab Unliganded  
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Deposited on : 2003-08-25  
Resolution : 1.79 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
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	recalc28949

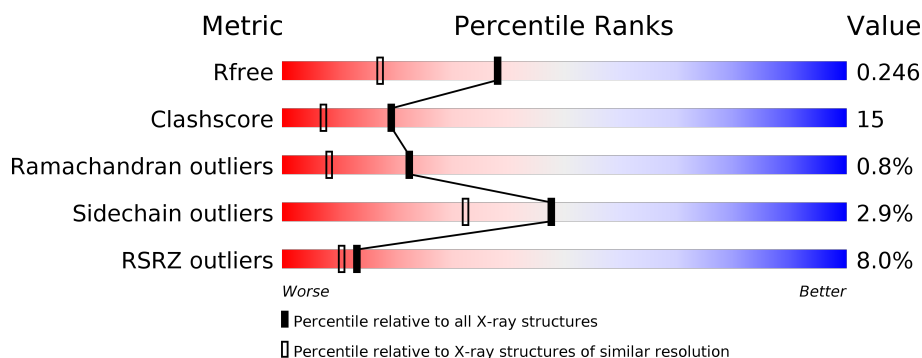
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.79 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))
$R_{free}$	100719	4827 (1.80-1.80)
Clashscore	112137	5742 (1.80-1.80)
Ramachandran outliers	110173	5676 (1.80-1.80)
Sidechain outliers	110143	5675 (1.80-1.80)
RSRZ outliers	101464	4906 (1.80-1.80)

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	B	226	<div> <div>5%</div> <div> <div></div> <div>79%</div> <div>18%</div> <div></div> </div> </div>
1	D	226	<div> <div>11%</div> <div> <div></div> <div>75%</div> <div>23%</div> <div></div> </div> </div>
2	A	219	<div> <div>7%</div> <div> <div></div> <div>74%</div> <div>24%</div> <div></div> </div> </div>
2	C	219	<div> <div>9%</div> <div> <div></div> <div>73%</div> <div>26%</div> <div></div> </div> </div>

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7379 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 S45-2 Fab (IgG1k) heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	226	Total	C	N	O	S	0	0	0
			1718	1085	284	340	9			
1	D	226	Total	C	N	O	S	0	0	0
			1718	1085	284	340	9			

- Molecule 2 is a protein called S45-2 Fab (IgG1k) light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	219	Total	C	N	O	S	0	0	0
			1707	1066	289	344	8			
2	C	219	Total	C	N	O	S	0	0	0
			1707	1066	289	344	8			

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Mg	0	0
			1	1		
3	A	1	Total	Mg	0	0
			1	1		
3	D	1	Total	Mg	0	0
			1	1		
3	C	1	Total	Mg	0	0
			1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	154	Total	O	0	0
			154	154		
4	B	181	Total	O	0	0
			181	181		

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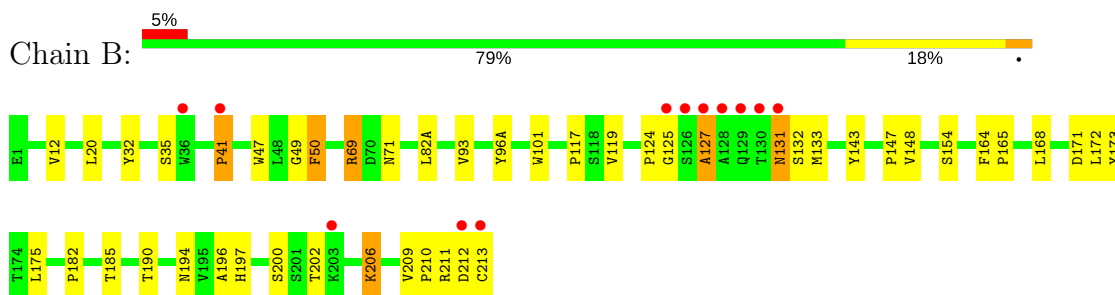
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	99	Total	O	0	0
			99	99		
4	D	91	Total	O	0	0
			91	91		

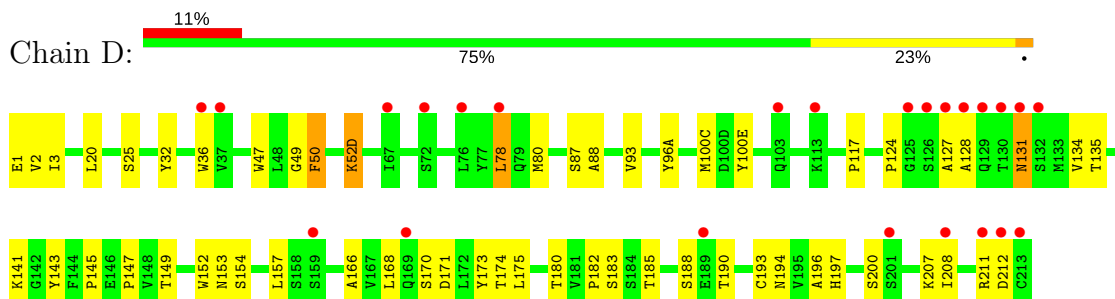
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

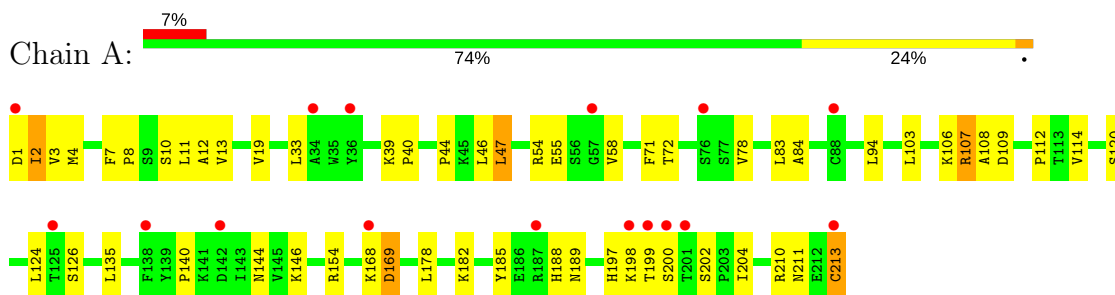
- Molecule 1: S45-2 Fab (IgG1k) heavy chain



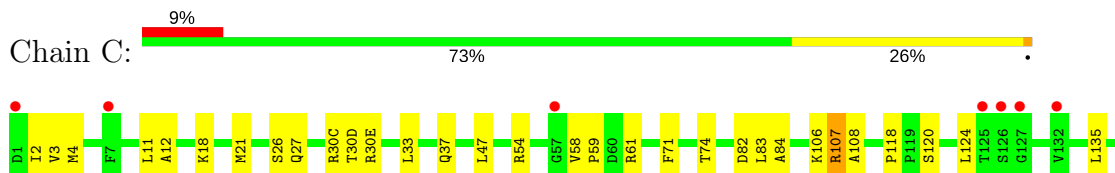
- Molecule 1: S45-2 Fab (IgG1k) heavy chain

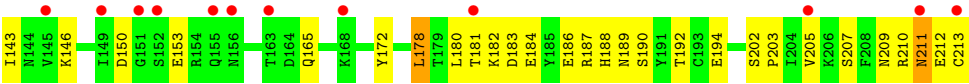


- Molecule 2: S45-2 Fab (IgG1k) light chain



- Molecule 2: S45-2 Fab (IgG1k) light chain





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	76.40Å 170.30Å 77.10Å 90.00° 114.40° 90.00°	Depositor
Resolution (Å)	19.18 – 1.79 19.18 – 1.79	Depositor EDS
% Data completeness (in resolution range)	88.6 (19.18-1.79) 88.6 (19.18-1.79)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.86 (at 1.79Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.220 , 0.247 0.218 , 0.246	Depositor DCC
$R_{free}$ test set	7500 reflections (10.07%)	DCC
Wilson B-factor (Å <sup>2</sup> )	25.4	Xtriage
Anisotropy	0.068	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 41.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7379	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.94% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

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

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

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	B	0.38	0/1763	0.70	0/2406
1	D	0.34	0/1763	0.66	0/2406
2	A	0.37	0/1744	0.66	0/2361
2	C	0.34	0/1744	0.64	0/2361
All	All	0.36	0/7014	0.67	0/9534

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1718	0	1671	41	0
1	D	1718	0	1671	41	0
2	A	1707	0	1653	64	0
2	C	1707	0	1653	52	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	154	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	181	0	0	1	0
4	C	99	0	0	0	0
4	D	91	0	0	0	0
All	All	7379	0	6648	196	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 15.

All (196) 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:A:2:ILE:HG22	2:A:4:MET:HE1	1.39	1.02
1:D:154:SER:H	1:D:194:ASN:HD21	1.09	1.00
2:A:2:ILE:HG22	2:A:4:MET:CE	2.00	0.91
1:B:69:ARG:HH21	1:B:71:ASN:HD21	1.19	0.90
1:B:154:SER:H	1:B:194:ASN:HD21	1.17	0.87
2:A:168:LYS:HA	2:A:168:LYS:NZ	1.91	0.85
2:A:210:ARG:HB3	2:A:210:ARG:HH11	1.40	0.85
2:A:8:PRO:HG2	2:A:11:LEU:HD21	1.62	0.80
1:D:154:SER:H	1:D:194:ASN:ND2	1.83	0.77
1:D:93:VAL:HG21	1:D:100(C):MET:HB3	1.69	0.74
2:A:2:ILE:CG2	2:A:4:MET:HE1	2.17	0.74
2:A:168:LYS:HZ2	2:A:169:ASP:H	1.34	0.74
2:A:210:ARG:HB3	2:A:210:ARG:NH1	2.03	0.74
1:B:69:ARG:HG3	1:B:69:ARG:HH21	1.53	0.72
2:A:210:ARG:CB	2:A:210:ARG:HH11	2.04	0.71
2:A:109:ASP:HB3	2:A:199:THR:HG21	1.73	0.71
1:B:197:HIS:HB3	1:B:202:THR:CG2	2.20	0.71
2:A:46:LEU:HD22	2:A:55:GLU:HB2	1.73	0.71
1:D:131:ASN:HD22	1:D:131:ASN:H	1.39	0.70
2:C:210:ARG:C	2:C:212:GLU:H	1.94	0.69
2:A:168:LYS:HZ2	2:A:169:ASP:N	1.90	0.69
1:B:69:ARG:NH2	1:B:71:ASN:HD21	1.91	0.68
2:C:209:ASN:O	2:C:210:ARG:HB3	1.92	0.68
2:A:10:SER:O	2:A:11:LEU:HD22	1.94	0.68
2:C:2:ILE:HG22	2:C:4:MET:CE	2.24	0.68
2:A:46:LEU:HD23	2:A:47:LEU:N	2.08	0.68
1:B:69:ARG:HH21	1:B:71:ASN:ND2	1.91	0.68
2:A:114:VAL:HG22	2:A:135:LEU:HD22	1.76	0.67
2:A:168:LYS:HA	2:A:168:LYS:HZ3	1.59	0.67
1:D:211:ARG:NH2	2:C:118:PRO:HG2	2.10	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:107:ARG:HD3	2:C:108:ALA:O	1.95	0.67
1:B:125:GLY:HA2	1:B:211:ARG:HB2	1.76	0.66
2:A:3:VAL:O	2:A:4:MET:HE2	1.96	0.66
2:A:168:LYS:HA	2:A:168:LYS:HZ2	1.61	0.66
2:C:2:ILE:HG22	2:C:4:MET:HE1	1.78	0.65
1:D:93:VAL:CG2	1:D:100(C):MET:HB3	2.27	0.64
2:A:189:ASN:HD21	2:A:211:ASN:ND2	1.95	0.64
2:C:135:LEU:HD23	2:C:143:ILE:HD13	1.78	0.64
2:A:33:LEU:HD22	2:A:71:PHE:CG	2.33	0.64
2:A:72:THR:HG23	4:A:681:HOH:O	1.97	0.64
2:C:194:GLU:HG2	2:C:205:VAL:HG12	1.78	0.64
2:A:107:ARG:HD3	2:A:108:ALA:O	1.98	0.63
2:C:165:GLN:HG3	2:C:172:TYR:CZ	2.33	0.63
2:A:189:ASN:HD21	2:A:211:ASN:HD22	1.45	0.62
1:B:200:SER:OG	1:B:202:THR:HG22	1.99	0.62
2:C:184:GLU:HG2	2:C:187:ARG:NH2	2.15	0.62
2:A:188:HIS:O	2:A:210:ARG:NH1	2.33	0.62
1:D:135:THR:OG1	1:D:180:THR:HG22	1.99	0.62
1:B:69:ARG:HG3	1:B:69:ARG:NH2	2.15	0.61
2:A:13:VAL:HG11	2:A:19:VAL:HG22	1.81	0.61
1:D:131:ASN:H	1:D:131:ASN:ND2	1.99	0.61
1:D:131:ASN:N	1:D:131:ASN:HD22	1.98	0.60
2:A:124:LEU:HD12	2:A:182:LYS:HG3	1.84	0.60
2:C:30(E):ARG:HG2	2:C:30(E):ARG:HH11	1.66	0.59
1:B:131:ASN:HD22	1:B:131:ASN:N	2.00	0.59
1:D:197:HIS:HD2	1:D:200:SER:OG	1.85	0.59
1:B:119:VAL:CG1	1:B:206:LYS:HG3	2.33	0.58
1:B:117:PRO:HB3	1:B:143:TYR:HB3	1.85	0.58
1:B:154:SER:H	1:B:194:ASN:ND2	1.94	0.58
1:B:197:HIS:HB3	1:B:202:THR:HG23	1.85	0.58
1:D:168:LEU:HB2	1:D:173:TYR:CE1	2.39	0.58
2:C:120:SER:O	2:C:124:LEU:HD23	2.02	0.57
2:C:33:LEU:HD22	2:C:71:PHE:CG	2.39	0.57
1:D:134:VAL:HG23	1:D:183:SER:HA	1.86	0.57
2:A:46:LEU:HD23	2:A:46:LEU:C	2.25	0.57
2:C:2:ILE:CG2	2:C:4:MET:HE1	2.35	0.57
1:D:124:PRO:O	1:D:211:ARG:HG3	2.05	0.57
1:D:117:PRO:HB3	1:D:143:TYR:HB3	1.87	0.56
1:D:145:PRO:O	1:D:197:HIS:HE1	1.88	0.56
2:C:186:GLU:HA	2:C:210:ARG:HE	1.71	0.56
2:C:3:VAL:HG12	2:C:26:SER:HB3	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:109:ASP:HB3	2:A:199:THR:CG2	2.36	0.56
2:A:189:ASN:ND2	2:A:211:ASN:HD22	2.04	0.55
1:B:101:TRP:CD2	2:A:44:PRO:HG2	2.41	0.55
1:D:149:THR:OG1	1:D:196:ALA:HB3	2.07	0.55
2:C:3:VAL:CG1	2:C:26:SER:HB3	2.37	0.55
2:C:37:GLN:HB3	2:C:47:LEU:HD11	1.89	0.54
2:C:146:LYS:HD2	2:C:153:GLU:CD	2.28	0.54
1:D:93:VAL:HG23	1:D:100(E):TYR:O	2.07	0.54
2:C:135:LEU:HD23	2:C:143:ILE:CD1	2.38	0.54
1:B:47:TRP:CZ2	1:B:49:GLY:HA2	2.44	0.53
2:C:210:ARG:C	2:C:212:GLU:N	2.61	0.53
2:A:19:VAL:HG21	2:A:78:VAL:HG21	1.90	0.53
2:C:150:ASP:HA	2:C:190:SER:HB3	1.90	0.53
1:D:182:PRO:HG2	1:D:185:THR:CG2	2.37	0.53
2:C:12:ALA:HB1	2:C:106:LYS:HE3	1.91	0.52
1:B:182:PRO:HG2	1:B:185:THR:HG23	1.91	0.52
1:B:125:GLY:HA3	1:B:211:ARG:NH1	2.24	0.51
1:B:124:PRO:HB3	1:B:127:ALA:HB3	1.92	0.51
1:B:206:LYS:HB3	1:B:206:LYS:NZ	2.26	0.51
1:B:148:VAL:HG23	1:B:196:ALA:O	2.11	0.51
2:C:54:ARG:HG2	2:C:58:VAL:HB	1.93	0.50
2:A:12:ALA:C	2:A:106:LYS:HE3	2.31	0.50
2:A:46:LEU:HD22	2:A:55:GLU:CB	2.41	0.50
2:A:2:ILE:HG22	2:A:4:MET:HE3	1.92	0.50
1:B:131:ASN:ND2	1:B:131:ASN:N	2.58	0.50
2:A:12:ALA:O	2:A:106:LYS:HE3	2.12	0.49
2:C:18:LYS:NZ	2:C:74:THR:HG21	2.27	0.49
2:C:178:LEU:HD22	2:C:180:LEU:HG	1.94	0.49
1:D:47:TRP:CZ2	1:D:49:GLY:HA2	2.47	0.49
2:A:168:LYS:NZ	2:A:169:ASP:H	2.06	0.49
2:A:168:LYS:CA	2:A:168:LYS:HZ2	2.25	0.49
2:C:192:THR:HG22	2:C:207:SER:CB	2.42	0.48
1:D:127:ALA:O	1:D:128:ALA:HB3	2.13	0.48
1:B:131:ASN:O	1:B:133:MET:N	2.45	0.48
2:A:140:PRO:HG3	2:A:198:LYS:HE3	1.95	0.48
2:C:3:VAL:O	2:C:4:MET:HE2	2.13	0.48
2:C:211:ASN:C	2:C:213:CYS:H	2.15	0.48
2:C:2:ILE:HG23	2:C:27:GLN:HG3	1.94	0.48
2:A:3:VAL:C	2:A:4:MET:HE2	2.34	0.48
2:C:107:ARG:CD	2:C:108:ALA:O	2.62	0.48
2:A:19:VAL:CG2	2:A:78:VAL:HG21	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:83:LEU:C	2:A:83:LEU:HD23	2.34	0.48
1:D:1:GLU:HG3	1:D:3:ILE:HD11	1.95	0.48
1:D:185:THR:C	1:D:188:SER:HB3	2.35	0.47
2:A:13:VAL:HG21	2:A:19:VAL:HG21	1.96	0.47
2:C:30(C):ARG:C	2:C:30(E):ARG:H	2.17	0.47
1:D:78:LEU:HD22	1:D:80:MET:CG	2.44	0.47
1:B:35:SER:HB2	1:B:93:VAL:CG2	2.45	0.47
2:A:146:LYS:HB3	2:A:146:LYS:NZ	2.30	0.47
1:B:206:LYS:HB3	1:B:206:LYS:HZ2	1.80	0.47
2:A:168:LYS:O	2:A:169:ASP:CG	2.54	0.47
2:C:30(E):ARG:HG2	2:C:30(E):ARG:NH1	2.30	0.46
2:C:12:ALA:CB	2:C:106:LYS:HE3	2.45	0.46
1:D:152:TRP:CZ3	1:D:208:ILE:HD11	2.50	0.46
1:D:175:LEU:C	1:D:175:LEU:HD12	2.36	0.46
2:A:197:HIS:CD2	2:A:198:LYS:H	2.34	0.46
2:A:1:ASP:O	2:A:2:ILE:O	2.34	0.46
2:C:11:LEU:HD11	2:C:21:MET:HG2	1.98	0.46
1:D:170:SER:O	1:D:171:ASP:HB2	2.15	0.46
2:A:13:VAL:HG21	2:A:19:VAL:CG2	2.47	0.45
2:A:185:TYR:CE2	2:A:210:ARG:HD2	2.52	0.45
2:A:46:LEU:CD2	2:A:55:GLU:HB2	2.45	0.45
2:A:213:CYS:SG	2:A:213:CYS:OXT	2.74	0.45
1:B:171:ASP:O	1:B:172:LEU:HD23	2.17	0.45
1:B:32:TYR:CE1	1:B:96(A):TYR:HB3	2.52	0.45
2:A:197:HIS:C	2:A:199:THR:H	2.19	0.45
2:C:192:THR:CB	2:C:207:SER:HB3	2.47	0.45
1:D:32:TYR:CE1	1:D:96(A):TYR:HB2	2.52	0.45
1:B:125:GLY:HA3	1:B:211:ARG:CZ	2.47	0.45
2:C:30(C):ARG:O	2:C:30(D):THR:OG1	2.30	0.44
1:B:175:LEU:HD12	1:B:175:LEU:C	2.38	0.44
1:B:190:THR:HG23	4:B:344:HOH:O	2.16	0.44
2:C:83:LEU:C	2:C:83:LEU:HD13	2.37	0.44
1:D:87:SER:O	1:D:88:ALA:HB2	2.18	0.44
1:B:209:VAL:HG13	1:B:210:PRO:HD2	1.99	0.44
2:C:37:GLN:CB	2:C:47:LEU:HD11	2.47	0.44
1:D:50:PHE:C	1:D:50:PHE:CD1	2.91	0.44
2:A:54:ARG:HD3	2:A:58:VAL:O	2.18	0.44
1:D:141:LYS:HG3	1:D:174:THR:OG1	2.18	0.44
2:A:39:LYS:HB3	2:A:40:PRO:HD2	1.99	0.44
2:A:3:VAL:C	2:A:4:MET:CE	2.86	0.44
1:B:182:PRO:HG2	1:B:185:THR:CG2	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:165:GLN:HG3	2:C:172:TYR:CE2	2.53	0.44
2:A:120:SER:O	2:A:124:LEU:HD23	2.18	0.43
2:C:18:LYS:HZ2	2:C:74:THR:CG2	2.31	0.43
1:D:2:VAL:O	1:D:3:ILE:HD13	2.17	0.43
2:A:7:PHE:HA	2:A:8:PRO:C	2.38	0.43
1:B:12:VAL:HG11	1:B:82(A):LEU:HD13	2.01	0.43
2:A:83:LEU:O	2:A:84:ALA:HB2	2.18	0.43
1:B:168:LEU:HB2	1:B:173:TYR:CE1	2.53	0.43
2:C:189:ASN:O	2:C:209:ASN:O	2.36	0.43
2:C:61:ARG:NH1	2:C:82:ASP:OD1	2.52	0.43
1:D:78:LEU:HD22	1:D:80:MET:HG2	2.01	0.43
1:B:47:TRP:CH2	1:B:49:GLY:HA2	2.52	0.43
2:C:107:ARG:HD3	2:C:108:ALA:N	2.33	0.43
1:D:152:TRP:CZ3	1:D:193:CYS:HB3	2.54	0.43
2:A:46:LEU:CD2	2:A:46:LEU:C	2.86	0.43
1:B:50:PHE:C	1:B:50:PHE:CD1	2.92	0.43
2:A:112:PRO:HG2	2:A:204:ILE:HD12	2.02	0.42
1:B:212:ASP:O	1:B:213:CYS:O	2.38	0.42
1:D:50:PHE:HD1	1:D:50:PHE:C	2.23	0.42
2:C:202:SER:HA	2:C:203:PRO:HD3	1.94	0.42
1:D:190:THR:HG23	1:D:207:LYS:HE2	2.01	0.42
2:A:8:PRO:HG2	2:A:11:LEU:CD2	2.43	0.42
1:B:164:PHE:HA	1:B:165:PRO:HD3	1.92	0.41
1:D:36:TRP:CE2	1:D:78:LEU:HB2	2.55	0.41
2:C:150:ASP:OD2	2:C:188:HIS:HB3	2.19	0.41
2:C:192:THR:HB	2:C:207:SER:HB3	2.01	0.41
2:C:181:THR:HG22	2:C:182:LYS:N	2.36	0.41
1:B:50:PHE:C	1:B:50:PHE:HD1	2.24	0.41
2:A:54:ARG:HG2	2:A:58:VAL:HB	2.02	0.41
1:D:153:ASN:ND2	1:D:157:LEU:HD23	2.35	0.41
1:B:131:ASN:H	1:B:131:ASN:HD22	1.68	0.41
2:C:183:ASP:O	2:C:187:ARG:HG3	2.20	0.41
1:B:119:VAL:HG12	1:B:206:LYS:HG3	2.01	0.41
1:D:52(D):LYS:HD2	1:D:52(D):LYS:N	2.36	0.41
2:A:146:LYS:CB	2:A:146:LYS:HZ2	2.34	0.41
2:A:200:SER:HB2	2:A:202:SER:O	2.21	0.41
1:D:153:ASN:HD22	1:D:157:LEU:HD23	1.86	0.41
1:D:3:ILE:HB	1:D:25:SER:OG	2.21	0.41
2:A:144:ASN:HB2	4:A:622:HOH:O	2.21	0.40
2:C:58:VAL:HA	2:C:59:PRO:HD3	1.94	0.40
2:C:210:ARG:O	2:C:212:GLU:N	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:83:LEU:O	2:C:84:ALA:HB2	2.21	0.40
1:D:166:ALA:HB2	1:D:175:LEU:HD23	2.04	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	B	224/226 (99%)	215 (96%)	6 (3%)	3 (1%)	14	3
1	D	224/226 (99%)	209 (93%)	14 (6%)	1 (0%)	38	23
2	A	217/219 (99%)	206 (95%)	8 (4%)	3 (1%)	13	3
2	C	217/219 (99%)	207 (95%)	10 (5%)	0	100	100
All	All	882/890 (99%)	837 (95%)	38 (4%)	7 (1%)	22	8

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	41	PRO
1	B	127	ALA
1	B	132	SER
1	D	212	ASP
2	A	2	ILE
2	A	126	SER
2	A	169	ASP

### 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	B	196/196 (100%)	189 (96%)	7 (4%)	40	23
1	D	196/196 (100%)	190 (97%)	6 (3%)	45	29
2	A	194/194 (100%)	187 (96%)	7 (4%)	40	23
2	C	194/194 (100%)	191 (98%)	3 (2%)	70	61
All	All	780/780 (100%)	757 (97%)	23 (3%)	48	32

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	20	LEU
1	B	41	PRO
1	B	50	PHE
1	B	69	ARG
1	B	131	ASN
1	B	147	PRO
1	B	206	LYS
1	D	20	LEU
1	D	50	PHE
1	D	52(D)	LYS
1	D	78	LEU
1	D	131	ASN
1	D	147	PRO
2	A	47	LEU
2	A	94	LEU
2	A	103	LEU
2	A	107	ARG
2	A	154	ARG
2	A	178	LEU
2	A	213	CYS
2	C	107	ARG
2	C	178	LEU
2	C	211	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	71	ASN
1	B	103	GLN

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Mol	Chain	Res	Type
1	B	131	ASN
1	B	194	ASN
1	D	71	ASN
1	D	73	GLN
1	D	129	GLN
1	D	131	ASN
1	D	194	ASN
1	D	197	HIS
2	A	42	GLN
2	A	79	GLN
2	A	137	ASN
2	A	156	ASN
2	A	197	HIS
2	A	209	ASN
2	A	211	ASN
2	C	93	ASN
2	C	209	ASN
2	C	211	ASN

### 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](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	B	226/226 (100%)	0.43	12 (5%) 27 22	17, 23, 42, 81	0
1	D	226/226 (100%)	0.69	24 (10%) 7 5	18, 30, 54, 84	0
2	A	219/219 (100%)	0.49	16 (7%) 16 13	17, 27, 45, 62	0
2	C	219/219 (100%)	0.67	19 (8%) 11 9	19, 31, 53, 62	0
All	All	890/890 (100%)	0.57	71 (7%) 13 10	17, 28, 50, 84	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	130	THR	13.5
1	B	128	ALA	12.8
1	B	213	CYS	11.7
1	B	126	SER	11.6
1	D	213	CYS	11.6
1	D	128	ALA	11.5
1	D	131	ASN	9.9
1	B	129	GLN	9.8
2	C	213	CYS	9.5
2	A	1	ASP	7.9
1	D	127	ALA	7.2
2	A	213	CYS	7.1
1	B	125	GLY	6.7
1	B	127	ALA	6.6
2	A	199	THR	6.5
1	D	129	GLN	6.4
2	A	200	SER	5.8
1	D	130	THR	5.7
2	A	198	LYS	5.7
2	C	1	ASP	5.6
1	D	126	SER	4.6

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Mol	Chain	Res	Type	RSRZ
1	D	125	GLY	4.5
1	B	131	ASN	4.5
2	A	201	THR	3.8
2	C	211	ASN	3.6
2	A	168	LYS	3.5
1	D	212	ASP	3.5
2	C	155	GLN	3.5
2	C	126	SER	3.4
1	D	211	ARG	3.4
2	C	7	PHE	3.2
1	D	113	LYS	3.0
2	A	76	SER	3.0
2	C	152	SER	3.0
1	B	203	LYS	3.0
1	B	41	PRO	2.9
1	D	72	SER	2.6
1	D	76	LEU	2.6
2	A	187	ARG	2.6
1	B	36	TRP	2.6
1	D	132	SER	2.6
2	C	125	THR	2.5
1	D	201	SER	2.5
2	C	145	VAL	2.5
1	D	36	TRP	2.5
1	D	78	LEU	2.4
1	D	169	GLN	2.4
2	C	168	LYS	2.4
2	C	57	GLY	2.4
2	A	34	ALA	2.4
2	A	57	GLY	2.4
1	D	159	SER	2.3
2	A	36	TYR	2.3
2	C	127	GLY	2.3
2	A	125	THR	2.3
2	C	205	VAL	2.2
2	C	181	THR	2.2
2	A	138	PHE	2.2
1	D	103	GLN	2.2
1	D	208	ILE	2.2
2	C	149	ILE	2.2
1	D	67	ILE	2.2
1	B	212	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
2	A	88	CYS	2.1
1	D	37	VAL	2.1
2	C	132	VAL	2.1
1	D	189	GLU	2.1
2	A	142	ASP	2.1
2	C	156	ASN	2.0
2	C	163	THR	2.0
2	C	151	GLY	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<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	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	MG	D	214	1/1	0.98	0.11	0.35	27,27,27,27	0
3	MG	C	214	1/1	0.96	0.07	-1.25	33,33,33,33	0
3	MG	B	214	1/1	0.99	0.05	-1.60	24,24,24,24	0
3	MG	A	214	1/1	0.99	0.04	-2.28	25,25,25,25	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.