



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:40 AM GMT

PDB ID : 3BQU  
Title : Crystal Structure of the 2F5 Fab'-3H6 Fab Complex  
Authors : Bryson, S.; Julien, J.-P.; Isenman, D.E.; Kunert, R.; Katinger, H.; Pai, E.F.  
Deposited on : 2007-12-20  
Resolution : 3.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

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

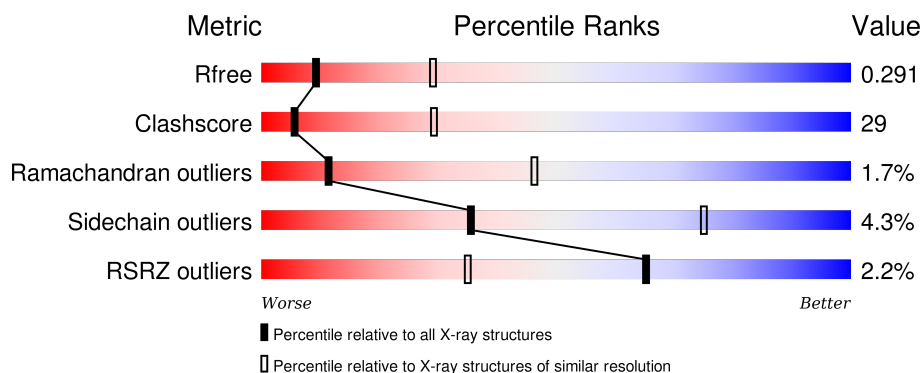
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	214	<div> <div>44%</div> <div>49%</div> <div>6%</div> </div>
2	B	235	<div> <div>50%</div> <div>39%</div> <div>9%</div> </div>
3	C	233	<div> <div>5%</div> <div>38%</div> <div>39%</div> <div>20%</div> </div>
4	D	241	<div> <div>51%</div> <div>37%</div> <div>10%</div> </div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6322 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 2F5 Fab' light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	211	Total	C	N	O	S	0	0	0
			1624	1015	278	327	4			

- Molecule 2 is a protein called 2F5 Fab' heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	214	Total	C	N	O	S	0	0	0
			1612	1028	271	307	6			

- Molecule 3 is a protein called 3H6 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	186	Total	C	N	O	S	0	0	0
			1445	903	235	301	6			

- Molecule 4 is a protein called 3H6 Fab heavy chain.

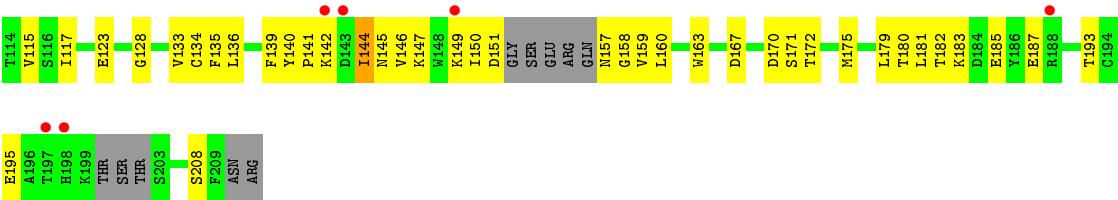
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	217	Total	C	N	O	S	0	0	0
			1636	1042	265	320	9			

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).

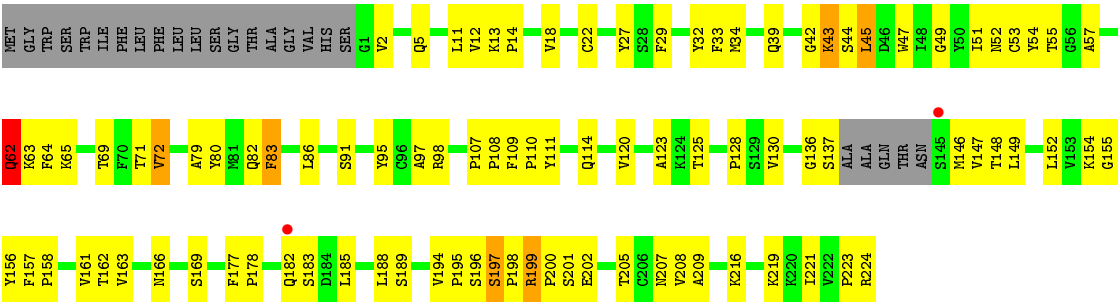


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	D	1	Total	O	S	0	0
			5	4	1		





• Molecule 4: 3H6 Fab heavy chain



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	67.44Å 98.33Å 154.39Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.00 35.93 – 2.99	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-3.00) 96.8 (35.93-2.99)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.78 (at 3.00Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.276 , 0.295 0.279 , 0.291	Depositor DCC
$R_{free}$ test set	1054 reflections (5.14%)	DCC
Wilson B-factor (Å <sup>2</sup> )	74.3	Xtriage
Anisotropy	0.041	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 42.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 20664 reflections	Xtriage
$F_o, F_c$ correlation	0.88	EDS
Total number of atoms	6322	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.55% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

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	0.26	0/1661	0.51	0/2259
2	B	0.26	0/1649	0.53	0/2253
3	C	0.27	0/1476	0.51	0/2007
4	D	0.28	0/1684	0.53	0/2299
All	All	0.27	0/6470	0.52	0/8818

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

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	1624	0	1574	107	0
2	B	1612	0	1630	87	0
3	C	1445	0	1355	96	0
4	D	1636	0	1590	88	0
5	D	5	0	0	0	0
All	All	6322	0	6149	365	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 29.



All (365) 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)
4:D:199:ARG:HD2	4:D:200:PRO:HA	1.49	0.95
1:A:11:LEU:HD21	1:A:104:VAL:HG22	1.53	0.90
4:D:43:LYS:HE2	4:D:43:LYS:HA	1.54	0.89
1:A:170:ASP:HB3	1:A:172:THR:HG22	1.55	0.88
3:C:6:GLN:HG3	3:C:101:GLY:H	1.42	0.85
4:D:125:THR:HG22	4:D:158:PRO:HD3	1.58	0.85
4:D:155:GLY:HA2	4:D:185:LEU:HD21	1.59	0.84
2:B:92:THR:HB	2:B:129:THR:HA	1.63	0.81
2:B:138:PRO:HB3	2:B:164:TYR:HB3	1.61	0.80
2:B:175:SER:H	2:B:216:ASN:HD21	1.31	0.77
4:D:55:THR:HG23	4:D:57:ALA:H	1.48	0.77
3:C:144:ILE:HD13	3:C:145:ASN:N	2.01	0.75
4:D:197:SER:OG	4:D:198:PRO:HD3	1.87	0.75
2:B:158:GLY:HA2	2:B:173:TRP:CH2	2.22	0.75
3:C:90:GLN:HE21	3:C:92:ASP:N	1.86	0.74
3:C:93:ASN:ND2	3:C:94:LEU:H	1.84	0.74
1:A:79:ARG:HB3	1:A:80:PRO:HD2	1.70	0.73
2:B:89:PRO:O	2:B:92:THR:HG23	1.89	0.73
4:D:52:ASN:CG	4:D:55:THR:HG22	2.10	0.72
2:B:52:ILE:HD13	2:B:53:ILE:N	2.04	0.72
3:C:21:ILE:HD12	3:C:102:THR:HG21	1.72	0.72
1:A:158:ASN:H	1:A:158:ASN:HD22	1.37	0.72
1:A:66:GLY:HA3	1:A:71:PHE:HA	1.71	0.71
3:C:6:GLN:HE22	3:C:88:CYS:H	1.37	0.71
3:C:37:GLN:HB2	3:C:47:LEU:HD11	1.73	0.70
3:C:28:ASP:O	3:C:29:ILE:HG23	1.91	0.70
4:D:147:VAL:HG13	4:D:196:SER:HB3	1.74	0.70
4:D:195:PRO:O	4:D:198:PRO:HD2	1.91	0.70
2:B:158:GLY:HA2	2:B:173:TRP:HH2	1.54	0.69
3:C:6:GLN:NE2	3:C:99:GLY:HA3	2.07	0.69
1:A:18:ARG:HE	1:A:76:SER:HA	1.56	0.69
4:D:5:GLN:HA	4:D:114:GLN:HE21	1.58	0.69
1:A:118:PHE:HB2	1:A:133:VAL:HG13	1.72	0.69
2:B:214:THR:HG22	2:B:229:ARG:HD3	1.74	0.69
1:A:22:THR:HG22	1:A:72:THR:HG22	1.73	0.69
2:B:33:GLY:HA3	2:B:103:PRO:HD2	1.74	0.68
4:D:155:GLY:HA2	4:D:185:LEU:CD2	2.23	0.68
3:C:6:GLN:HG3	3:C:100:GLY:N	2.08	0.68
4:D:18:VAL:HG12	4:D:86:LEU:HD11	1.76	0.68
3:C:179:LEU:HG	3:C:181:LEU:CD1	2.24	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:4:LEU:HD23	2:B:24:PHE:HB3	1.76	0.67
3:C:33:MET:SD	3:C:88:CYS:HB3	2.35	0.67
1:A:55:GLU:HB3	1:A:58:VAL:HG21	1.76	0.67
1:A:37:ARG:HB2	1:A:47:LEU:HD11	1.77	0.67
2:B:175:SER:N	2:B:216:ASN:HD21	1.93	0.66
3:C:6:GLN:HE21	3:C:99:GLY:HA3	1.61	0.66
4:D:62:GLN:OE1	4:D:65:LYS:HD2	1.95	0.66
4:D:42:GLY:O	4:D:43:LYS:HB2	1.97	0.65
1:A:122:ASP:O	1:A:123:GLU:HB3	1.96	0.65
4:D:43:LYS:HE2	4:D:43:LYS:CA	2.26	0.65
3:C:4:VAL:HG22	3:C:25:THR:HG22	1.79	0.65
3:C:34:ASN:HD22	3:C:89:LEU:HD12	1.62	0.64
3:C:6:GLN:HG3	3:C:101:GLY:N	2.13	0.64
4:D:97:ALA:HB1	4:D:109:PHE:HB3	1.79	0.63
1:A:19:ILE:HD13	1:A:78:LEU:HD11	1.80	0.63
3:C:6:GLN:NE2	3:C:88:CYS:HB2	2.13	0.63
3:C:115:VAL:HA	3:C:135:PHE:O	1.97	0.63
3:C:140:TYR:CD1	3:C:141:PRO:HA	2.34	0.63
2:B:37:GLY:HA2	2:B:52:ILE:HA	1.82	0.62
3:C:52:ASN:HB3	3:C:64:SER:O	2.00	0.62
4:D:198:PRO:O	4:D:202:GLU:HB2	2.00	0.61
4:D:13:LYS:CG	4:D:14:PRO:HD2	2.30	0.61
1:A:90:GLN:HE22	1:A:93:PHE:H	1.48	0.61
2:B:179:THR:O	2:B:182:VAL:HG12	2.00	0.61
4:D:148:THR:C	4:D:149:LEU:HD12	2.21	0.61
1:A:113:PRO:HB3	1:A:139:PHE:HB3	1.83	0.60
1:A:137:ASN:HD22	1:A:138:ASN:H	1.48	0.60
3:C:6:GLN:HE22	3:C:88:CYS:HB2	1.66	0.60
2:B:136:LYS:NZ	2:B:136:LYS:HB2	2.15	0.60
2:B:40:ARG:HB2	2:B:50:LEU:HD11	1.82	0.60
1:A:2:LEU:HD23	1:A:3:GLN:N	2.17	0.60
3:C:54:LEU:HD21	3:C:62:PHE:HB2	1.83	0.60
3:C:179:LEU:HG	3:C:181:LEU:HD11	1.83	0.60
1:A:158:ASN:H	1:A:158:ASN:ND2	1.98	0.60
4:D:221:ILE:HD12	4:D:221:ILE:N	2.18	0.59
3:C:93:ASN:HD22	3:C:94:LEU:H	1.47	0.59
2:B:162:LYS:HG3	2:B:163:ASP:N	2.17	0.59
4:D:128:PRO:HB3	4:D:156:TYR:HB3	1.84	0.59
4:D:136:GLY:HA2	4:D:224:ARG:HD3	1.84	0.59
2:B:11:LEU:HD12	2:B:129:THR:O	2.03	0.59
3:C:31:ASP:HB2	3:C:51:GLY:HA2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:137:ASN:HD22	1:A:138:ASN:N	1.99	0.59
1:A:133:VAL:HG23	1:A:177:SER:O	2.02	0.59
1:A:158:ASN:N	1:A:158:ASN:HD22	1.98	0.58
1:A:14:SER:HB2	1:A:17:ASP:OD1	2.03	0.58
2:B:197:LEU:HD12	2:B:197:LEU:C	2.24	0.58
4:D:13:LYS:HG3	4:D:14:PRO:HD2	1.84	0.58
3:C:48:ILE:HD13	3:C:64:SER:HB2	1.84	0.58
3:C:55:ARG:HD2	3:C:56:PRO:HD2	1.85	0.58
3:C:48:ILE:CG2	3:C:52:ASN:HA	2.33	0.58
1:A:134:CYS:HB2	1:A:148:TRP:CH2	2.38	0.58
3:C:24:ILE:HA	3:C:69:THR:O	2.04	0.58
2:B:214:THR:CG2	2:B:229:ARG:HD3	2.34	0.58
2:B:229:ARG:HG3	2:B:230:VAL:N	2.19	0.58
1:A:30:THR:HG23	1:A:31:SER:H	1.68	0.58
4:D:12:VAL:HG21	4:D:86:LEU:HD12	1.86	0.57
4:D:83:PHE:HB3	4:D:86:LEU:HD21	1.85	0.57
2:B:218:ASN:HD22	2:B:219:HIS:N	2.02	0.57
1:A:75:ILE:N	1:A:75:ILE:HD12	2.20	0.57
1:A:162:SER:OG	2:B:186:PRO:HG2	2.05	0.57
3:C:6:GLN:HE22	3:C:88:CYS:CB	2.17	0.57
2:B:40:ARG:HG2	2:B:41:GLN:N	2.20	0.57
3:C:19:VAL:O	3:C:74:THR:HA	2.04	0.57
4:D:53:CYS:HA	4:D:72:VAL:HG21	1.86	0.57
1:A:112:ALA:HB2	1:A:200:GLY:O	2.05	0.57
1:A:135:LEU:HD22	2:B:200:VAL:HG11	1.87	0.56
3:C:6:GLN:CG	3:C:101:GLY:H	2.16	0.56
2:B:29:LEU:HD12	2:B:55:SER:HA	1.88	0.56
1:A:38:GLN:O	1:A:84:ALA:HB1	2.06	0.56
3:C:20:THR:HA	3:C:73:PHE:O	2.04	0.56
1:A:125:LEU:O	1:A:183:LYS:HD2	2.06	0.56
3:C:90:GLN:HE21	3:C:92:ASP:H	1.54	0.56
2:B:29:LEU:O	2:B:55:SER:HB2	2.05	0.56
3:C:98:PHE:CD2	4:D:45:LEU:HD23	2.40	0.56
1:A:138:ASN:HD21	2:B:183:HIS:HE1	1.54	0.55
2:B:39:ILE:HD12	2:B:39:ILE:N	2.21	0.55
3:C:8:PRO:O	3:C:102:THR:HB	2.06	0.55
1:A:61:ARG:O	1:A:75:ILE:HA	2.06	0.55
4:D:194:VAL:HG23	4:D:195:PRO:HD2	1.88	0.54
1:A:113:PRO:HB3	1:A:139:PHE:CD2	2.42	0.54
3:C:6:GLN:HE22	3:C:88:CYS:N	2.06	0.54
1:A:14:SER:O	1:A:17:ASP:HB2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:2:VAL:HG13	4:D:27:TYR:CD2	2.42	0.54
4:D:14:PRO:HA	4:D:86:LEU:O	2.07	0.54
4:D:152:LEU:CD1	4:D:154:LYS:HB2	2.37	0.54
2:B:24:PHE:HE2	2:B:80:VAL:HG23	1.71	0.54
2:B:138:PRO:HD3	2:B:219:HIS:ND1	2.22	0.54
4:D:123:ALA:HB3	4:D:157:PHE:CE2	2.43	0.54
2:B:117:ASN:O	2:B:118:ALA:HB2	2.07	0.54
4:D:69:THR:HB	4:D:82:GLN:HB3	1.89	0.53
4:D:107:PRO:HB2	4:D:108:PRO:HA	1.88	0.53
4:D:2:VAL:HG13	4:D:27:TYR:HD2	1.73	0.53
4:D:146:MET:HE2	4:D:195:PRO:HA	1.90	0.53
1:A:122:ASP:C	1:A:124:GLN:H	2.11	0.53
1:A:29:VAL:HG11	1:A:90:GLN:HB2	1.91	0.53
1:A:18:ARG:HH21	1:A:76:SER:HA	1.74	0.53
1:A:71:PHE:N	1:A:71:PHE:CD1	2.77	0.53
2:B:138:PRO:HB3	2:B:164:TYR:CB	2.36	0.53
4:D:149:LEU:HD23	4:D:221:ILE:HG21	1.90	0.53
2:B:204:PRO:HB2	2:B:207:SER:HB2	1.90	0.53
1:A:141:PRO:HB2	1:A:143:GLU:HG2	1.90	0.53
1:A:142:ARG:HB2	1:A:173:TYR:CE1	2.44	0.52
1:A:59:PRO:HB3	1:A:61:ARG:NH1	2.25	0.52
3:C:167:ASP:O	3:C:171:SER:HA	2.10	0.52
2:B:77:LYS:O	2:B:79:GLN:HG3	2.09	0.52
1:A:79:ARG:HB2	1:A:82:ASP:OD2	2.09	0.52
1:A:9:SER:O	1:A:102:THR:HA	2.09	0.52
1:A:120:PRO:HD3	1:A:132:VAL:HG22	1.92	0.52
1:A:18:ARG:HG2	1:A:18:ARG:HH11	1.75	0.52
1:A:63:SER:HB3	1:A:74:THR:OG1	2.10	0.52
4:D:130:VAL:CG2	4:D:208:VAL:HG11	2.40	0.51
4:D:130:VAL:HG21	4:D:208:VAL:HG11	1.91	0.51
3:C:136:LEU:N	3:C:136:LEU:HD12	2.24	0.51
2:B:163:ASP:HB3	2:B:194:LEU:HD13	1.93	0.51
4:D:71:THR:HB	4:D:80:TYR:HB2	1.93	0.51
4:D:199:ARG:NH1	4:D:223:PRO:HG3	2.26	0.51
2:B:65:LEU:HD22	2:B:65:LEU:N	2.25	0.51
4:D:163:VAL:HA	4:D:207:ASN:O	2.11	0.51
3:C:42:GLU:HB2	3:C:43:PRO:HD2	1.93	0.51
2:B:103:PRO:HG3	2:B:116:VAL:HG11	1.92	0.51
4:D:149:LEU:HD12	4:D:149:LEU:N	2.25	0.51
1:A:119:PRO:HB3	1:A:209:PHE:CE2	2.46	0.51
3:C:5:THR:O	3:C:23:CYS:HA	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:53:ILE:HD13	2:B:73:LYS:HB3	1.93	0.51
1:A:30:THR:HG23	1:A:31:SER:N	2.26	0.50
3:C:183:LYS:O	3:C:187:GLU:HG2	2.11	0.50
3:C:38:GLN:HE22	4:D:39:GLN:HE22	1.59	0.50
2:B:41:GLN:O	2:B:93:ALA:HB1	2.12	0.50
2:B:106:LEU:HB2	2:B:111:ILE:HD13	1.93	0.50
4:D:33:PHE:CD1	4:D:52:ASN:HA	2.46	0.50
4:D:130:VAL:HG21	4:D:208:VAL:CG1	2.41	0.50
1:A:115:VAL:HA	1:A:135:LEU:O	2.12	0.50
2:B:52:ILE:HD12	2:B:54:TYR:CZ	2.47	0.50
1:A:2:LEU:C	1:A:2:LEU:HD23	2.32	0.50
2:B:6:GLU:HG2	2:B:95:TYR:O	2.11	0.50
1:A:151:ASP:OD2	1:A:189:HIS:HB3	2.12	0.50
4:D:12:VAL:O	4:D:120:VAL:HA	2.12	0.49
2:B:42:PRO:HA	2:B:93:ALA:HB2	1.94	0.49
2:B:165:PHE:CE1	2:B:166:PRO:HB3	2.47	0.49
4:D:194:VAL:CG2	4:D:195:PRO:HD2	2.43	0.49
2:B:28:SER:C	2:B:30:SER:H	2.15	0.49
3:C:117:ILE:HD12	3:C:133:VAL:O	2.12	0.49
1:A:11:LEU:HD23	1:A:103:ARG:O	2.13	0.49
2:B:218:ASN:ND2	2:B:225:LYS:HG2	2.26	0.49
1:A:54:LEU:HD13	1:A:55:GLU:O	2.13	0.49
3:C:157:ASN:OD1	3:C:158:GLY:N	2.46	0.49
2:B:92:THR:HG22	2:B:130:ILE:H	1.77	0.49
2:B:172:SER:OG	2:B:216:ASN:HB2	2.12	0.49
3:C:11:LEU:HD12	3:C:11:LEU:C	2.33	0.49
4:D:188:LEU:HD23	4:D:189:SER:N	2.28	0.49
4:D:199:ARG:HD2	4:D:200:PRO:CA	2.31	0.49
1:A:37:ARG:HG3	1:A:86:TYR:CZ	2.48	0.49
1:A:6:GLN:HG2	1:A:88:CYS:SG	2.53	0.49
2:B:174:ASN:ND2	2:B:178:LEU:HD12	2.28	0.49
4:D:162:THR:O	4:D:208:VAL:HA	2.13	0.48
2:B:174:ASN:HD22	2:B:178:LEU:HD12	1.78	0.48
4:D:209:ALA:HB2	4:D:216:LYS:HG2	1.95	0.48
3:C:6:GLN:NE2	3:C:88:CYS:H	2.10	0.48
1:A:183:LYS:O	1:A:187:GLU:HG2	2.13	0.48
2:B:38:TRP:C	2:B:39:ILE:HD12	2.34	0.48
3:C:32:ASP:HB3	3:C:91:SER:HB2	1.95	0.48
4:D:63:LYS:HD2	4:D:64:PHE:CE1	2.48	0.48
3:C:149:LYS:HD2	3:C:149:LYS:C	2.33	0.48
3:C:72:VAL:HG12	3:C:73:PHE:N	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:93:ASN:ND2	3:C:94:LEU:N	2.58	0.48
3:C:34:ASN:OD1	3:C:49:SER:HA	2.14	0.48
4:D:110:PRO:HB2	4:D:111:TYR:CD1	2.49	0.48
1:A:61:ARG:HA	1:A:76:SER:OG	2.13	0.48
3:C:48:ILE:CD1	3:C:64:SER:HB2	2.44	0.48
1:A:180:THR:O	1:A:181:LEU:HD23	2.14	0.48
3:C:89:LEU:HD11	4:D:107:PRO:HG3	1.96	0.48
1:A:80:PRO:HG2	1:A:81:GLU:H	1.79	0.47
1:A:91:LEU:HD12	1:A:91:LEU:N	2.29	0.47
2:B:6:GLU:OE2	2:B:123:GLY:HA3	2.14	0.47
3:C:11:LEU:HD11	3:C:104:LEU:CD1	2.44	0.47
3:C:48:ILE:HG21	3:C:52:ASN:HA	1.96	0.47
2:B:136:LYS:HZ2	2:B:136:LYS:HB2	1.76	0.47
1:A:116:PHE:CD2	2:B:156:ALA:HB3	2.49	0.47
2:B:138:PRO:CB	2:B:164:TYR:HB3	2.37	0.47
3:C:94:LEU:HD12	3:C:94:LEU:N	2.29	0.47
3:C:39:LYS:HG2	3:C:84:ALA:HB2	1.96	0.47
3:C:150:ILE:O	3:C:151:ASP:C	2.51	0.47
4:D:52:ASN:O	4:D:53:CYS:HB2	2.14	0.47
2:B:41:GLN:C	2:B:93:ALA:HB1	2.34	0.47
3:C:38:GLN:O	3:C:84:ALA:HB1	2.14	0.47
2:B:142:PRO:HD3	2:B:228:LYS:HE3	1.96	0.47
3:C:133:VAL:HG12	3:C:134:CYS:N	2.29	0.47
2:B:157:LEU:HD23	2:B:157:LEU:N	2.29	0.47
2:B:169:VAL:O	2:B:169:VAL:HG13	2.14	0.47
3:C:139:PHE:HE1	3:C:142:LYS:HA	1.78	0.47
1:A:23:CYS:HB2	1:A:35:TRP:CH2	2.49	0.46
2:B:40:ARG:HH21	2:B:84:MET:HE1	1.81	0.46
4:D:39:GLN:HG3	4:D:44:SER:O	2.16	0.46
1:A:147:GLN:CG	1:A:154:LEU:HD11	2.46	0.46
4:D:188:LEU:HD23	4:D:188:LEU:C	2.36	0.46
1:A:24:ARG:C	1:A:24:ARG:HD3	2.36	0.46
4:D:205:THR:HG23	4:D:219:LYS:C	2.35	0.46
1:A:6:GLN:NE2	1:A:88:CYS:SG	2.87	0.46
3:C:34:ASN:ND2	3:C:89:LEU:HD12	2.28	0.46
3:C:90:GLN:NE2	3:C:93:ASN:H	2.14	0.46
2:B:190:GLN:NE2	2:B:196:SER:HB2	2.31	0.46
2:B:55:SER:O	2:B:73:LYS:NZ	2.44	0.46
1:A:138:ASN:ND2	2:B:183:HIS:HE1	2.13	0.46
3:C:24:ILE:N	3:C:24:ILE:HD12	2.31	0.46
2:B:4:LEU:HD12	2:B:121:VAL:HG12	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:5:GLN:CA	4:D:114:GLN:HE21	2.25	0.46
1:A:175:LEU:HD23	1:A:176:SER:N	2.30	0.46
1:A:90:GLN:NE2	1:A:92:HIS:H	2.13	0.45
4:D:34:MET:HB3	4:D:51:ILE:HG22	1.98	0.45
1:A:8:PRO:O	1:A:102:THR:HG22	2.16	0.45
3:C:182:THR:HG22	3:C:183:LYS:N	2.31	0.45
2:B:4:LEU:HD23	2:B:24:PHE:CB	2.45	0.45
4:D:197:SER:C	4:D:199:ARG:H	2.17	0.45
1:A:79:ARG:NE	1:A:80:PRO:HD2	2.32	0.45
1:A:50:ASP:O	1:A:51:ALA:HB3	2.15	0.45
3:C:30:ASP:N	3:C:30:ASP:OD1	2.47	0.45
1:A:43:PRO:HB3	2:B:96:PHE:CE2	2.52	0.45
3:C:159:VAL:HG22	3:C:160:LEU:N	2.32	0.45
1:A:155:GLN:HB3	1:A:158:ASN:HD21	1.81	0.45
1:A:198:HIS:ND1	1:A:199:GLN:N	2.64	0.45
1:A:122:ASP:O	1:A:123:GLU:CB	2.64	0.45
1:A:77:THR:HG23	1:A:77:THR:O	2.17	0.45
1:A:164:THR:HG23	2:B:185:PHE:CD2	2.52	0.45
1:A:198:HIS:CE1	1:A:200:GLY:H	2.35	0.44
2:B:138:PRO:HD2	2:B:224:THR:HB	1.98	0.44
3:C:108:ARG:HG3	3:C:140:TYR:CD2	2.52	0.44
3:C:63:SER:OG	3:C:74:THR:HG22	2.17	0.44
1:A:175:LEU:HD23	1:A:175:LEU:C	2.37	0.44
3:C:123:GLU:N	3:C:123:GLU:OE1	2.50	0.44
4:D:42:GLY:O	4:D:43:LYS:CB	2.65	0.44
3:C:8:PRO:CG	3:C:11:LEU:HD23	2.47	0.44
3:C:144:ILE:HD13	3:C:144:ILE:C	2.38	0.44
3:C:90:GLN:NE2	3:C:93:ASN:N	2.65	0.44
1:A:79:ARG:HB3	1:A:80:PRO:CD	2.45	0.44
1:A:33:LEU:HD12	1:A:89:GLN:O	2.16	0.44
1:A:151:ASP:O	1:A:152:ASN:HB2	2.18	0.44
4:D:182:GLN:O	4:D:183:SER:HB2	2.18	0.44
4:D:11:LEU:C	4:D:11:LEU:HD13	2.37	0.44
1:A:54:LEU:HD11	1:A:58:VAL:HB	2.00	0.44
1:A:92:HIS:HD2	1:A:93:PHE:CE1	2.35	0.44
3:C:28:ASP:O	3:C:29:ILE:CG2	2.63	0.44
4:D:136:GLY:O	4:D:137:SER:C	2.55	0.44
3:C:38:GLN:NE2	4:D:39:GLN:HE22	2.16	0.44
3:C:193:THR:OG1	3:C:208:SER:HB3	2.17	0.44
2:B:12:VAL:HB	2:B:130:ILE:HD13	2.00	0.44
2:B:91:ASP:HB2	2:B:130:ILE:HG13	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:181:LEU:HD23	3:C:185:GLU:HG3	2.01	0.43
1:A:54:LEU:CD1	1:A:58:VAL:HB	2.48	0.43
3:C:163:TRP:CD1	3:C:175:MET:HB3	2.53	0.43
3:C:6:GLN:OE1	3:C:101:GLY:HA2	2.18	0.43
3:C:93:ASN:HD22	3:C:94:LEU:N	2.14	0.43
1:A:124:GLN:HB2	2:B:141:PHE:CD2	2.53	0.43
4:D:52:ASN:OD1	4:D:54:TYR:HB3	2.18	0.43
2:B:69:LEU:HD21	2:B:84:MET:HE3	2.00	0.43
2:B:42:PRO:HA	2:B:93:ALA:CB	2.48	0.43
1:A:24:ARG:O	1:A:24:ARG:HD3	2.18	0.43
2:B:22:CYS:HB2	2:B:38:TRP:CZ2	2.54	0.43
1:A:150:VAL:O	1:A:151:ASP:HB2	2.19	0.43
1:A:167:ASP:OD1	1:A:170:ASP:HB2	2.19	0.43
1:A:137:ASN:ND2	1:A:138:ASN:N	2.66	0.43
2:B:157:LEU:HD23	2:B:201:VAL:O	2.18	0.43
2:B:60:ARG:HA	2:B:60:ARG:HD3	1.79	0.43
1:A:122:ASP:O	1:A:124:GLN:N	2.49	0.43
4:D:45:LEU:HA	4:D:45:LEU:HD12	1.88	0.43
1:A:108:ARG:NE	1:A:109:THR:O	2.51	0.43
4:D:166:ASN:HB2	4:D:169:SER:HB2	2.00	0.43
4:D:52:ASN:ND2	4:D:55:THR:HG22	2.33	0.43
2:B:201:VAL:O	2:B:201:VAL:HG13	2.19	0.43
1:A:108:ARG:HG2	1:A:109:THR:N	2.34	0.43
1:A:33:LEU:HD22	1:A:71:PHE:CD1	2.54	0.42
1:A:49:TYR:HE2	1:A:55:GLU:HA	1.84	0.42
1:A:121:SER:C	1:A:122:ASP:O	2.55	0.42
3:C:180:THR:C	3:C:181:LEU:HD12	2.40	0.42
1:A:55:GLU:HG3	1:A:56:SER:N	2.33	0.42
3:C:39:LYS:HB3	3:C:40:PRO:HD2	2.00	0.42
3:C:113:PRO:CA	3:C:139:PHE:HB3	2.49	0.42
4:D:27:TYR:CE1	4:D:29:PHE:HA	2.54	0.42
4:D:155:GLY:CA	4:D:185:LEU:HD21	2.42	0.42
2:B:24:PHE:HZ	2:B:29:LEU:HD23	1.84	0.42
4:D:157:PHE:HA	4:D:158:PRO:HA	1.84	0.42
2:B:204:PRO:O	2:B:207:SER:HB3	2.20	0.42
1:A:42:SER:OG	1:A:43:PRO:HD2	2.20	0.42
3:C:147:LYS:HB2	3:C:195:GLU:HB2	2.02	0.42
1:A:103:ARG:HH11	1:A:103:ARG:HG3	1.85	0.42
3:C:43:PRO:HB3	4:D:95:TYR:CE1	2.55	0.42
4:D:47:TRP:CZ2	4:D:49:GLY:HA2	2.55	0.42
4:D:32:TYR:CG	4:D:98:ARG:HD2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:34:ALA:HA	1:A:48:ILE:O	2.20	0.42
4:D:62:GLN:HA	4:D:65:LYS:HG3	2.01	0.42
2:B:106:LEU:O	2:B:107:PHE:HB2	2.20	0.42
4:D:62:GLN:HA	4:D:65:LYS:CD	2.50	0.41
1:A:132:VAL:HB	1:A:179:LEU:HB3	2.02	0.41
2:B:28:SER:C	2:B:30:SER:N	2.72	0.41
3:C:6:GLN:CG	3:C:99:GLY:HA3	2.49	0.41
3:C:35:TRP:CZ3	3:C:88:CYS:SG	3.12	0.41
2:B:52:ILE:HD12	2:B:54:TYR:CE1	2.56	0.41
1:A:124:GLN:HG2	1:A:129:THR:O	2.19	0.41
2:B:137:GLY:HA2	2:B:222:SER:OG	2.20	0.41
4:D:197:SER:H	4:D:198:PRO:CD	2.33	0.41
2:B:33:GLY:HA3	2:B:103:PRO:CD	2.47	0.41
3:C:8:PRO:HG3	3:C:11:LEU:HD23	2.03	0.41
4:D:177:PHE:HA	4:D:178:PRO:HD3	1.93	0.41
3:C:35:TRP:CH2	3:C:73:PHE:HB2	2.55	0.41
3:C:21:ILE:HB	3:C:73:PHE:HB3	2.02	0.41
2:B:175:SER:H	2:B:216:ASN:ND2	2.10	0.41
1:A:36:TYR:HA	1:A:45:GLN:O	2.20	0.41
3:C:135:PHE:C	3:C:136:LEU:HD12	2.41	0.41
1:A:111:ALA:O	1:A:139:PHE:HA	2.20	0.41
4:D:177:PHE:CD1	4:D:177:PHE:N	2.89	0.41
4:D:52:ASN:C	4:D:54:TYR:H	2.24	0.41
2:B:53:ILE:HG13	2:B:58:ASP:O	2.21	0.41
4:D:152:LEU:HD11	4:D:154:LYS:HB2	2.03	0.41
3:C:170:ASP:OD1	3:C:172:THR:HG23	2.21	0.41
4:D:22:CYS:HB3	4:D:79:ALA:HB3	2.01	0.41
4:D:197:SER:O	4:D:201:SER:HB2	2.21	0.41
1:A:190:LYS:HG3	1:A:191:VAL:HG23	2.03	0.41
4:D:33:PHE:CE1	4:D:52:ASN:HA	2.56	0.40
1:A:90:GLN:C	1:A:91:LEU:HD12	2.42	0.40
3:C:35:TRP:CH2	3:C:88:CYS:SG	3.15	0.40
1:A:122:ASP:C	1:A:124:GLN:N	2.73	0.40
3:C:128:GLY:HA2	3:C:183:LYS:HD2	2.03	0.40
2:B:7:SER:OG	2:B:21:THR:HB	2.21	0.40
3:C:21:ILE:HG22	3:C:22:ARG:N	2.35	0.40
1:A:18:ARG:NE	1:A:76:SER:HA	2.30	0.40
4:D:161:VAL:HG13	4:D:208:VAL:HG23	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	A	209/214 (98%)	186 (89%)	19 (9%)	4 (2%)	10	43
2	B	206/235 (88%)	172 (84%)	32 (16%)	2 (1%)	19	61
3	C	174/233 (75%)	148 (85%)	23 (13%)	3 (2%)	11	46
4	D	213/241 (88%)	188 (88%)	20 (9%)	5 (2%)	8	36
All	All	802/923 (87%)	694 (86%)	94 (12%)	14 (2%)	11	46

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	43	LYS
1	A	122	ASP
1	A	138	ASN
2	B	163	ASP
3	C	30	ASP
3	C	92	ASP
4	D	91	SER
4	D	197	SER
1	A	40	PRO
3	C	32	ASP
4	D	62	GLN
2	B	16	GLN
4	D	45	LEU
1	A	59	PRO

### 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	185/187 (99%)	176 (95%)	9 (5%)	31	71
2	B	188/203 (93%)	178 (95%)	10 (5%)	28	67
3	C	168/210 (80%)	160 (95%)	8 (5%)	31	71
4	D	187/205 (91%)	183 (98%)	4 (2%)	61	89
All	All	728/805 (90%)	697 (96%)	31 (4%)	35	75

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	ASP
1	A	24	ARG
1	A	71	PHE
1	A	90	GLN
1	A	108	ARG
1	A	137	ASN
1	A	143	GLU
1	A	158	ASN
1	A	170	ASP
2	B	52	ILE
2	B	56	ASP
2	B	86	ARG
2	B	90	VAL
2	B	92	THR
2	B	99	HIS
2	B	136	LYS
2	B	218	ASN
2	B	227	ASP
2	B	229	ARG
3	C	6	GLN
3	C	30	ASP
3	C	31	ASP
3	C	82	ASP
3	C	93	ASN
3	C	97	THR
3	C	144	ILE
3	C	146	VAL
4	D	62	GLN
4	D	72	VAL
4	D	83	PHE
4	D	199	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	3	GLN
1	A	38	GLN
1	A	90	GLN
1	A	92	HIS
1	A	96	HIS
1	A	137	ASN
1	A	138	ASN
1	A	158	ASN
1	A	166	GLN
1	A	199	GLN
2	B	16	GLN
2	B	41	GLN
2	B	78	ASN
2	B	174	ASN
2	B	183	HIS
2	B	190	GLN
2	B	216	ASN
2	B	218	ASN
3	C	6	GLN
3	C	52	ASN
3	C	90	GLN
3	C	93	ASN
3	C	161	ASN
3	C	166	GLN
4	D	3	GLN
4	D	5	GLN
4	D	77	ASN
4	D	114	GLN
4	D	175	HIS

### 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

1 ligand is 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	$\# Z  > 2$
5	SO4	D	225	-	4,4,4	0.22	0	6,6,6	0.09	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
5	SO4	D	225	-	-	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.

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	A	211/214 (98%)	0.06	1 (0%) 91 76	43, 68, 84, 109	0
2	B	214/235 (91%)	0.02	3 (1%) 78 51	37, 60, 83, 97	0
3	C	186/233 (79%)	0.53	12 (6%) 22 8	57, 82, 100, 116	0
4	D	217/241 (90%)	-0.00	2 (0%) 85 64	35, 55, 82, 101	0
All	All	828/923 (89%)	0.14	18 (2%) 65 35	35, 65, 92, 116	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	133	THR	4.0
3	C	23	CYS	3.4
3	C	24	ILE	3.1
3	C	198	HIS	3.1
1	A	193	GLU	2.8
4	D	145	SER	2.6
3	C	142	LYS	2.5
2	B	117	ASN	2.5
3	C	81	GLU	2.5
3	C	111	ALA	2.4
3	C	143	ASP	2.3
3	C	188	ARG	2.3
3	C	110	ASP	2.3
3	C	149	LYS	2.1
2	B	1	ARG	2.1
4	D	182	GLN	2.1
3	C	197	THR	2.1
3	C	68	GLY	2.1

## 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( $\text{\AA}^2$ )	Q<0.9
5	SO4	D	225	5/5	0.97	0.14	-2.62	70,70,70,70	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.