Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 09:08 AM GMT

PDB ID	:	3H9J
Title	:	Crystal structure of E. coli MccB + AMPCPP + SeMeT MccA
Authors	:	Regni, C.A.; Roush, R.F.; Miller, D.; Nourse, A.; Walsh, C.T.; Schulman, B.A.
Deposited on	:	2009-04-30
Resolution	:	2.30 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:

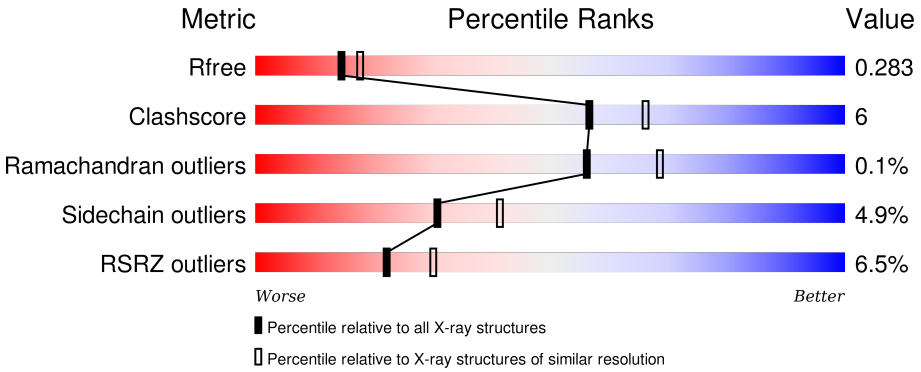
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	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 2.30 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	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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	353	5% 82% 12%
1	B	353	8% 80% 14% 5%
1	C	353	3% 84% 10%
1	D	353	9% 80% 13% 5%
2	E	7	14% 86%

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Mol	Chain	Length	Quality of chain
2	F	7	
2	G	7	
2	H	7	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 10848 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 MccB protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	339	Total	C	N	O	S	0	0	0
			2616	1671	446	488	11			
1	B	336	Total	C	N	O	S	0	0	0
			2569	1646	432	480	11			
1	C	344	Total	C	N	O	S	0	0	0
			2658	1698	453	496	11			
1	D	334	Total	C	N	O	S	0	1	0
			2564	1638	439	476	11			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	EXPRESSION TAG	UNP Q47506
A	-1	SER	-	EXPRESSION TAG	UNP Q47506
A	0	HIS	-	EXPRESSION TAG	UNP Q47506
B	-2	GLY	-	EXPRESSION TAG	UNP Q47506
B	-1	SER	-	EXPRESSION TAG	UNP Q47506
B	0	HIS	-	EXPRESSION TAG	UNP Q47506
C	-2	GLY	-	EXPRESSION TAG	UNP Q47506
C	-1	SER	-	EXPRESSION TAG	UNP Q47506
C	0	HIS	-	EXPRESSION TAG	UNP Q47506
D	-2	GLY	-	EXPRESSION TAG	UNP Q47506
D	-1	SER	-	EXPRESSION TAG	UNP Q47506
D	0	HIS	-	EXPRESSION TAG	UNP Q47506

- Molecule 2 is a protein called Microcin C7 ANALOG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	1	Total	C	N	O	Se	0	0	0
			8	5	1	1	1			
2	F	1	Total	C	N	O	Se	0	0	0
			8	5	1	1	1			

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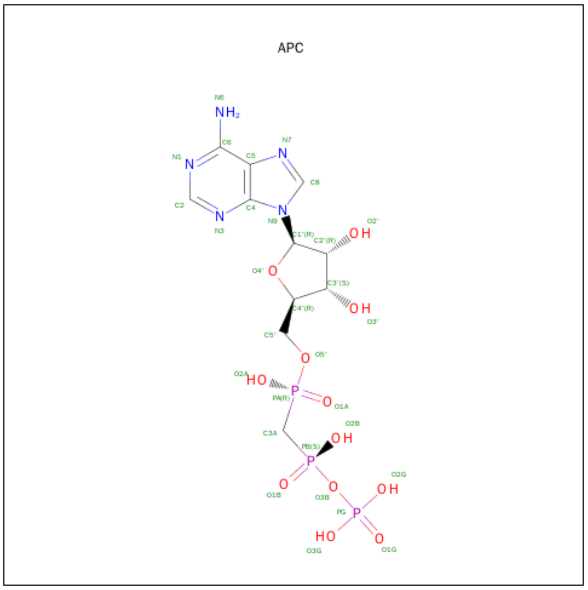
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
2	G	7	Total C N O Se 52 28 12 11 1	0	0	0
2	H	1	Total C N O Se 8 5 1 1 1	0	0	0

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 4 is DIPHOSPHOMETHYLPHOSPHONIC ACID ADENOSYL ESTER (three-letter code: APC) (formula: $C_{11}H_{18}N_5O_{12}P_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N O P 31 11 5 12 3	0	0
4	B	1	Total C N O P 31 11 5 12 3	0	0
4	C	1	Total C N O P 31 11 5 12 3	0	0

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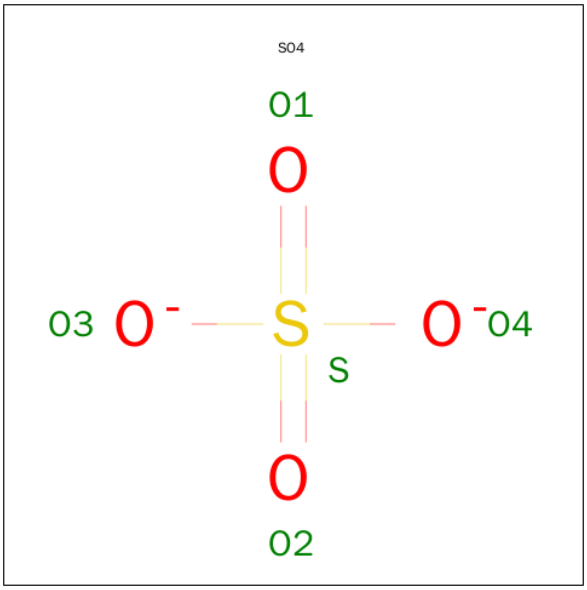
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	1	Total C N O P 31 11 5 12 3	0	0
4	D	1	Total C O P 9 1 6 2	0	0

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

- Molecule 6 is water.

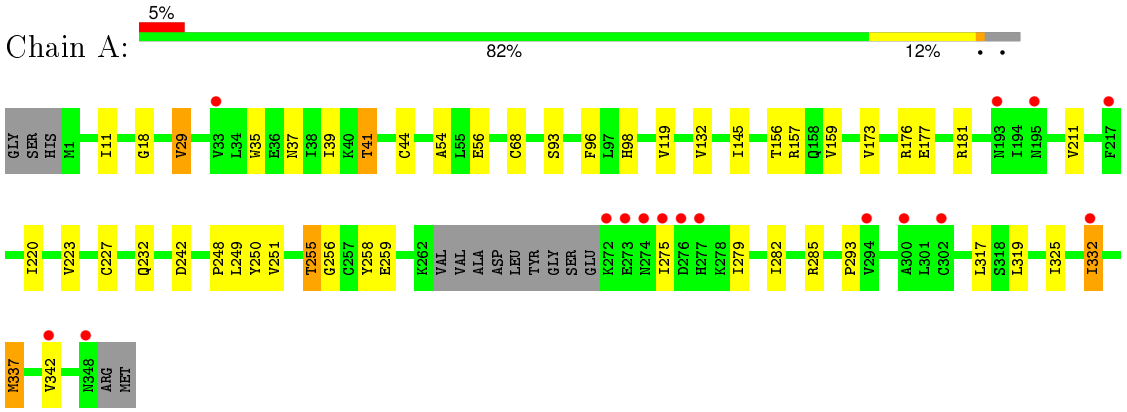
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	62	Total O 62 62	0	0
6	B	44	Total O 44 44	0	0
6	C	69	Total O 69 69	0	0
6	D	47	Total O 47 47	0	0
6	G	1	Total O 1 1	0	0

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.

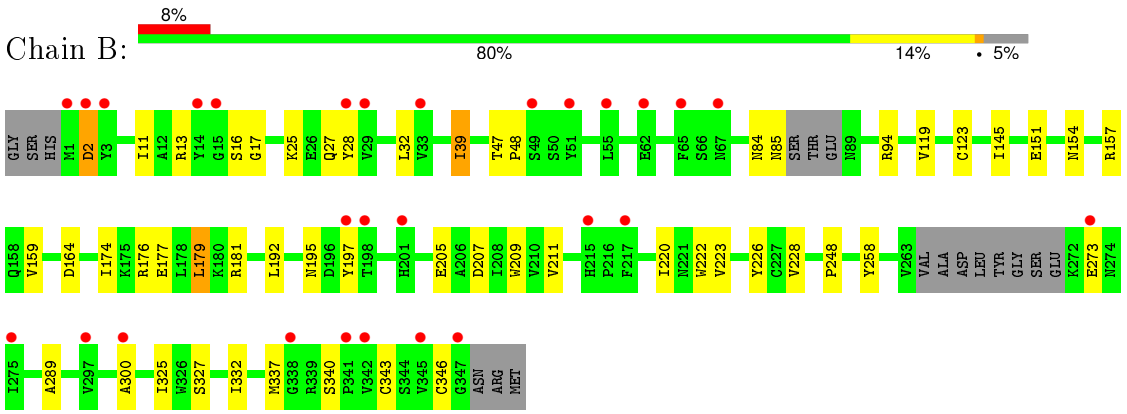
- Molecule 1: MccB protein

Chain A:



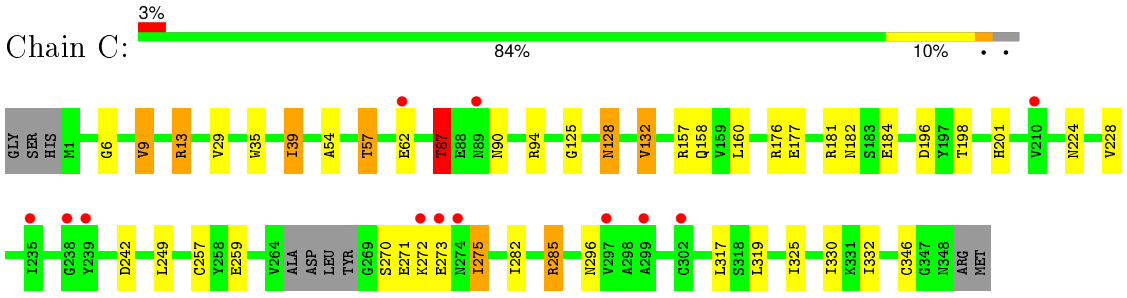
- Molecule 1: MccB protein

Chain B:



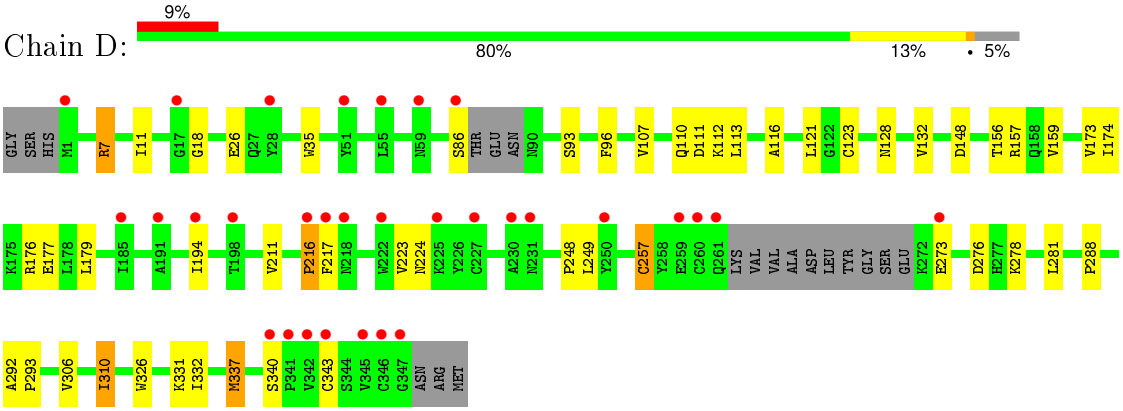
- Molecule 1: MccB protein

Chain C:



• Molecule 1: MccB protein

Chain D:



• Molecule 2: Microcin C7 ANALOG

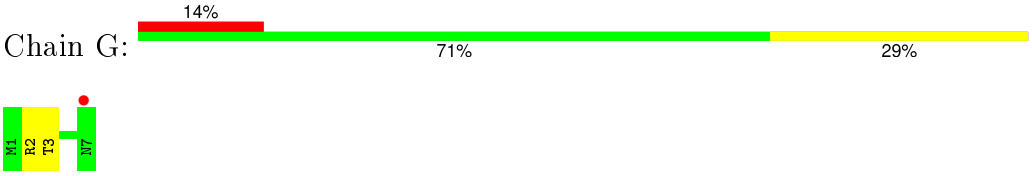
Chain E:

• Molecule 2: Microcin C7 ANALOG

Chain F:

• Molecule 2: Microcin C7 ANALOG

Chain G:



• Molecule 2: Microcin C7 ANALOG

Chain H:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	55.84Å 138.00Å 80.82Å 90.00° 92.21° 90.00°	Depositor
Resolution (Å)	39.97 – 2.30 44.28 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.2 (39.97-2.30) 99.2 (44.28-2.30)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.95 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.196 , 0.255 0.228 , 0.283	Depositor DCC
R_{free} test set	2715 reflections (5.32%)	DCC
Wilson B-factor (Å^2)	37.9	Xtriage
Anisotropy	0.330	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 36.0	EDS
Estimated twinning fraction	0.035 for h,-k,-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Outliers	0 of 53756 reflections	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	10848	wwPDB-VP
Average B, all atoms (Å^2)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.22% 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: APC, ZN, 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	0.48	0/2671	0.59	0/3630
1	B	0.49	1/2622 (0.0%)	0.57	0/3566
1	C	0.51	0/2713	0.60	0/3681
1	D	0.70	3/2623 (0.1%)	0.60	0/3563
2	E	0.64	0/7	0.60	0/7
2	F	0.63	0/7	0.50	0/7
2	G	0.54	0/51	0.59	0/65
2	H	0.67	0/7	0.49	0/7
All	All	0.55	4/10701 (0.0%)	0.59	0/14526

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	273[A]	GLU	CG-CD	-17.20	1.26	1.51
1	D	273[B]	GLU	CG-CD	-17.20	1.26	1.51
1	D	86	SER	CB-OG	9.28	1.54	1.42
1	B	273	GLU	CD-OE2	7.03	1.33	1.25

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	2616	0	2555	42	0
1	B	2569	0	2490	39	0
1	C	2658	0	2615	33	0
1	D	2564	0	2494	33	0
2	E	8	0	11	0	0
2	F	8	0	11	0	0
2	G	52	0	51	1	0
2	H	8	0	11	0	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	31	0	14	1	0
4	B	31	0	14	0	0
4	C	62	0	28	1	0
4	D	9	0	2	0	0
5	B	5	0	0	0	0
6	A	62	0	0	1	0
6	B	44	0	0	4	0
6	C	69	0	0	3	0
6	D	47	0	0	1	0
6	G	1	0	0	0	0
All	All	10848	0	10296	128	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 6.

All (128) 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:A:181:ARG:NH1	1:B:159:VAL:O	1.95	0.98
1:C:285:ARG:HH11	1:C:285:ARG:HG2	1.37	0.89
1:C:13:ARG:HG3	1:C:13:ARG:HH11	1.41	0.86
1:A:248:PRO:HG3	1:A:337:MET:HE1	1.59	0.82
1:A:248:PRO:HG3	1:A:337:MET:CE	2.14	0.76
1:B:94:ARG:O	6:B:400:HOH:O	2.02	0.75
1:D:156:THR:HG22	1:D:157:ARG:HG3	1.67	0.75
1:C:128:ASN:O	1:C:132:VAL:HG23	1.87	0.74
1:D:121:LEU:HD11	1:D:194:ILE:HD11	1.70	0.74
1:B:258:TYR:HA	1:B:337:MET:HE3	1.72	0.72
1:C:157:ARG:HB2	6:C:421:HOH:O	1.90	0.72
1:A:279:ILE:HG13	1:B:39:ILE:HD12	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:29:VAL:HG22	1:A:35:TRP:HB2	1.71	0.71
1:A:159:VAL:O	1:B:181:ARG:NH1	2.25	0.70
1:C:296:ASN:ND2	6:C:421:HOH:O	2.22	0.68
1:D:248:PRO:HG3	1:D:337:MET:HE1	1.76	0.68
1:C:87:THR:HG23	1:C:90:ASN:HB2	1.77	0.67
1:C:132:VAL:HG22	1:C:160:LEU:HD11	1.78	0.66
1:C:285:ARG:NH1	1:C:285:ARG:HG2	2.09	0.65
1:C:181:ARG:NH1	1:D:159:VAL:O	2.30	0.65
1:B:258:TYR:HA	1:B:337:MET:CE	2.27	0.64
4:A:359:APC:O3B	4:A:359:APC:H5'2	1.96	0.64
1:D:248:PRO:HG3	1:D:337:MET:CE	2.28	0.64
1:B:211:VAL:HG21	1:B:223:VAL:HG11	1.80	0.63
1:A:317:LEU:HD11	1:B:327:SER:O	2.00	0.62
1:C:272:LYS:HB2	1:C:275:ILE:HD13	1.83	0.61
1:C:94:ARG:HH22	1:D:288:PRO:HD2	1.65	0.61
1:C:177:GLU:OE1	1:C:181:ARG:NH2	2.34	0.61
1:D:96:PHE:CE1	1:D:110:GLN:HG3	2.36	0.61
1:B:176:ARG:NH1	1:B:177:GLU:OE2	2.34	0.60
1:C:272:LYS:HB2	1:C:275:ILE:CD1	2.31	0.59
1:C:282:ILE:HG21	1:D:11:ILE:HD12	1.85	0.59
1:A:251:VAL:H	1:A:255:THR:CG2	2.16	0.59
1:C:35:TRP:O	1:C:39:ILE:HG23	2.03	0.58
1:D:123:CYS:HB3	1:D:174:ILE:HD12	1.86	0.58
1:B:248:PRO:HG3	1:B:337:MET:CE	2.34	0.57
1:C:325:ILE:HG12	1:C:332:ILE:HG12	1.86	0.57
1:C:13:ARG:HG3	1:C:13:ARG:NH1	2.15	0.57
1:D:123:CYS:HB3	1:D:174:ILE:CD1	2.35	0.57
1:D:110:GLN:NE2	6:D:376:HOH:O	2.37	0.56
1:A:41:THR:HG21	1:A:68:CYS:HB2	1.88	0.56
1:C:330:ILE:HG23	1:D:332:ILE:HG21	1.86	0.56
1:A:275:ILE:HD11	1:B:13:ARG:HH21	1.69	0.56
1:D:96:PHE:HE1	1:D:110:GLN:HG3	1.69	0.56
1:B:119:VAL:HG13	1:B:145:ILE:HD12	1.86	0.56
1:D:306:VAL:O	1:D:310:ILE:HG23	2.05	0.55
1:A:37:ASN:O	1:A:41:THR:HG23	2.06	0.55
1:A:176:ARG:NH1	1:A:177:GLU:OE2	2.40	0.54
1:B:157:ARG:NH1	6:B:397:HOH:O	2.40	0.54
1:A:332:ILE:HD11	1:B:332:ILE:HG22	1.89	0.54
1:B:154:ASN:HA	6:B:397:HOH:O	2.07	0.54
1:C:6:GLY:O	1:C:9:VAL:HG13	2.09	0.54
1:C:270:SER:OG	1:C:275:ILE:HD11	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:340:SER:HB3	1:D:343:CYS:HB2	1.90	0.53
1:A:332:ILE:HD11	1:B:332:ILE:N	2.23	0.53
1:B:248:PRO:HG3	1:B:337:MET:HE2	1.91	0.52
1:A:211:VAL:HG21	1:A:223:VAL:HG11	1.92	0.52
1:C:39:ILE:HD11	1:D:278:LYS:HB2	1.91	0.51
4:C:359:APC:H3A2	6:C:414:HOH:O	2.10	0.51
1:A:250:TYR:HA	1:A:255:THR:HG21	1.93	0.51
1:D:113:LEU:HA	1:D:310:ILE:HD11	1.92	0.51
1:C:182:ASN:OD1	1:C:184:GLU:HB2	2.12	0.50
1:C:177:GLU:HB3	1:C:181:ARG:HH21	1.77	0.50
1:B:205:GLU:HA	6:B:371:HOH:O	2.12	0.49
1:A:35:TRP:CZ2	1:A:39:ILE:HD11	2.47	0.49
1:A:258:TYR:HA	1:A:337:MET:CE	2.43	0.49
1:B:228:VAL:HG11	1:B:346:CYS:HB3	1.94	0.49
1:B:340:SER:HB3	1:B:343:CYS:HB2	1.94	0.48
1:D:211:VAL:HG21	1:D:223:VAL:HG11	1.95	0.48
1:C:224:ASN:OD1	1:C:257:CYS:HB2	2.13	0.48
1:A:251:VAL:H	1:A:255:THR:HG21	1.78	0.48
1:D:116:ALA:HB2	1:D:310:ILE:HD13	1.94	0.48
1:A:293:PRO:HB3	1:B:300:ALA:O	2.13	0.48
1:D:326:TRP:CE2	1:D:331:LYS:HE3	2.49	0.47
1:A:248:PRO:HG3	1:A:337:MET:HE2	1.95	0.47
1:A:342:VAL:HG12	1:A:342:VAL:O	2.16	0.46
1:D:113:LEU:HD23	1:D:310:ILE:CG1	2.45	0.46
1:B:179:LEU:HA	1:B:179:LEU:HD12	1.85	0.46
1:D:292:ALA:HB3	1:D:293:PRO:HD3	1.98	0.45
1:C:198:THR:O	1:C:201:HIS:ND1	2.45	0.45
1:A:37:ASN:O	1:A:41:THR:CG2	2.64	0.45
1:A:119:VAL:HG13	1:A:145:ILE:HD12	1.98	0.45
1:B:325:ILE:HG12	1:B:332:ILE:HG13	1.99	0.45
1:C:224:ASN:O	1:C:228:VAL:HG23	2.16	0.45
1:D:112:LYS:C	1:D:310:ILE:HD11	2.37	0.44
1:D:224:ASN:HD21	1:D:257:CYS:HB2	1.83	0.44
1:A:227:CYS:HB3	1:A:232:GLN:O	2.18	0.44
1:A:282:ILE:HG21	1:B:11:ILE:HD12	1.99	0.44
1:B:17:GLY:HA2	1:B:32:LEU:HD13	2.01	0.43
1:A:220:ILE:HD12	1:A:258:TYR:CZ	2.53	0.43
1:A:173:VAL:HG13	1:A:176:ARG:HH21	1.83	0.43
1:A:332:ILE:CD1	1:B:332:ILE:HG22	2.48	0.43
1:B:2:ASP:OD1	1:B:48:PRO:HB2	2.18	0.43
1:A:93:SER:O	1:A:96:PHE:HB2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:228:VAL:HG11	1:C:346:CYS:HA	2.00	0.43
1:B:123:CYS:HB3	1:B:174:ILE:HD12	2.00	0.43
1:A:44:CYS:HB3	1:A:54:ALA:HB1	2.01	0.42
1:A:156:THR:HG21	6:A:421:HOH:O	2.18	0.42
1:B:248:PRO:HG3	1:B:337:MET:HE1	2.01	0.42
1:A:255:THR:HG23	1:A:256:GLY:O	2.18	0.42
1:A:258:TYR:HA	1:A:337:MET:HE1	2.02	0.42
1:C:54:ALA:O	1:C:57:THR:HG22	2.20	0.42
1:D:93:SER:O	1:D:96:PHE:HB2	2.20	0.42
1:A:98:HIS:HA	1:B:289:ALA:HB1	2.01	0.42
1:A:332:ILE:HD11	1:B:332:ILE:H	1.84	0.41
1:D:176:ARG:NH1	1:D:177:GLU:OE2	2.51	0.41
1:C:125:GLY:HA2	1:C:158:GLN:HG2	2.02	0.41
1:D:216:PRO:HB2	1:D:217:PHE:H	1.64	0.41
1:A:279:ILE:CG1	1:B:39:ILE:HD12	2.47	0.41
1:A:251:VAL:H	1:A:255:THR:HG22	1.85	0.41
1:A:275:ILE:CD1	1:B:13:ARG:HH21	2.32	0.41
1:B:209:TRP:CH2	1:B:226:TYR:CE2	3.08	0.41
1:B:197:TYR:HB2	1:B:222:TRP:CD1	2.55	0.41
1:B:16:SER:HB3	1:B:28:TYR:OH	2.20	0.41
1:C:285:ARG:O	1:D:7:ARG:HD2	2.21	0.41
1:A:18:GLY:HA3	1:A:35:TRP:CE2	2.55	0.41
1:A:220:ILE:HD12	1:A:258:TYR:OH	2.21	0.41
1:C:332:ILE:HG13	1:D:332:ILE:HG13	2.03	0.41
1:B:84:ASN:O	1:B:85:ASN:C	2.59	0.41
1:D:26:GLU:OE1	2:G:2:ARG:HD3	2.20	0.41
1:D:18:GLY:HA3	1:D:35:TRP:CE2	2.56	0.41
1:C:296:ASN:HD22	1:C:296:ASN:N	2.19	0.41
1:B:151:GLU:H	1:B:154:ASN:ND2	2.19	0.40
1:D:173:VAL:HG13	1:D:176:ARG:NH2	2.35	0.40
1:B:25:LYS:O	1:B:27:GLN:HG3	2.21	0.40
1:A:325:ILE:HG13	1:A:332:ILE:HG23	2.01	0.40
1:C:196:ASP:OD2	1:C:198:THR:OG1	2.32	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	335/353 (95%)	327 (98%)	8 (2%)	0	100	100
1	B	330/353 (94%)	319 (97%)	11 (3%)	0	100	100
1	C	340/353 (96%)	330 (97%)	9 (3%)	1 (0%)	46	57
1	D	329/353 (93%)	319 (97%)	9 (3%)	1 (0%)	46	57
2	G	5/7 (71%)	5 (100%)	0	0	100	100
All	All	1339/1419 (94%)	1300 (97%)	37 (3%)	2 (0%)	56	68

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	216	PRO
1	C	87	THR

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	279/304 (92%)	265 (95%)	14 (5%)	30	41
1	B	270/304 (89%)	261 (97%)	9 (3%)	45	61
1	C	285/304 (94%)	266 (93%)	19 (7%)	20	26
1	D	271/304 (89%)	259 (96%)	12 (4%)	35	46
2	E	1/4 (25%)	1 (100%)	0	100	100
2	F	1/4 (25%)	1 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	G	5/4 (125%)	4 (80%)	1 (20%)	1 1
2	H	1/4 (25%)	1 (100%)	0	100 100
All	All	1113/1232 (90%)	1058 (95%)	55 (5%)	31 41

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	ILE
1	A	29	VAL
1	A	41	THR
1	A	56	GLU
1	A	132	VAL
1	A	157	ARG
1	A	242	ASP
1	A	249	LEU
1	A	255	THR
1	A	259	GLU
1	A	285	ARG
1	A	319	LEU
1	A	332	ILE
1	A	337	MET
1	B	2	ASP
1	B	39	ILE
1	B	47	THR
1	B	164	ASP
1	B	179	LEU
1	B	192	LEU
1	B	195	ASN
1	B	207	ASP
1	B	220	ILE
1	C	9	VAL
1	C	13	ARG
1	C	29	VAL
1	C	39	ILE
1	C	57	THR
1	C	62	GLU
1	C	87	THR
1	C	128	ASN
1	C	132	VAL
1	C	176	ARG
1	C	242	ASP

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Mol	Chain	Res	Type
1	C	249	LEU
1	C	259	GLU
1	C	271	GLU
1	C	273	GLU
1	C	275	ILE
1	C	285	ARG
1	C	317	LEU
1	C	319	LEU
1	D	7	ARG
1	D	107	VAL
1	D	111	ASP
1	D	128	ASN
1	D	132	VAL
1	D	148	ASP
1	D	179	LEU
1	D	249	LEU
1	D	257	CYS
1	D	281	LEU
1	D	310	ILE
1	D	337	MET
2	G	3	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	85	ASN
1	A	295	ASN
1	A	296	ASN
1	B	27	GLN
1	B	31	ASN
1	B	154	ASN
1	B	195	ASN
1	C	129	HIS
1	C	147	ASN
1	C	231	ASN
1	C	295	ASN
1	C	296	ASN
1	C	333	HIS
1	D	154	ASN
1	D	193	ASN
1	D	224	ASN

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

Of 10 ligands modelled in this entry, 4 are monoatomic - leaving 6 for Mogul analysis.

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	$\#\|Z\| > 2$
4	APC	A	359	-	25,33,33	1.33	2 (8%)	30,52,52	2.49	7 (23%)
4	APC	B	359	-	25,33,33	1.32	2 (8%)	30,52,52	2.40	8 (26%)
5	SO4	B	360	-	4,4,4	0.17	0	6,6,6	0.10	0
4	APC	C	359	-	25,33,33	1.49	3 (12%)	30,52,52	2.25	5 (16%)
4	APC	C	360	-	25,33,33	1.33	2 (8%)	30,52,52	2.46	6 (20%)
4	APC	D	359	-	6,8,33	1.76	2 (33%)	12,13,52	1.64	4 (33%)

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
4	APC	A	359	-	-	0/15/38/38	0/3/3/3
4	APC	B	359	-	-	0/15/38/38	0/3/3/3
5	SO4	B	360	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	APC	C	359	-	-	0/15/38/38	0/3/3/3
4	APC	C	360	-	-	0/15/38/38	0/3/3/3
4	APC	D	359	-	-	0/6/6/38	0/0/0/3

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	359	APC	PB-O2B	-2.02	1.51	1.56
4	D	359	APC	PA-O5'	2.63	1.61	1.54
4	D	359	APC	PB-O3B	2.71	1.61	1.54
4	A	359	APC	PB-O3B	2.87	1.61	1.58
4	C	360	APC	PB-O3B	3.08	1.61	1.58
4	C	359	APC	PA-O5'	3.59	1.61	1.57
4	B	359	APC	PB-O3B	3.63	1.62	1.58
4	B	359	APC	PA-O5'	3.87	1.61	1.57
4	C	360	APC	PA-O5'	3.98	1.61	1.57
4	A	359	APC	PA-O5'	4.43	1.62	1.57
4	C	359	APC	PB-O3B	4.67	1.63	1.58

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	359	APC	N3-C2-N1	-11.24	120.29	128.89
4	C	360	APC	N3-C2-N1	-10.66	120.73	128.89
4	B	359	APC	N3-C2-N1	-10.62	120.76	128.89
4	C	359	APC	N3-C2-N1	-9.94	121.29	128.89
4	C	360	APC	C2'-C1'-N9	-3.93	108.28	114.29
4	C	359	APC	O5'-PA-O1A	-3.37	105.01	113.98
4	B	359	APC	O5'-PA-O1A	-2.97	106.07	113.98
4	A	359	APC	C1'-N9-C4	-2.95	122.49	126.94
4	C	360	APC	PG-O3B-PB	-2.94	122.81	132.67
4	A	359	APC	PG-O3B-PB	-2.89	122.98	132.67
4	C	360	APC	O5'-PA-O1A	-2.84	106.42	113.98
4	D	359	APC	O5'-PA-O1A	-2.84	105.14	112.40
4	A	359	APC	O5'-PA-O1A	-2.64	106.97	113.98
4	B	359	APC	PG-O3B-PB	-2.47	124.38	132.67
4	D	359	APC	O3B-PB-O1B	-2.47	106.08	112.40
4	B	359	APC	C2'-C1'-N9	-2.44	110.57	114.29
4	A	359	APC	C4-C5-N7	-2.26	107.40	109.48
4	C	359	APC	C1'-N9-C4	-2.22	123.59	126.94
4	B	359	APC	C4-C5-N7	-2.16	107.49	109.48
4	B	359	APC	C1'-N9-C4	-2.15	123.69	126.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	C	359	APC	C4-C5-N7	-2.01	107.63	109.48
4	A	359	APC	O3G-PG-O2G	2.17	115.63	107.38
4	D	359	APC	O2A-PA-O1A	2.38	118.49	112.40
4	C	360	APC	O2B-PB-O1B	2.45	117.82	110.12
4	C	359	APC	O2B-PB-O1B	2.56	118.17	110.12
4	A	359	APC	O2B-PB-O1B	2.56	118.18	110.12
4	C	360	APC	O2A-PA-O1A	2.60	118.30	110.12
4	B	359	APC	O2A-PA-O1A	2.62	118.37	110.12
4	B	359	APC	O2B-PB-O1B	2.64	118.43	110.12
4	D	359	APC	O2B-PB-O1B	2.74	119.42	112.40

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	359	APC	1	0
4	C	359	APC	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{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	339/353 (96%)	0.47	16 (4%) 35 44	33, 43, 55, 62	0
1	B	336/353 (95%)	0.64	28 (8%) 14 20	31, 42, 55, 66	0
1	C	344/353 (97%)	0.44	12 (3%) 48 56	31, 42, 56, 67	0
1	D	334/353 (94%)	0.64	31 (9%) 11 16	28, 42, 56, 66	0
2	E	0/7	-	-	-	-
2	F	0/7	-	-	-	-
2	G	6/7 (85%)	1.61	1 (16%) 2 4	64, 65, 67, 67	0
2	H	0/7	-	-	-	-
All	All	1359/1440 (94%)	0.55	88 (6%) 22 30	28, 42, 56, 67	0

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	342	VAL	6.7
1	C	89	ASN	6.7
1	D	343	CYS	6.0
1	B	342	VAL	5.2
1	D	341	PRO	5.1
1	D	347	GLY	4.8
1	D	217	PHE	4.8
1	D	1	MET	4.6
1	B	197	TYR	4.5
1	D	340	SER	4.5
1	B	217	PHE	4.4
1	D	198	THR	4.3
1	D	345	VAL	4.1
1	A	275	ILE	4.1
1	D	222	TRP	4.0
1	D	17	GLY	3.9
1	B	1	MET	3.9

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Mol	Chain	Res	Type	RSRZ
1	B	55	LEU	3.8
1	B	198	THR	3.7
1	B	15	GLY	3.7
1	B	347	GLY	3.7
1	B	28	TYR	3.6
1	D	346	CYS	3.6
1	B	29	VAL	3.5
1	B	3	TYR	3.4
1	A	272	LYS	3.4
1	D	261	GLN	3.3
1	D	230	ALA	3.3
1	B	51	TYR	3.2
1	B	215	HIS	3.0
1	D	86	SER	3.0
1	D	185	ILE	2.9
1	D	273[A]	GLU	2.9
1	C	273	GLU	2.9
1	A	33	VAL	2.9
1	C	272	LYS	2.8
1	D	51	TYR	2.8
2	G	7	ASN	2.8
1	D	231	ASN	2.7
1	B	62	GLU	2.7
1	B	338	GLY	2.6
1	A	217	PHE	2.6
1	A	195	ASN	2.6
1	C	274	ASN	2.6
1	D	218	ASN	2.6
1	B	14	TYR	2.6
1	D	55	LEU	2.6
1	A	332	ILE	2.6
1	A	274	ASN	2.5
1	C	297	VAL	2.5
1	C	238	GLY	2.5
1	C	62	GLU	2.5
1	D	59	ASN	2.5
1	D	28	TYR	2.5
1	D	191	ALA	2.5
1	D	227	CYS	2.5
1	B	65	PHE	2.5
1	B	201	HIS	2.4
1	B	33	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	302	CYS	2.4
1	D	216	PRO	2.4
1	A	277	HIS	2.4
1	A	342	VAL	2.3
1	D	194	ILE	2.3
1	B	341	PRO	2.3
1	B	275	ILE	2.3
1	A	348	ASN	2.3
1	B	49	SER	2.3
1	C	299	ALA	2.2
1	D	250	TYR	2.2
1	C	235	ILE	2.2
1	B	297	VAL	2.2
1	C	239	TYR	2.2
1	B	273	GLU	2.2
1	D	259	GLU	2.1
1	A	276	ASP	2.1
1	B	300	ALA	2.1
1	A	193	ASN	2.1
1	A	273	GLU	2.1
1	B	2	ASP	2.1
1	B	67	ASN	2.1
1	D	260	CYS	2.1
1	A	302	CYS	2.1
1	A	300	ALA	2.1
1	B	345	VAL	2.1
1	C	210	VAL	2.1
1	D	225	LYS	2.0
1	A	294	VAL	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
4	APC	B	359	31/31	0.74	0.23	1.30	81,82,94,94	0
4	APC	D	359	9/31	0.87	0.20	1.25	89,90,90,90	0
4	APC	C	360	31/31	0.76	0.23	0.27	85,89,105,106	0
4	APC	A	359	31/31	0.89	0.14	-0.75	53,55,74,74	0
5	SO4	B	360	5/5	0.86	0.14	-1.07	95,95,96,96	0
4	APC	C	359	31/31	0.90	0.12	-1.20	37,42,70,71	0
3	ZN	B	500	1/1	0.97	0.06	-1.78	58,58,58,58	0
3	ZN	A	500	1/1	0.98	0.03	-1.94	46,46,46,46	0
3	ZN	D	500	1/1	0.60	0.07	-2.53	86,86,86,86	0
3	ZN	C	500	1/1	0.99	0.05	-2.69	34,34,34,34	0

6.5 Other polymers (i)

There are no such residues in this entry.