Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 08:17 PM GMT

PDB ID	:	4RG6
Title	:	Crystal structure of APC3-APC16 complex
Authors	:	Yamaguchi, M.; Yu, S.; Miller, D.J.; Schulman, B.A.
Deposited on	:	2014-09-29
Resolution	:	3.30 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:

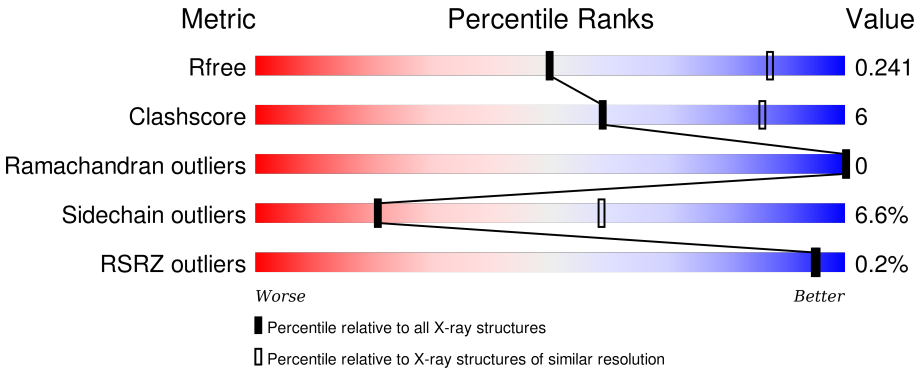
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.30 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	2060 (3.40-3.20)
Clashscore	102246	1058 (3.38-3.22)
Ramachandran outliers	100387	1038 (3.38-3.22)
Sidechain outliers	100360	1037 (3.38-3.22)
RSRZ outliers	91569	2070 (3.40-3.20)

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	560	71% 12% • 15%
1	B	560	72% 12% • 16%
2	S	43	5% 72% 9% 19%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7598 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 Cell division cycle protein 27 homolog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	474	Total	C	N	O	S	0	0	0
			3623	2318	604	676	25			
1	B	473	Total	C	N	O	S	0	0	0
			3701	2372	619	685	25			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	EXPRESSION TAG	UNP P30260
A	0	SER	-	EXPRESSION TAG	UNP P30260
B	-1	GLY	-	EXPRESSION TAG	UNP P30260
B	0	SER	-	EXPRESSION TAG	UNP P30260

- Molecule 2 is a protein called Anaphase-promoting complex subunit 16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	S	35	Total	C	N	O	S	0	0	0
			274	177	47	49	1			

There are 7 discrepancies between the modelled and reference sequences:

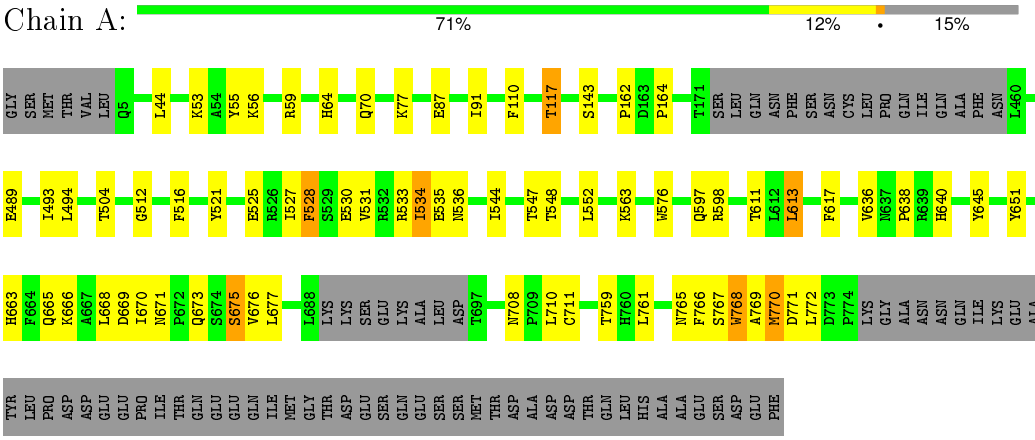
Chain	Residue	Modelled	Actual	Comment	Reference
S	73	MET	-	INITIATING METHIONINE	UNP Q96DE5
S	110	GLU	-	EXPRESSION TAG	UNP Q96DE5
S	111	ASN	-	EXPRESSION TAG	UNP Q96DE5
S	112	LEU	-	EXPRESSION TAG	UNP Q96DE5
S	113	TYR	-	EXPRESSION TAG	UNP Q96DE5
S	114	PHE	-	EXPRESSION TAG	UNP Q96DE5
S	115	GLN	-	EXPRESSION TAG	UNP Q96DE5

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.

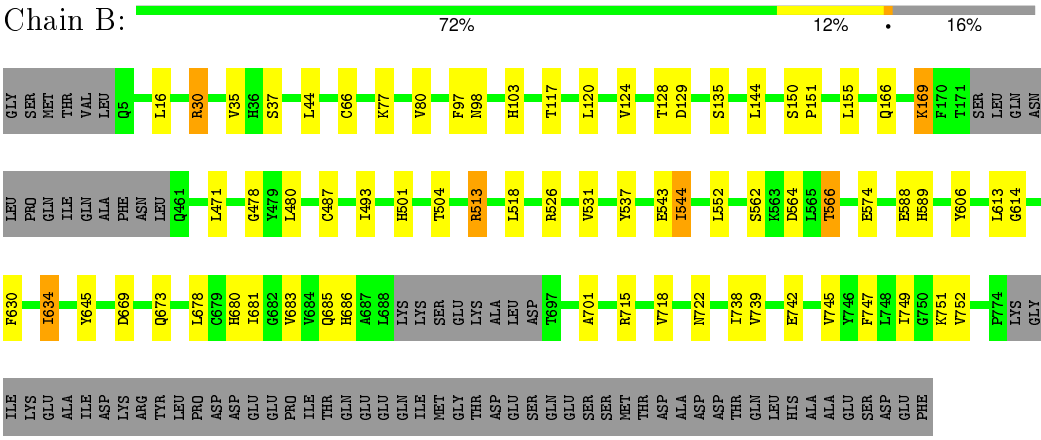
- Molecule 1: Cell division cycle protein 27 homolog

Chain A:



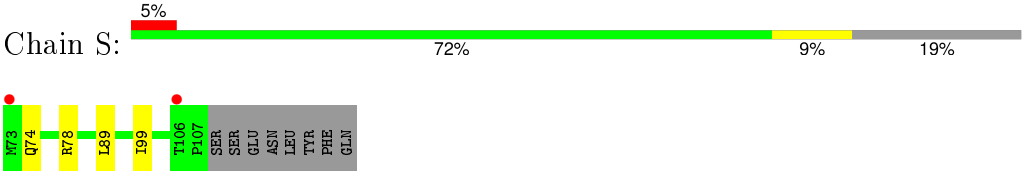
- Molecule 1: Cell division cycle protein 27 homolog

Chain B:



- Molecule 2: Anaphase-promoting complex subunit 16

Chain S:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α, β, γ	116.66Å 116.66Å 184.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.30 49.39 – 3.30	Depositor EDS
% Data completeness (in resolution range)	99.8 (50.00-3.30) 99.9 (49.39-3.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$< I/\sigma(I) >$ [1]	3.63 (at 3.33Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.203 , 0.242 0.204 , 0.241	Depositor DCC
R_{free} test set	1867 reflections (5.29%)	DCC
Wilson B-factor (Å^2)	100.7	Xtriage
Anisotropy	0.025	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 54.3	EDS
Estimated twinning fraction	0.042 for h,-k,-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Outliers	0 of 37127 reflections	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	7598	wwPDB-VP
Average B, all atoms (Å^2)	107.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.83% 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

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	0.34	0/3709	0.52	0/5041
1	B	0.35	0/3788	0.54	0/5135
2	S	0.38	0/278	0.57	0/374
All	All	0.35	0/7775	0.53	0/10550

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	3623	0	3344	54	0
1	B	3701	0	3509	33	0
2	S	274	0	266	4	0
All	All	7598	0	7119	86	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 (86) 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:668:LEU:HA	1:A:671:ASN:O	1.28	1.25

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:668:LEU:CA	1:A:671:ASN:O	2.11	0.97
1:A:765:ASN:O	1:A:769:ALA:HB2	1.66	0.94
1:A:531:VAL:HA	1:A:534:ILE:CG2	2.00	0.90
1:A:531:VAL:HA	1:A:534:ILE:HG22	1.53	0.89
1:A:55:TYR:O	1:A:59:ARG:HG2	1.80	0.81
1:A:768:TRP:HD1	1:A:769:ALA:N	1.83	0.75
1:A:531:VAL:CA	1:A:534:ILE:HG22	2.18	0.73
1:A:645:TYR:OH	1:A:675:SER:HB3	1.89	0.72
1:B:166:GLN:OE1	1:B:169:LYS:HE3	1.91	0.70
1:A:768:TRP:HA	1:A:771:ASP:HB2	1.74	0.70
1:B:562:SER:O	1:B:566:THR:HB	1.94	0.68
1:A:766:PHE:O	1:A:770:MET:HG3	1.93	0.68
1:A:768:TRP:CD1	1:A:769:ALA:N	2.62	0.67
1:A:673:GLN:O	1:A:673:GLN:HG3	1.94	0.66
1:A:768:TRP:C	1:A:768:TRP:CD1	2.70	0.65
1:B:478:GLY:N	1:B:493:ILE:HD11	2.11	0.65
1:A:765:ASN:O	1:A:769:ALA:CB	2.43	0.63
1:B:701:ALA:HB3	1:B:715:ARG:NH2	2.15	0.62
1:B:742:GLU:O	1:B:745:VAL:HG12	2.01	0.60
1:B:645:TYR:HB3	1:B:678:LEU:CD2	2.32	0.60
1:A:665:GLN:O	1:A:669:ASP:HB2	2.02	0.59
1:A:531:VAL:HA	1:A:534:ILE:HG21	1.85	0.58
1:B:718:VAL:O	1:B:722:ASN:ND2	2.38	0.56
1:A:768:TRP:C	1:A:768:TRP:HD1	2.07	0.56
1:B:80:VAL:HG21	1:B:120:LEU:HD11	1.86	0.56
1:B:501:HIS:O	1:B:504:THR:HG22	2.06	0.56
1:A:481:ALA:O	1:A:484:SER:O	2.24	0.56
1:A:661:GLU:OE1	1:A:711:CYS:N	2.38	0.55
1:A:516:PHE:CD2	1:A:548:THR:HG22	2.42	0.54
1:A:162:PRO:O	1:A:164:PRO:HD3	2.09	0.53
2:S:74:GLN:HG3	2:S:78:ARG:HE	1.74	0.53
1:A:665:GLN:OE1	1:A:710:LEU:HD11	2.10	0.52
1:B:645:TYR:HB3	1:B:678:LEU:HD22	1.92	0.52
1:B:745:VAL:O	1:B:749:ILE:HG13	2.11	0.51
1:A:534:ILE:O	1:A:534:ILE:HD12	2.10	0.51
1:B:513:ARG:HA	1:B:544:ILE:HD11	1.92	0.51
1:B:478:GLY:CA	1:B:493:ILE:HD11	2.41	0.51
1:A:531:VAL:C	1:A:534:ILE:HG22	2.32	0.50
1:A:668:LEU:C	1:A:671:ASN:O	2.49	0.49
1:A:530:GLU:O	1:A:534:ILE:HG22	2.12	0.49
1:A:651:TYR:CE2	1:A:663:HIS:CE1	3.01	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:97:PHE:O	1:B:98:ASN:OD1	2.32	0.48
1:A:59:ARG:HG3	1:B:537:TYR:HB3	1.96	0.48
1:B:739:VAL:HG13	1:B:739:VAL:O	2.13	0.48
1:A:512:GLY:HA2	1:A:527:ILE:HD11	1.96	0.48
1:A:676:VAL:HG13	1:A:677:LEU:N	2.29	0.48
1:B:487:CYS:HB2	1:B:518:LEU:HD21	1.96	0.47
1:A:766:PHE:O	1:A:770:MET:CG	2.62	0.46
1:A:666:LYS:O	1:A:670:ILE:HG13	2.16	0.46
1:A:651:TYR:CD1	1:A:659:LEU:HD11	2.50	0.46
1:A:651:TYR:CE2	1:A:663:HIS:HE1	2.34	0.46
1:B:749:ILE:O	1:B:752:VAL:HG12	2.16	0.46
1:A:772:LEU:HD12	1:A:772:LEU:O	2.16	0.45
1:B:471:LEU:HD21	1:B:501:HIS:ND1	2.31	0.45
1:A:87:GLU:O	1:A:91:ILE:HG13	2.17	0.45
1:A:544:ILE:O	1:A:548:THR:HG23	2.17	0.45
1:B:681:ILE:O	1:B:685:GLN:HG3	2.17	0.45
1:A:528:PHE:HA	1:A:531:VAL:HG12	1.98	0.45
1:B:124:VAL:O	1:B:128:THR:HG23	2.17	0.45
1:B:673:GLN:HG3	1:B:747:PHE:CE2	2.52	0.44
1:A:613:LEU:HD22	1:A:617:PHE:CE2	2.52	0.44
1:A:611:THR:HG1	1:A:640:HIS:CD2	2.35	0.44
1:B:680:HIS:O	1:B:683:VAL:HG22	2.17	0.44
1:A:489:GLU:O	1:A:493:ILE:HG12	2.18	0.43
1:A:665:GLN:O	1:A:669:ASP:CB	2.67	0.43
1:B:480:LEU:O	1:B:480:LEU:HD23	2.18	0.43
1:A:521:TYR:HB2	1:A:552:LEU:HD21	2.00	0.43
1:B:471:LEU:HD21	1:B:501:HIS:CE1	2.54	0.43
1:A:576:TRP:CH2	2:S:89:LEU:HD21	2.54	0.43
1:B:630:PHE:O	1:B:634:ILE:HG13	2.19	0.43
1:B:589:HIS:CE1	1:B:619:LEU:HD22	2.54	0.42
1:A:766:PHE:O	1:A:769:ALA:HB3	2.18	0.42
1:A:504:THR:HG21	1:B:30:ARG:NH2	2.33	0.42
1:A:563:LYS:HD2	2:S:78:ARG:HD2	2.01	0.42
1:B:614:GLY:HA3	1:B:630:PHE:CE1	2.54	0.42
1:A:761:LEU:N	1:A:761:LEU:HD12	2.34	0.42
1:A:597:GLN:HG2	2:S:99:ILE:HG21	2.01	0.41
1:A:533:ARG:HG3	1:A:534:ILE:N	2.35	0.41
1:B:543:GLU:OE2	1:B:606:TYR:OH	2.39	0.41
1:B:166:GLN:OE1	1:B:169:LYS:CE	2.66	0.41
1:B:35:VAL:C	1:B:37:SER:H	2.23	0.41
1:A:110:PHE:CG	1:A:117:THR:HG21	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:64:HIS:N	1:A:64:HIS:CD2	2.89	0.41
1:B:150:SER:N	1:B:151:PRO:CD	2.84	0.41
1:A:53:LYS:HB3	1:A:56:LYS:HG3	2.03	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	468/560 (84%)	440 (94%)	28 (6%)	0	100	100
1	B	467/560 (83%)	438 (94%)	29 (6%)	0	100	100
2	S	33/43 (77%)	31 (94%)	2 (6%)	0	100	100
All	All	968/1163 (83%)	909 (94%)	59 (6%)	0	100	100

There are no Ramachandran outliers to report.

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	356/485 (73%)	334 (94%)	22 (6%)	23	61
1	B	377/485 (78%)	349 (93%)	28 (7%)	17	52
2	S	26/38 (68%)	26 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	759/1008 (75%)	709 (93%)	50 (7%)	21 59

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	LEU
1	A	70	GLN
1	A	77	LYS
1	A	117	THR
1	A	143	SER
1	A	494	LEU
1	A	525	GLU
1	A	528	PHE
1	A	534	ILE
1	A	535	GLU
1	A	536	ASN
1	A	547	THR
1	A	598	ARG
1	A	613	LEU
1	A	636	VAL
1	A	638	PRO
1	A	675	SER
1	A	708	ASN
1	A	759	THR
1	A	767	SER
1	A	768	TRP
1	A	770	MET
1	B	16	LEU
1	B	30	ARG
1	B	44	LEU
1	B	66	CYS
1	B	77	LYS
1	B	103	HIS
1	B	117	THR
1	B	129	ASP
1	B	135	SER
1	B	144	LEU
1	B	155	LEU
1	B	169	LYS
1	B	513	ARG
1	B	526	ARG
1	B	531	VAL

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Mol	Chain	Res	Type
1	B	544	ILE
1	B	552	LEU
1	B	564	ASP
1	B	566	THR
1	B	574	GLU
1	B	588	GLU
1	B	613	LEU
1	B	627	LEU
1	B	634	ILE
1	B	669	ASP
1	B	686	HIS
1	B	738	ILE
1	B	751	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	663	HIS
1	A	671	ASN
1	B	708	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)

There are no ligands in this entry.

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	474/560 (84%)	-0.27	0 100 100	68, 113, 158, 232	0
1	B	473/560 (84%)	-0.24	0 100 100	69, 96, 148, 208	0
2	S	35/43 (81%)	0.03	2 (5%) 27 22	80, 117, 150, 169	0
All	All	982/1163 (84%)	-0.24	2 (0%) 95 95	68, 103, 155, 232	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	S	73	MET	3.0
2	S	106	THR	2.8

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

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

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.