Full wwPDB X-ray Structure Validation Report (i)

Oct 27, 2016 – 11:28 AM EDT

PDB ID	:	4OVM
Title	:	Crystal structure of SgcJ protein from Streptomyces carzinostaticus
Authors	:	Chang, C.; Bigelow, L.; Clancy, S.; Bingman, C.; Yennamalli, R.; Lohman, J.R.; Ma, M.; Shen, B.; Phillips Jr., G.N.; Babnigg, G.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG); Enzyme Discovery for Natural Product Biosynthesis (NatPro)
Deposited on	:	2013-11-20
Resolution	:	2.72 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:

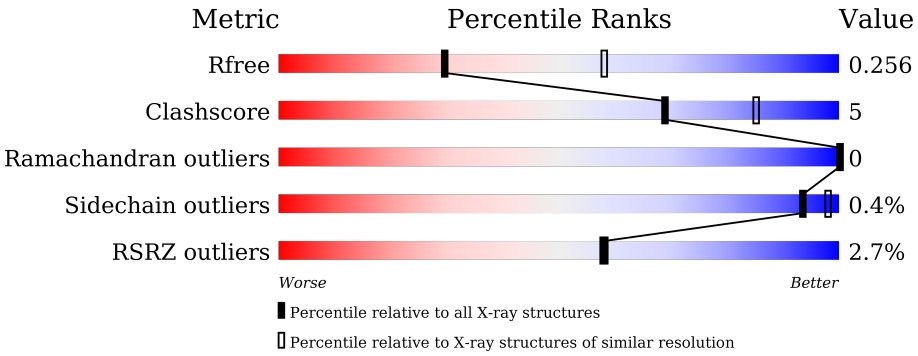
MolProbity	:	4.02b-467
Mogul	:	unknown
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20027939
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20027939

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 2.72 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.



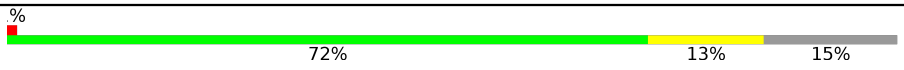
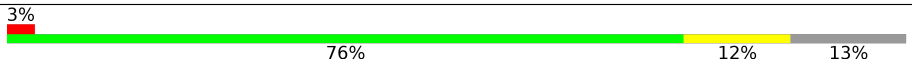
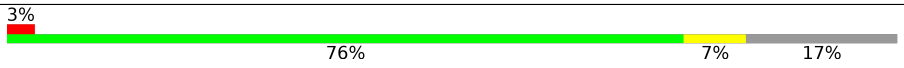
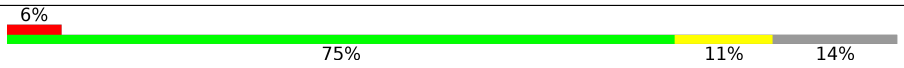
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2439 (2.74-2.70)
Clashscore	102246	2771 (2.74-2.70)
Ramachandran outliers	100387	2726 (2.74-2.70)
Sidechain outliers	100360	2727 (2.74-2.70)
RSRZ outliers	91569	2443 (2.74-2.70)

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	144	2% 83% 6% 11%
1	B	144	77% 10% 13%
1	C	144	80% 10% 10%
1	D	144	74% 13% 13%
1	E	144	76% 12% 13%
1	F	144	3% 82% 8% 10%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	G	144	
1	H	144	
1	I	144	
1	J	144	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9240 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 uncharacterized protein SgcJ.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	128	Total	C	N	O	S	Se	0	0	0
			955	611	165	173	1	5			
1	B	126	Total	C	N	O	S	Se	0	0	0
			929	591	157	175	1	5			
1	C	129	Total	C	N	O	S	Se	0	0	0
			963	613	166	178	1	5			
1	D	125	Total	C	N	O	S	Se	0	0	0
			902	582	150	164	1	5			
1	E	126	Total	C	N	O	S	Se	0	0	0
			936	598	157	175	1	5			
1	F	129	Total	C	N	O	S	Se	0	0	0
			942	605	163	168	1	5			
1	G	122	Total	C	N	O	S	Se	0	0	0
			903	582	152	163	1	5			
1	H	126	Total	C	N	O	S	Se	0	0	0
			931	595	163	167	1	5			
1	I	120	Total	C	N	O	S	Se	0	0	0
			872	562	143	161	1	5			
1	J	124	Total	C	N	O	S	Se	0	0	0
			897	577	149	165	1	5			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	O	0	0
			1	1		
2	B	2	Total	O	0	0
			2	2		
2	C	1	Total	O	0	0
			1	1		
2	D	1	Total	O	0	0
			1	1		

Continued on next page...

Continued from previous page...

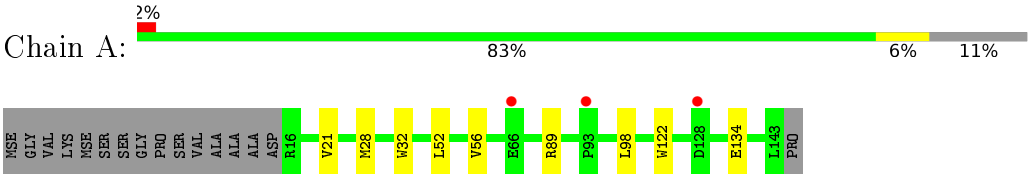
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	E	1	Total O 1 1	0	0
2	G	1	Total O 1 1	0	0
2	H	2	Total O 2 2	0	0
2	J	1	Total O 1 1	0	0

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.

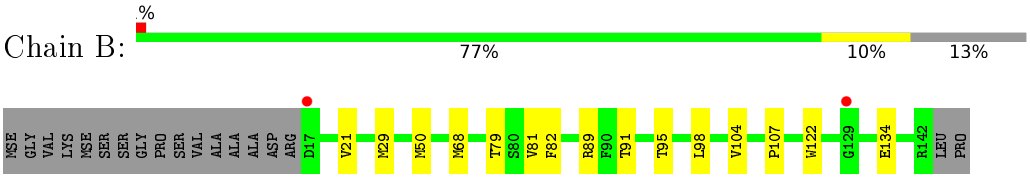
- Molecule 1: uncharacterized protein SgcJ

Chain A:



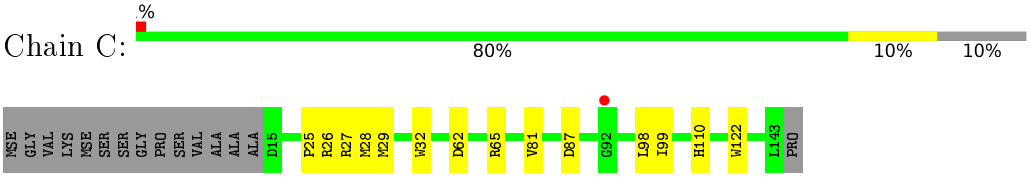
- Molecule 1: uncharacterized protein SgcJ

Chain B:



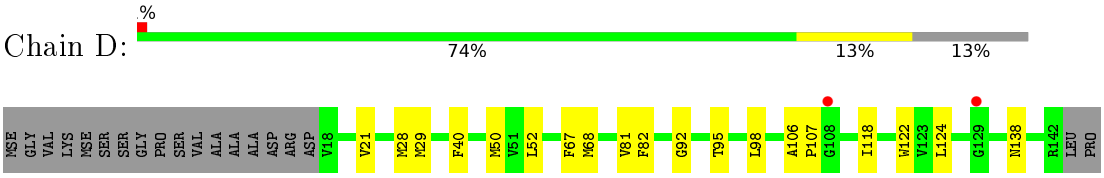
- Molecule 1: uncharacterized protein SgcJ

Chain C:



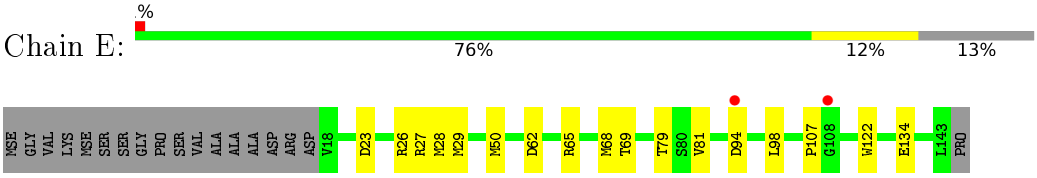
- Molecule 1: uncharacterized protein SgcJ

Chain D:



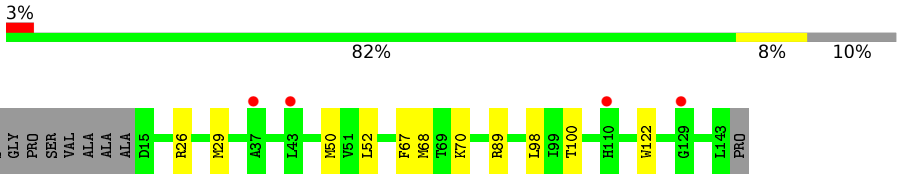
- Molecule 1: uncharacterized protein SgcJ

Chain E:



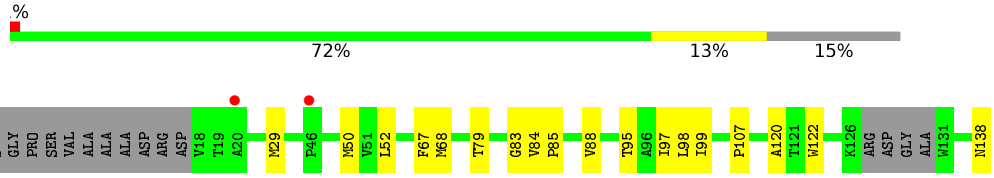
- Molecule 1: uncharacterized protein SgcJ

Chain F:



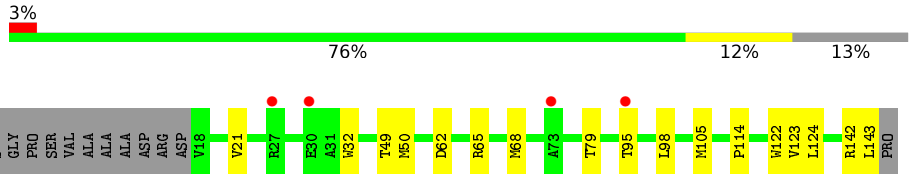
• Molecule 1: uncharacterized protein SgcJ

Chain G:



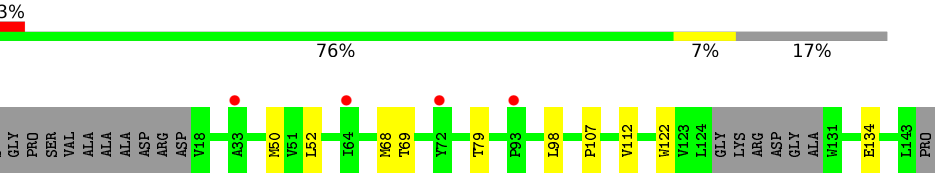
• Molecule 1: uncharacterized protein SgcJ

Chain H:



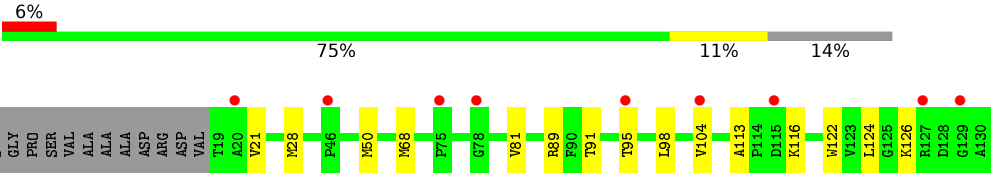
• Molecule 1: uncharacterized protein SgcJ

Chain I:



• Molecule 1: uncharacterized protein SgcJ

Chain J:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	98.32Å 52.83Å 131.80Å 90.00° 90.14° 90.00°	Depositor
Resolution (Å)	37.99 – 2.72 37.99 – 2.72	Depositor EDS
% Data completeness (in resolution range)	88.6 (37.99-2.72) 88.3 (37.99-2.72)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	5.46 (at 2.72Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, R_{free}	0.216 , 0.256 0.217 , 0.256	Depositor DCC
R_{free} test set	1933 reflections (5.91%)	DCC
Wilson B-factor (Å^2)	43.5	Xtriage
Anisotropy	0.011	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 37.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.024 for h,-k,-l	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	9240	wwPDB-VP
Average B, all atoms (Å^2)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 20.98 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 7.7228e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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	0.21	0/975	0.39	0/1320
1	B	0.21	0/948	0.39	0/1286
1	C	0.22	0/983	0.39	0/1331
1	D	0.21	0/922	0.40	0/1253
1	E	0.24	0/956	0.40	0/1296
1	F	0.21	0/962	0.41	0/1305
1	G	0.21	0/922	0.39	0/1250
1	H	0.21	0/950	0.39	0/1287
1	I	0.21	0/890	0.39	0/1211
1	J	0.21	0/917	0.40	0/1246
All	All	0.21	0/9425	0.40	0/12785

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	955	0	934	6	0
1	B	929	0	894	9	0
1	C	963	0	931	8	0
1	D	902	0	865	11	0
1	E	936	0	903	9	0
1	F	942	0	913	10	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	903	0	878	13	0
1	H	931	0	915	11	0
1	I	872	0	833	6	0
1	J	897	0	856	9	0
2	A	1	0	0	0	0
2	B	2	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	G	1	0	0	0	0
2	H	2	0	0	0	0
2	J	1	0	0	0	0
All	All	9240	0	8922	84	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 5.

All (84) 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:D:98:LEU:HB3	1:D:122:TRP:HB2	1.57	0.87
1:J:98:LEU:HB3	1:J:122:TRP:HB2	1.60	0.83
1:E:98:LEU:HB2	1:E:122:TRP:HB2	1.65	0.77
1:A:98:LEU:HB2	1:A:122:TRP:HB2	1.66	0.77
1:H:98:LEU:HB2	1:H:122:TRP:HB2	1.69	0.74
1:J:113:ALA:HB3	1:J:116:LYS:HD2	1.70	0.73
1:F:98:LEU:HB3	1:F:122:TRP:HB2	1.75	0.67
1:C:26:ARG:NH1	1:I:112:VAL:O	2.27	0.67
1:B:29:MSE:HE3	1:B:82:PHE:HA	1.77	0.66
1:I:98:LEU:HB2	1:I:122:TRP:HB2	1.77	0.65
1:G:98:LEU:HB2	1:G:122:TRP:HB2	1.79	0.64
1:B:21:VAL:HG13	1:B:98:LEU:HD11	1.80	0.63
1:B:98:LEU:HB2	1:B:122:TRP:HB2	1.81	0.62
1:G:97:ILE:HD11	1:H:123:VAL:HG11	1.82	0.61
1:A:21:VAL:HG13	1:A:98:LEU:HD11	1.83	0.60
1:D:50:MSE:HE2	1:D:52:LEU:HD21	1.83	0.60
1:I:134:GLU:O	1:J:89:ARG:NH2	2.35	0.58
1:E:134:GLU:O	1:F:89:ARG:NH1	2.36	0.57
1:E:62:ASP:OD1	1:E:65:ARG:NH2	2.37	0.56
1:H:32:TRP:HE1	1:H:79:THR:HG23	1.69	0.56
1:F:50:MSE:HE2	1:F:52:LEU:HD11	1.86	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:29:MSE:HE3	1:D:82:PHE:HA	1.87	0.56
1:G:50:MSE:SE	1:G:68:MSE:HE3	2.56	0.56
1:F:100:THR:HG1	1:F:122:TRP:HE1	1.52	0.55
1:G:50:MSE:HE2	1:G:52:LEU:HD11	1.89	0.54
1:I:50:MSE:HE2	1:I:52:LEU:HD21	1.90	0.54
1:D:28:MSE:HE2	1:D:40:PHE:HE1	1.74	0.53
1:E:50:MSE:SE	1:E:68:MSE:HE3	2.59	0.53
1:F:68:MSE:HA	1:F:68:MSE:HE2	1.90	0.52
1:A:134:GLU:O	1:B:89:ARG:NH2	2.42	0.52
1:G:99:ILE:HD11	1:H:49:THR:HG21	1.92	0.52
1:D:21:VAL:HG13	1:D:124:LEU:HD12	1.92	0.51
1:D:92:GLY:H	1:D:95:THR:HG23	1.76	0.50
1:H:142:ARG:HG2	1:H:143:LEU:H	1.77	0.50
1:B:79:THR:HG22	1:B:107:PRO:HD3	1.93	0.49
1:G:120:ALA:HB2	1:G:138:ASN:HB3	1.93	0.49
1:C:28:MSE:HE2	1:C:81:VAL:HG11	1.95	0.49
1:H:62:ASP:OD1	1:H:65:ARG:NH2	2.44	0.48
1:B:50:MSE:SE	1:B:68:MSE:HE2	2.63	0.48
1:D:118:ILE:HD13	1:D:138:ASN:HD22	1.78	0.48
1:F:26:ARG:HA	1:F:29:MSE:HE3	1.94	0.48
1:H:21:VAL:HG13	1:H:124:LEU:HD12	1.95	0.48
1:G:67:PHE:HD2	1:G:68:MSE:HE2	1.79	0.47
1:G:67:PHE:CD2	1:G:68:MSE:HE2	2.49	0.47
1:A:52:LEU:HD12	1:A:56:VAL:HG11	1.96	0.46
1:E:79:THR:HG22	1:E:107:PRO:HD3	1.98	0.46
1:E:28:MSE:HE3	1:E:81:VAL:HG11	1.96	0.46
1:B:81:VAL:HG22	1:B:104:VAL:HA	1.98	0.46
1:J:50:MSE:HE1	1:J:68:MSE:HE1	1.97	0.46
1:C:62:ASP:OD1	1:C:65:ARG:NH2	2.49	0.46
1:D:68:MSE:HA	1:D:68:MSE:HE2	1.97	0.45
1:H:114:PRO:HB3	1:H:142:ARG:HH21	1.81	0.45
1:I:79:THR:HG22	1:I:107:PRO:HD3	1.98	0.45
1:E:28:MSE:CE	1:E:81:VAL:HG11	2.47	0.45
1:G:95:THR:HG21	1:H:95:THR:HG21	1.99	0.45
1:I:50:MSE:SE	1:I:68:MSE:HE3	2.67	0.44
1:G:79:THR:HG22	1:G:107:PRO:HD3	2.00	0.44
1:A:89:ARG:NH2	1:B:134:GLU:OE1	2.51	0.44
1:J:21:VAL:HG13	1:J:124:LEU:HD12	2.00	0.43
1:C:87:ASP:HB3	1:C:99:ILE:HB	2.00	0.43
1:J:81:VAL:HG22	1:J:104:VAL:HA	2.00	0.42
1:E:23:ASP:O	1:E:27:ARG:N	2.51	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:25:PRO:O	1:C:29:MSE:HG3	2.20	0.42
1:H:79:THR:OG1	1:H:105:MSE:O	2.24	0.42
1:F:70:LYS:HE3	1:F:70:LYS:HB2	1.83	0.42
1:C:27:ARG:HD3	1:C:27:ARG:HA	1.93	0.41
1:D:106:ALA:HB1	1:D:107:PRO:HD2	2.01	0.41
1:E:26:ARG:HA	1:E:29:MSE:HE3	2.02	0.41
1:D:67:PHE:CD2	1:D:68:MSE:HE3	2.56	0.41
1:J:91:THR:OG1	1:J:95:THR:OG1	2.38	0.41
1:F:67:PHE:CE2	1:F:68:MSE:HE3	2.55	0.41
1:F:50:MSE:HE2	1:F:52:LEU:HD21	2.02	0.41
1:A:28:MSE:HE3	1:A:32:TRP:CE3	2.55	0.41
1:C:98:LEU:HB2	1:C:122:TRP:HB2	2.03	0.41
1:H:50:MSE:SE	1:H:68:MSE:HE2	2.71	0.41
1:J:126:LYS:HD2	1:J:131:TRP:CZ2	2.55	0.41
1:G:29:MSE:HE1	1:G:83:GLY:O	2.21	0.41
1:D:29:MSE:HG2	1:D:81:VAL:HG12	2.03	0.40
1:J:28:MSE:SE	1:J:122:TRP:HH2	2.54	0.40
1:F:67:PHE:CD2	1:F:68:MSE:HE3	2.56	0.40
1:G:84:VAL:HA	1:G:85:PRO:HD3	1.88	0.40
1:B:91:THR:OG1	1:B:95:THR:OG1	2.34	0.40
1:C:28:MSE:HE3	1:C:32:TRP:CE3	2.56	0.40
1:G:88:VAL:HG22	1:G:98:LEU:HG	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	126/144 (88%)	124 (98%)	2 (2%)	0	100	100
1	B	124/144 (86%)	120 (97%)	4 (3%)	0	100	100
1	C	127/144 (88%)	124 (98%)	3 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	123/144 (85%)	119 (97%)	4 (3%)	0	100	100
1	E	124/144 (86%)	122 (98%)	2 (2%)	0	100	100
1	F	127/144 (88%)	124 (98%)	3 (2%)	0	100	100
1	G	118/144 (82%)	114 (97%)	4 (3%)	0	100	100
1	H	124/144 (86%)	121 (98%)	3 (2%)	0	100	100
1	I	116/144 (81%)	111 (96%)	5 (4%)	0	100	100
1	J	122/144 (85%)	118 (97%)	4 (3%)	0	100	100
All	All	1231/1440 (86%)	1197 (97%)	34 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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	96/104 (92%)	96 (100%)	0	100	100
1	B	94/104 (90%)	94 (100%)	0	100	100
1	C	97/104 (93%)	96 (99%)	1 (1%)	82	94
1	D	88/104 (85%)	88 (100%)	0	100	100
1	E	95/104 (91%)	93 (98%)	2 (2%)	61	86
1	F	92/104 (88%)	92 (100%)	0	100	100
1	G	91/104 (88%)	91 (100%)	0	100	100
1	H	93/104 (89%)	93 (100%)	0	100	100
1	I	87/104 (84%)	86 (99%)	1 (1%)	80	94
1	J	88/104 (85%)	88 (100%)	0	100	100
All	All	921/1040 (89%)	917 (100%)	4 (0%)	93	98

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	110	HIS
1	E	69	THR
1	E	94	ASP
1	I	69	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	35	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

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	123/144 (85%)	0.19	3 (2%)	62	62	37, 68, 99, 120	0
1	B	121/144 (84%)	0.22	2 (1%)	73	74	32, 63, 94, 106	0
1	C	124/144 (86%)	0.11	1 (0%)	87	88	38, 62, 96, 122	0
1	D	120/144 (83%)	0.21	2 (1%)	73	74	40, 82, 116, 132	0
1	E	121/144 (84%)	0.03	2 (1%)	73	74	34, 54, 84, 104	0
1	F	124/144 (86%)	0.17	4 (3%)	51	52	35, 72, 99, 119	0
1	G	117/144 (81%)	0.28	2 (1%)	73	74	43, 72, 97, 106	0
1	H	121/144 (84%)	0.28	4 (3%)	50	50	43, 78, 109, 121	0
1	I	115/144 (79%)	0.35	4 (3%)	48	48	45, 79, 107, 122	0
1	J	119/144 (82%)	0.54	9 (7%)	17	15	56, 83, 109, 119	0
All	All	1205/1440 (83%)	0.24	33 (2%)	58	58	32, 71, 105, 132	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	46	PRO	3.8
1	J	95	THR	3.7
1	B	129	GLY	3.4
1	A	66	GLU	3.0
1	D	108	GLY	2.6
1	J	127	ARG	2.6
1	E	94	ASP	2.6
1	H	73	ALA	2.5
1	I	64	ILE	2.5
1	H	27	ARG	2.5
1	A	128	ASP	2.5
1	J	115	ASP	2.5
1	J	20	ALA	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	J	129	GLY	2.5
1	I	93	PRO	2.4
1	F	129	GLY	2.4
1	F	43	LEU	2.4
1	E	108	GLY	2.4
1	F	37	ALA	2.3
1	D	129	GLY	2.3
1	I	33	ALA	2.3
1	A	93	PRO	2.2
1	G	20	ALA	2.2
1	J	78	GLY	2.2
1	J	104	VAL	2.2
1	C	92	GLY	2.2
1	G	46	PRO	2.1
1	I	72	TYR	2.1
1	F	110	HIS	2.1
1	H	95	THR	2.1
1	B	17	ASP	2.0
1	H	30	GLU	2.0
1	J	75	PRO	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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.