W O R L D W I D E

wwPDB

P R O T E I N   D A T A   B A N K

Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 08:33 PM GMT

PDB ID	:	4TRG
Title	:	the SNL domain of SidC
Authors	:	Hsu, F.S.; Luo, X.; Qiu, J.; Teng, Y.; Jin, J.; Smolka, M.B.; Luo, Z.Q.; Mao, Y.
Deposited on	:	2014-06-16
Resolution	:	2.59 Å(reported)

The following versions of software and data (see references (i)) 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
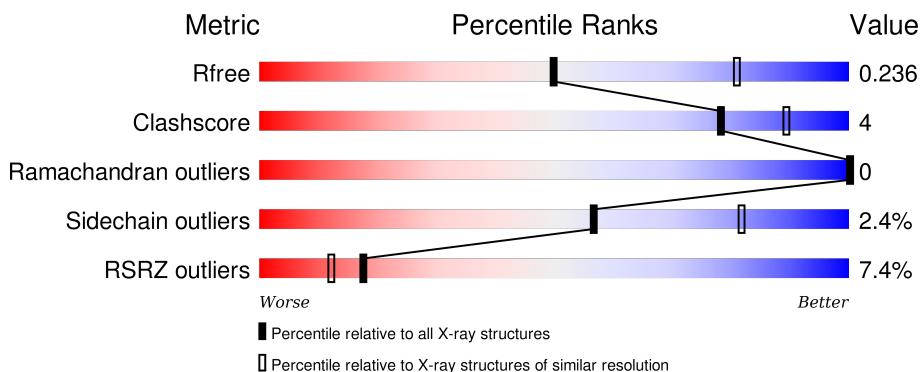
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION
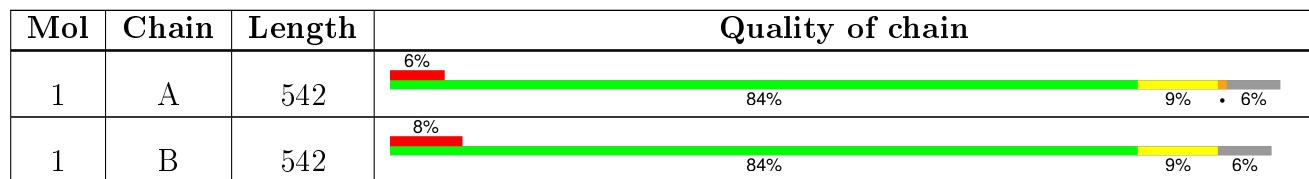
The reported resolution of this entry is 2.59 Å.

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	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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	542	
1	B	542	

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 8608 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 SidC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	509	Total 4146	C 2620	N 705	O 816	S 5	0	3	0
1	B	509	Total 4164	C 2630	N 707	O 822	S 5	0	5	0

- Molecule 2 is MERCURY (II) ION (three-letter code: HG) (formula: Hg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total 2	Hg 2	0	0
2	A	2	Total 2	Hg 2	0	0
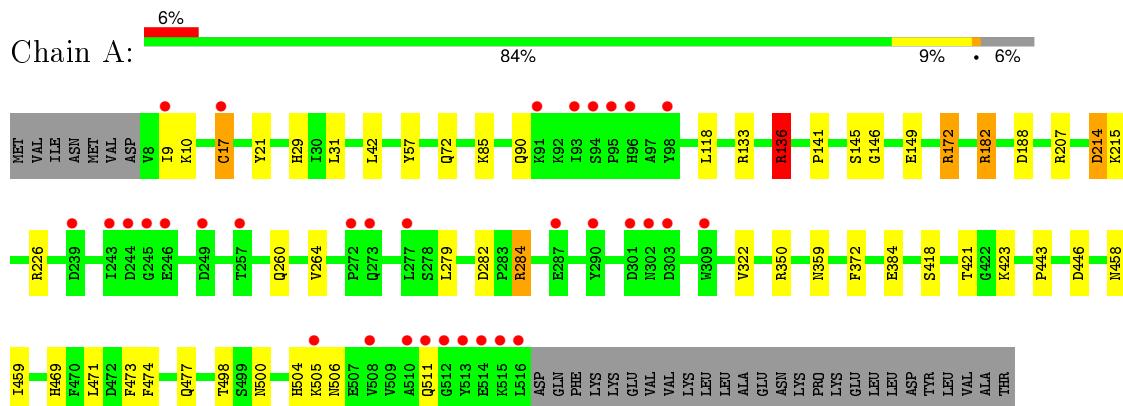
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	167	Total 167	O 167	0	0
3	B	127	Total 127	O 127	0	0
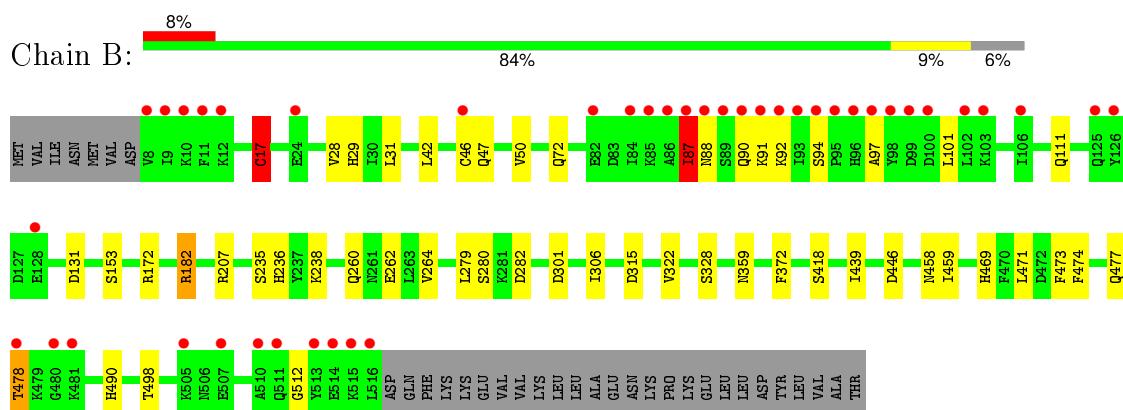
3 Residue-property plots ⓘ

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: SidC

- Molecule 1: SidC

4 Data and refinement statistics (i)

| Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	61.53Å 133.44Å 170.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.00 – 2.59 36.05 – 2.59	Depositor EDS
% Data completeness (in resolution range)	98.8 (36.00-2.59) 99.0 (36.05-2.59)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$< I/\sigma(I) >$ [1]	2.58 (at 2.58Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.189 , 0.231 0.197 , 0.236	Depositor DCC
R_{free} test set	2214 reflections (5.30%)	DCC
Wilson B-factor (Å^2)	36.7	Xtriage
Anisotropy	0.171	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 40.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< |L| > = 0.50, < L^2 > = 0.34$	Xtriage
Outliers	0 of 43949 reflections	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	8608	wwPDB-VP
Average B, all atoms (Å^2)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.07% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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 (i)

5.1 Standard geometry (i)

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

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	0.85	4/4233 (0.1%)	0.92	14/5713 (0.2%)
1	B	0.78	4/4251 (0.1%)	0.87	13/5737 (0.2%)
All	All	0.82	8/8484 (0.1%)	0.89	27/11450 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	17	CYS	CB-SG	9.55	1.98	1.82
1	A	17	CYS	CB-SG	8.32	1.96	1.82
1	A	149	GLU	CD-OE1	7.28	1.33	1.25
1	B	262	GLU	CD-OE1	6.92	1.33	1.25
1	A	145	SER	CB-OG	-6.66	1.33	1.42
1	B	46	CYS	CB-SG	6.63	1.93	1.82
1	B	280	SER	CB-OG	-5.89	1.34	1.42
1	A	17	CYS	CA-CB	5.53	1.66	1.53

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	136	ARG	NE-CZ-NH2	-12.56	114.02	120.30
1	A	182	ARG	NE-CZ-NH2	-12.17	114.21	120.30
1	A	172	ARG	NE-CZ-NH2	-12.05	114.28	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	136	ARG	NE-CZ-NH1	11.54	126.07	120.30
1	B	182	ARG	NE-CZ-NH2	-11.06	114.77	120.30
1	A	172	ARG	NE-CZ-NH1	11.02	125.81	120.30
1	B	172	ARG	NE-CZ-NH2	-9.02	115.79	120.30
1	B	172	ARG	NE-CZ-NH1	7.72	124.16	120.30
1	B	87	ILE	O-C-N	-7.64	110.47	122.70
1	B	182	ARG	NE-CZ-NH1	7.61	124.11	120.30
1	A	207	ARG	NE-CZ-NH1	7.59	124.10	120.30
1	A	284	ARG	CG-CD-NE	6.40	125.25	111.80
1	B	182	ARG	CG-CD-NE	-6.24	98.71	111.80
1	B	87	ILE	C-N-CA	-6.18	106.26	121.70
1	B	301	ASP	CB-CG-OD1	5.96	123.66	118.30
1	A	226	ARG	NE-CZ-NH2	-5.85	117.37	120.30
1	B	17	CYS	N-CA-CB	5.76	120.98	110.60
1	A	182	ARG	NE-CZ-NH1	5.63	123.12	120.30
1	A	17	CYS	N-CA-CB	5.58	120.65	110.60
1	B	207	ARG	NE-CZ-NH1	5.48	123.04	120.30
1	A	31	LEU	CA-CB-CG	-5.32	103.06	115.30
1	B	31	LEU	CA-CB-CG	-5.24	103.25	115.30
1	B	315	ASP	CB-CG-OD2	-5.17	113.64	118.30
1	A	188	ASP	CB-CG-OD1	-5.16	113.65	118.30
1	A	182	ARG	CG-CD-NE	-5.15	100.99	111.80
1	B	282	ASP	CB-CG-OD1	5.05	122.85	118.30
1	A	350	ARG	NE-CZ-NH1	5.02	122.81	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	87	ILE	Mainchain

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4146	0	4085	30	0
1	B	4164	0	4094	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	2	0	0	1	0
2	B	2	0	0	0	0
3	A	167	0	0	1	0
3	B	127	0	0	1	0
All	All	8608	0	8179	60	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 4.

All (60) 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:17:CYS:SG	1:A:72:GLN:HB3	2.09	0.91
1:A:133:ARG:HG2	3:A:715:HOH:O	1.76	0.84
1:B:28:VAL:H	1:B:111:GLN:HE22	1.32	0.75
1:A:17:CYS:SG	1:A:72:GLN:NE2	2.61	0.74
1:B:92:LYS:HD2	1:B:92:LYS:O	1.88	0.73
1:B:17:CYS:SG	1:B:72:GLN:NE2	2.63	0.71
1:A:17:CYS:SG	2:A:601:HG:HG	2.10	0.69
1:A:421:THR:HG22	1:A:423:LYS:H	1.57	0.69
1:B:260:GLN:HE21	1:B:279:LEU:H	1.40	0.69
1:A:504:HIS:CE1	1:A:505:LYS:HG3	2.29	0.68
1:A:282:ASP:OD2	1:A:284:ARG:NH1	2.27	0.68
1:B:474:PHE:O	1:B:478:THR:HB	1.94	0.67
1:B:28:VAL:H	1:B:111:GLN:NE2	1.94	0.65
1:A:473:PHE:CZ	1:A:477:GLN:HG3	2.35	0.60
1:B:92:LYS:C	1:B:92:LYS:HD2	2.21	0.60
1:A:421:THR:HG22	1:A:423:LYS:N	2.17	0.59
1:A:469:HIS:HD2	1:A:471:LEU:H	1.51	0.58
1:B:17:CYS:SG	1:B:72:GLN:HB3	2.43	0.58
1:B:260:GLN:NE2	1:B:279:LEU:H	2.01	0.58
1:A:21:TYR:HA	1:A:506:ASN:HD21	1.69	0.58
1:A:9:ILE:HD11	1:A:90:GLN:HG3	1.86	0.58
1:B:473:PHE:CZ	1:B:477:GLN:HG3	2.40	0.57
1:A:284:ARG:HG3	1:A:284:ARG:HH11	1.70	0.56
1:B:88:ASN:O	1:B:91:LYS:HB3	2.05	0.56
1:B:47:GLN:O	1:B:50:VAL:HG12	2.07	0.55
1:B:182:ARG:NH2	1:B:446:ASP:OD2	2.38	0.54
1:A:260:GLN:HE21	1:A:279:LEU:H	1.57	0.53
1:A:359:ASN:ND2	1:A:372:PHE:H	2.08	0.52
1:B:87:ILE:O	1:B:88:ASN:C	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:GLN:O	1:A:264:VAL:HG13	2.11	0.51
1:B:469:HIS:HD2	1:B:471:LEU:H	1.57	0.51
1:A:57:TYR:CD1	1:A:136:ARG:HD3	2.46	0.51
1:B:88:ASN:O	1:B:91:LYS:N	2.42	0.51
1:B:260:GLN:O	1:B:264:VAL:HG13	2.12	0.50
1:B:28:VAL:N	1:B:111:GLN:HE22	2.06	0.50
1:B:101:LEU:HD21	1:B:512:GLY:HA3	1.94	0.49
1:A:260:GLN:NE2	1:A:279:LEU:H	2.11	0.48
1:A:146:GLY:H	1:A:477:GLN:HE21	1.61	0.48
1:B:359:ASN:ND2	1:B:372:PHE:H	2.11	0.48
1:A:473:PHE:CE1	1:A:477:GLN:HG3	2.49	0.48
1:B:94:SER:HB3	1:B:97:ALA:HB3	1.95	0.48
1:A:182:ARG:NH2	1:A:446:ASP:OD2	2.40	0.48
1:B:87:ILE:HA	1:B:90:GLN:HB2	1.96	0.48
1:B:235:SER:HB2	1:B:236:HIS:CD2	2.50	0.45
1:A:421:THR:CG2	1:A:423:LYS:H	2.29	0.45
1:B:473:PHE:CE1	1:B:477:GLN:HG3	2.52	0.45
1:A:214:ASP:O	1:A:215:LYS:HB2	2.16	0.44
1:A:29:HIS:ND1	1:A:469:HIS:HE1	2.16	0.44
1:B:29:HIS:ND1	1:B:469:HIS:HE1	2.16	0.43
1:A:182:ARG:NH2	1:A:446:ASP:HB3	2.34	0.43
1:A:118:LEU:HD22	1:A:474:PHE:CZ	2.53	0.43
1:B:458:ASN:OD1	1:B:459:ILE:HG12	2.20	0.42
1:B:101:LEU:HD21	1:B:512:GLY:CA	2.49	0.42
1:B:306:ILE:HG12	3:B:744:HOH:O	2.20	0.42
1:A:458:ASN:OD1	1:A:459:ILE:HG12	2.20	0.41
1:A:9:ILE:HG22	1:A:10:LYS:N	2.35	0.41
1:A:141:PRO:O	1:A:172:ARG:HD2	2.20	0.41
1:B:92:LYS:C	1:B:92:LYS:CD	2.85	0.41
1:B:111:GLN:NE2	1:B:490:HIS:NE2	2.69	0.41
1:A:469:HIS:CD2	1:A:471:LEU:H	2.35	0.41

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	510/542 (94%)	500 (98%)	10 (2%)	0	100	100
1	B	512/542 (94%)	499 (98%)	13 (2%)	0	100	100
All	All	1022/1084 (94%)	999 (98%)	23 (2%)	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	463/491 (94%)	452 (98%)	11 (2%)	57	82
1	B	465/491 (95%)	454 (98%)	11 (2%)	57	82
All	All	928/982 (94%)	906 (98%)	22 (2%)	57	82

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	42	LEU
1	A	85	LYS
1	A	136	ARG
1	A	214	ASP
1	A	322	VAL
1	A	384	GLU
1	A	418	SER
1	A	443	PRO
1	A	498	THR
1	A	500	ASN
1	A	511	GLN
1	B	17	CYS
1	B	42	LEU
1	B	131	ASP
1	B	153	SER

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Mol	Chain	Res	Type
1	B	238	LYS
1	B	322	VAL
1	B	328	SER
1	B	418	SER
1	B	439	ILE
1	B	478	THR
1	B	498	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	72	GLN
1	A	221	ASN
1	A	260	GLN
1	A	302	ASN
1	A	359	ASN
1	A	411	HIS
1	A	469	HIS
1	A	477	GLN
1	A	500	ASN
1	A	504	HIS
1	A	506	ASN
1	B	71	HIS
1	B	72	GLN
1	B	111	GLN
1	B	130	ASN
1	B	142	GLN
1	B	221	ASN
1	B	236	HIS
1	B	260	GLN
1	B	359	ASN
1	B	381	HIS
1	B	469	HIS
1	B	477	GLN
1	B	500	ASN

5.3.3   RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

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

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (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 (i)

6.1 Protein, DNA and RNA chains (i)

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, 95th 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(Å²)	Q<0.9
1	A	509/542 (93%)	0.27	33 (6%)	22	16	15, 32, 84, 142	1 (0%)
1	B	509/542 (93%)	0.44	42 (8%)	14	9	16, 42, 129, 176	0
All	All	1018/1084 (93%)	0.35	75 (7%)	17	12	15, 38, 106, 176	1 (0%)

All (75) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	8	VAL	13.7
1	B	97	ALA	9.2
1	A	516	LEU	8.5
1	B	96	HIS	8.1
1	B	514	GLU	8.0
1	B	102	LEU	7.9
1	B	92	LYS	7.3
1	B	94	SER	6.9
1	B	103	LYS	6.9
1	B	95	PRO	6.8
1	B	9	ILE	6.7
1	A	95	PRO	6.5
1	A	512	GLY	6.2
1	A	510	ALA	6.1
1	B	90	GLN	6.1
1	B	91	LYS	6.0
1	B	99	ASP	6.0
1	B	106	ILE	5.9
1	B	93	ILE	5.8
1	A	513	TYR	5.7
1	B	89	SER	5.6
1	B	515	LYS	5.5
1	B	513	TYR	4.8
1	A	246	GLU	4.6

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Mol	Chain	Res	Type	RSRZ
1	B	516	LEU	4.5
1	A	303	ASP	4.3
1	B	98	TYR	4.1
1	B	85	LYS	4.0
1	B	481	LYS	4.0
1	B	87	ILE	3.9
1	A	244	ASP	3.8
1	A	515	LYS	3.8
1	B	84	ILE	3.7
1	B	511	GLN	3.7
1	B	88	ASN	3.6
1	B	126	TYR	3.6
1	A	514	GLU	3.6
1	A	511	GLN	3.5
1	A	243	ILE	3.5
1	A	302	ASN	3.4
1	B	12	LYS	3.3
1	A	94	SER	3.1
1	A	290	TYR	3.0
1	A	272	PRO	3.0
1	B	10	LYS	2.9
1	A	245	GLY	2.9
1	B	24	GLU	2.9
1	B	11	PHE	2.9
1	A	96	HIS	2.9
1	B	82	GLU	2.9
1	B	86	ALA	2.8
1	A	93	ILE	2.8
1	B	125	GLN	2.8
1	A	98	TYR	2.7
1	A	309	TRP	2.7
1	B	46	CYS	2.6
1	B	100	ASP	2.6
1	A	249	ASP	2.5
1	A	301	ASP	2.5
1	A	17	CYS	2.4
1	B	128[A]	GLU	2.4
1	B	507	GLU	2.4
1	A	273	GLN	2.4
1	A	505	LYS	2.4
1	B	505	LYS	2.4
1	B	480	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	239	ASP	2.2
1	A	257	THR	2.1
1	A	91	LYS	2.1
1	B	510	ALA	2.1
1	A	508	VAL	2.1
1	A	277	LEU	2.1
1	B	478	THR	2.0
1	A	287	GLU	2.0
1	A	9	ILE	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, 95th 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
2	HG	A	601	1/1	0.98	0.23	1.16	68,68,68,68	0
2	HG	B	601	1/1	0.93	0.10	-2.48	103,103,103,103	0
2	HG	B	602	1/1	0.97	0.18	-	102,102,102,102	1
2	HG	A	602	1/1	0.99	0.18	-	76,76,76,76	0

6.5 Other polymers (i)

There are no such residues in this entry.