Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2023 – 07:14 PM EDT

PDB ID	:	2PSO
Title	:	Human StarD13 (DLC2) lipid transfer and protein localization domain
Authors	:	Lehtio, L.; Busam, R.; Arrowsmith, C.H.; Berglund, H.; Collins, R.; Dahlgren, L.G.; Edwards, A.; Flodin, S.; Flores, A.; Graslund, S.; Hammarstrom, M.; Hallberg, B.M.; Holmberg-Schiavone, L.; Johansson, I.; Kallas, A.; Karlberg, T.; Kotenyova, T.; Moche, M.; Nordlund, P.; Nyman, T.; Ogg, D.; Sagemark, J.; Stenmark, P.; Sundstrom, M.; Thorsell, A.G.; Van den Berg, S.; Weigelt, J.; Welin, M.; Persson, C.; Structural Genomics Consortium (SGC)
Deposited on	:	2007-05-07
Resolution	:	2.80 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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

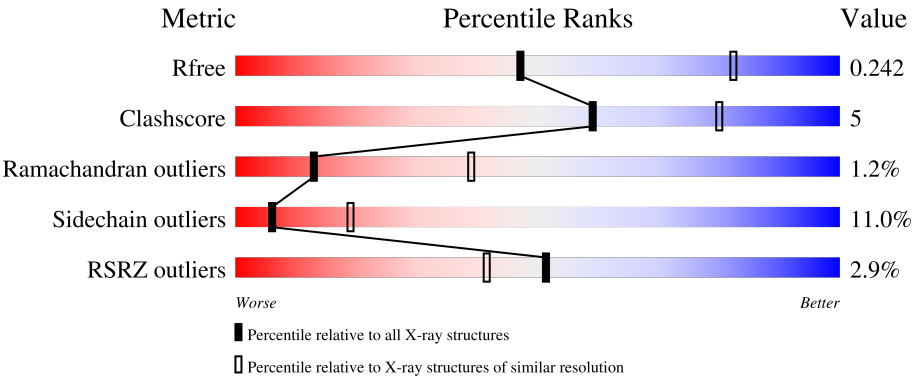
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)

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 2.80 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}	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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 of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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	237	3% 68% 13% • 17%
1	B	237	% 69% 10% • 16%
1	C	237	4% 62% 16% 21%

Validation Pipeline (wwPDB-VP) : 2.35

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 4477 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 StAR-related lipid transfer protein 13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	197	Total	C	N	O	S	0	0	0
			1517	962	268	279	8			
1	B	198	Total	C	N	O	S	0	0	0
			1535	979	267	282	7			
1	C	188	Total	C	N	O	S	0	0	0
			1425	911	250	258	6			

There are 78 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	877	MET	-	cloning artifact	UNP Q9Y3M8
A	878	HIS	-	cloning artifact	UNP Q9Y3M8
A	879	HIS	-	cloning artifact	UNP Q9Y3M8
A	880	HIS	-	cloning artifact	UNP Q9Y3M8
A	881	HIS	-	cloning artifact	UNP Q9Y3M8
A	882	HIS	-	cloning artifact	UNP Q9Y3M8
A	883	HIS	-	cloning artifact	UNP Q9Y3M8
A	884	SER	-	cloning artifact	UNP Q9Y3M8
A	885	SER	-	cloning artifact	UNP Q9Y3M8
A	886	GLY	-	cloning artifact	UNP Q9Y3M8
A	887	VAL	-	cloning artifact	UNP Q9Y3M8
A	888	ASP	-	cloning artifact	UNP Q9Y3M8
A	889	LEU	-	cloning artifact	UNP Q9Y3M8
A	890	GLY	-	cloning artifact	UNP Q9Y3M8
A	891	THR	-	cloning artifact	UNP Q9Y3M8
A	892	GLU	-	cloning artifact	UNP Q9Y3M8
A	893	ASN	-	cloning artifact	UNP Q9Y3M8
A	894	LEU	-	cloning artifact	UNP Q9Y3M8
A	895	TYR	-	cloning artifact	UNP Q9Y3M8
A	896	PHE	-	cloning artifact	UNP Q9Y3M8
A	897	GLN	-	cloning artifact	UNP Q9Y3M8
A	898	SER	-	cloning artifact	UNP Q9Y3M8
A	899	MET	-	cloning artifact	UNP Q9Y3M8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	900	GLU	-	cloning artifact	UNP Q9Y3M8
A	901	GLU	-	cloning artifact	UNP Q9Y3M8
A	902	SER	-	cloning artifact	UNP Q9Y3M8
B	877	MET	-	cloning artifact	UNP Q9Y3M8
B	878	HIS	-	cloning artifact	UNP Q9Y3M8
B	879	HIS	-	cloning artifact	UNP Q9Y3M8
B	880	HIS	-	cloning artifact	UNP Q9Y3M8
B	881	HIS	-	cloning artifact	UNP Q9Y3M8
B	882	HIS	-	cloning artifact	UNP Q9Y3M8
B	883	HIS	-	cloning artifact	UNP Q9Y3M8
B	884	SER	-	cloning artifact	UNP Q9Y3M8
B	885	SER	-	cloning artifact	UNP Q9Y3M8
B	886	GLY	-	cloning artifact	UNP Q9Y3M8
B	887	VAL	-	cloning artifact	UNP Q9Y3M8
B	888	ASP	-	cloning artifact	UNP Q9Y3M8
B	889	LEU	-	cloning artifact	UNP Q9Y3M8
B	890	GLY	-	cloning artifact	UNP Q9Y3M8
B	891	THR	-	cloning artifact	UNP Q9Y3M8
B	892	GLU	-	cloning artifact	UNP Q9Y3M8
B	893	ASN	-	cloning artifact	UNP Q9Y3M8
B	894	LEU	-	cloning artifact	UNP Q9Y3M8
B	895	TYR	-	cloning artifact	UNP Q9Y3M8
B	896	PHE	-	cloning artifact	UNP Q9Y3M8
B	897	GLN	-	cloning artifact	UNP Q9Y3M8
B	898	SER	-	cloning artifact	UNP Q9Y3M8
B	899	MET	-	cloning artifact	UNP Q9Y3M8
B	900	GLU	-	cloning artifact	UNP Q9Y3M8
B	901	GLU	-	cloning artifact	UNP Q9Y3M8
B	902	SER	-	cloning artifact	UNP Q9Y3M8
C	877	MET	-	cloning artifact	UNP Q9Y3M8
C	878	HIS	-	cloning artifact	UNP Q9Y3M8
C	879	HIS	-	cloning artifact	UNP Q9Y3M8
C	880	HIS	-	cloning artifact	UNP Q9Y3M8
C	881	HIS	-	cloning artifact	UNP Q9Y3M8
C	882	HIS	-	cloning artifact	UNP Q9Y3M8
C	883	HIS	-	cloning artifact	UNP Q9Y3M8
C	884	SER	-	cloning artifact	UNP Q9Y3M8
C	885	SER	-	cloning artifact	UNP Q9Y3M8
C	886	GLY	-	cloning artifact	UNP Q9Y3M8
C	887	VAL	-	cloning artifact	UNP Q9Y3M8
C	888	ASP	-	cloning artifact	UNP Q9Y3M8
C	889	LEU	-	cloning artifact	UNP Q9Y3M8

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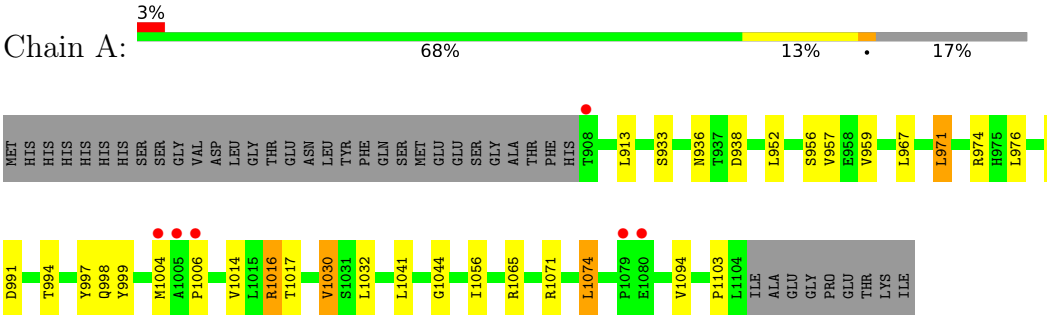
Chain	Residue	Modelled	Actual	Comment	Reference
C	890	GLY	-	cloning artifact	UNP Q9Y3M8
C	891	THR	-	cloning artifact	UNP Q9Y3M8
C	892	GLU	-	cloning artifact	UNP Q9Y3M8
C	893	ASN	-	cloning artifact	UNP Q9Y3M8
C	894	LEU	-	cloning artifact	UNP Q9Y3M8
C	895	TYR	-	cloning artifact	UNP Q9Y3M8
C	896	PHE	-	cloning artifact	UNP Q9Y3M8
C	897	GLN	-	cloning artifact	UNP Q9Y3M8
C	898	SER	-	cloning artifact	UNP Q9Y3M8
C	899	MET	-	cloning artifact	UNP Q9Y3M8
C	900	GLU	-	cloning artifact	UNP Q9Y3M8
C	901	GLU	-	cloning artifact	UNP Q9Y3M8
C	902	SER	-	cloning artifact	UNP Q9Y3M8

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

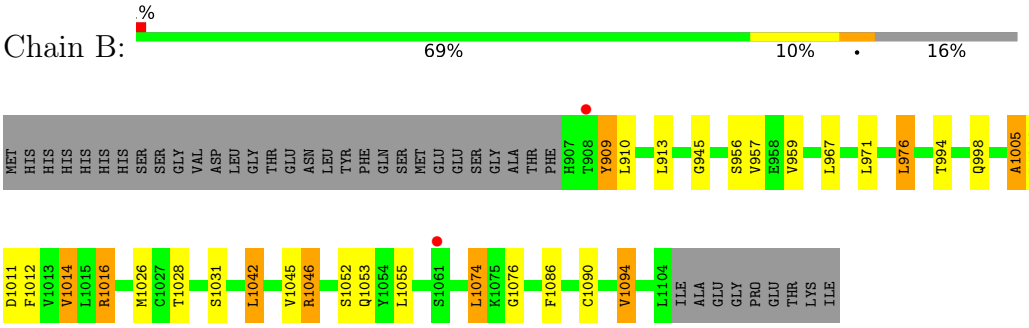
• Molecule 1: StAR-related lipid transfer protein 13

Chain A:



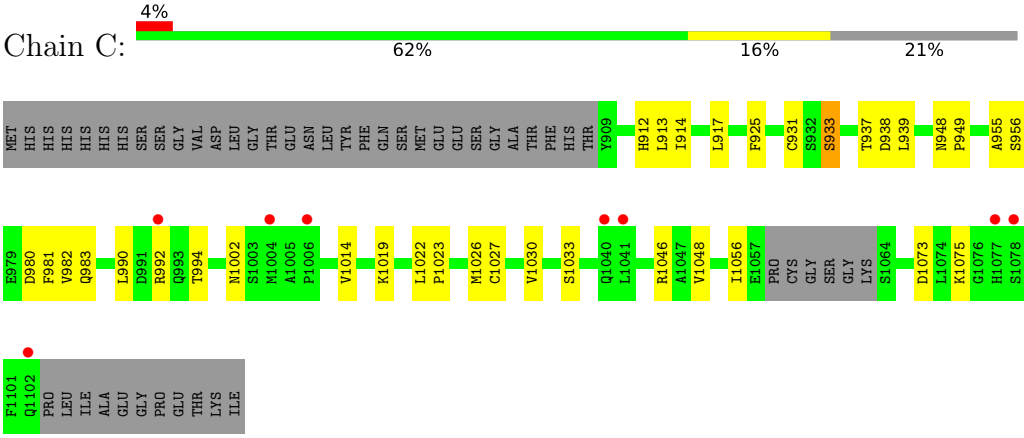
• Molecule 1: StAR-related lipid transfer protein 13

Chain B:



• Molecule 1: StAR-related lipid transfer protein 13

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α, β, γ	78.24Å 78.24Å 212.72Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.79 – 2.80 19.59 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.8 (19.79-2.80) 99.8 (19.59-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	3.06 (at 2.79Å)	Xtriage
Refinement program	REFMAC 5.3.0032	Depositor
R, R_{free}	0.210 , 0.244 0.206 , 0.242	Depositor DCC
R_{free} test set	1571 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å^2)	75.1	Xtriage
Anisotropy	0.248	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 52.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.055 for h,-k,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	4477	wwPDB-VP
Average B, all atoms (Å^2)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.40% 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, 0.333 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	0.57	0/1554	0.76	0/2118
1	B	0.60	0/1573	0.74	1/2143 (0.0%)
1	C	0.42	0/1458	0.60	0/1990
All	All	0.54	0/4585	0.71	1/6251 (0.0%)

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

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	1074	LEU	CA-CB-CG	5.16	127.17	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	945	GLY	Peptide

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	1517	0	1440	11	0
1	B	1535	0	1471	16	0
1	C	1425	0	1349	15	0
All	All	4477	0	4260	41	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 (41) 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:B:1005:ALA:HB1	1:B:1006:PRO:HD3	1.50	0.90
1:B:957:VAL:HG13	1:B:1094:VAL:HG13	1.68	0.74
1:B:1005:ALA:HB1	1:B:1006:PRO:CD	2.18	0.73
1:B:1005:ALA:CB	1:B:1006:PRO:CD	2.72	0.67
1:A:983:GLN:O	1:A:999:TYR:HA	1.95	0.66
1:A:997:TYR:HB2	1:A:1016:ARG:HD2	1.80	0.63
1:A:991:ASP:OD1	1:A:994:THR:HG23	2.05	0.57
1:B:1005:ALA:CB	1:B:1006:PRO:HD3	2.30	0.57
1:C:914:ILE:HA	1:C:917:LEU:HD12	1.88	0.55
1:A:982:VAL:HG12	1:A:983:GLN:HG2	1.88	0.54
1:C:933:SER:OG	1:C:937:THR:OG1	2.26	0.53
1:C:980:ASP:HB3	1:C:1002:ASN:H	1.76	0.50
1:C:1022:LEU:HB2	1:C:1026:MET:O	2.11	0.50
1:B:1011:ASP:OD2	1:B:1046:ARG:NH1	2.45	0.50
1:A:952:LEU:HD12	1:A:1071:ARG:HB2	1.94	0.49
1:B:1028:THR:HG22	1:B:1055:LEU:HD23	1.95	0.49
1:B:1014:VAL:HG13	1:B:1016:ARG:HG2	1.97	0.46
1:C:948:ASN:HA	1:C:949:PRO:HD3	1.79	0.45
1:A:938:ASP:HB2	1:A:956:SER:HB2	1.98	0.45
1:C:1027:CYS:HB2	1:C:1056:ILE:HB	1.99	0.44
1:A:971:LEU:HD22	1:A:971:LEU:O	2.18	0.43
1:B:1008:PRO:HD2	1:B:1010:ARG:HH21	1.83	0.43
1:C:982:VAL:HG12	1:C:983:GLN:HG3	1.99	0.42
1:B:1086:PHE:CE1	1:B:1090:CYS:SG	3.12	0.42
1:C:931:CYS:HB2	1:C:939:LEU:HB3	2.01	0.42
1:C:938:ASP:O	1:C:955:ALA:HA	2.19	0.42
1:A:1074:LEU:HD22	1:A:1074:LEU:H	1.84	0.42
1:A:967:LEU:C	1:A:967:LEU:HD13	2.40	0.42
1:B:998:GLN:HA	1:B:1012:PHE:O	2.20	0.42
1:B:976:LEU:HD12	1:B:976:LEU:HA	1.84	0.42
1:C:978:ASP:HB3	1:C:981:PHE:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1053:GLN:HG3	1:C:914:ILE:HD13	2.01	0.41
1:A:974:ARG:HD3	1:A:981:PHE:CE1	2.55	0.41
1:B:1042:LEU:HA	1:B:1042:LEU:HD12	1.78	0.41
1:C:1048:VAL:HB	1:C:1073:ASP:HB3	2.03	0.41
1:B:909:TYR:HD1	1:B:910:LEU:N	2.19	0.40
1:C:1022:LEU:HA	1:C:1023:PRO:HD2	1.84	0.40
1:A:1016:ARG:HA	1:A:1030:VAL:O	2.20	0.40
1:C:937:THR:HG22	1:C:957:VAL:CG1	2.51	0.40
1:B:1010:ARG:HD3	1:B:1045:VAL:HB	2.03	0.40
1:C:990:LEU:HD23	1:C:990:LEU:HA	1.82	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	195/237 (82%)	170 (87%)	21 (11%)	4 (2%)	7 23
1	B	196/237 (83%)	177 (90%)	17 (9%)	2 (1%)	15 44
1	C	184/237 (78%)	162 (88%)	21 (11%)	1 (0%)	29 61
All	All	575/711 (81%)	509 (88%)	59 (10%)	7 (1%)	13 39

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	1005	ALA
1	A	1041	LEU
1	A	1103	PRO
1	C	925	PHE
1	B	1076	GLY
1	A	1006	PRO
1	A	1044	GLY

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	158/209 (76%)	140 (89%)	18 (11%)	5	18
1	B	161/209 (77%)	143 (89%)	18 (11%)	6	18
1	C	145/209 (69%)	130 (90%)	15 (10%)	7	21
All	All	464/627 (74%)	413 (89%)	51 (11%)	6	19

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	913	LEU
1	A	933	SER
1	A	936	ASN
1	A	957	VAL
1	A	959	VAL
1	A	971	LEU
1	A	976	LEU
1	A	998	GLN
1	A	1004	MET
1	A	1014	VAL
1	A	1016	ARG
1	A	1017	THR
1	A	1030	VAL
1	A	1032	LEU
1	A	1056	ILE
1	A	1065	ARG
1	A	1074	LEU
1	A	1094	VAL
1	B	909	TYR
1	B	913	LEU
1	B	956	SER
1	B	959	VAL
1	B	967	LEU
1	B	971	LEU
1	B	976	LEU
1	B	994	THR

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Mol	Chain	Res	Type
1	B	1010	ARG
1	B	1014	VAL
1	B	1016	ARG
1	B	1026	MET
1	B	1031	SER
1	B	1042	LEU
1	B	1046	ARG
1	B	1052	SER
1	B	1074	LEU
1	B	1094	VAL
1	C	912	HIS
1	C	913	LEU
1	C	933	SER
1	C	956	SER
1	C	967	LEU
1	C	992	ARG
1	C	994	THR
1	C	1014	VAL
1	C	1019	LYS
1	C	1030	VAL
1	C	1033	SER
1	C	1046	ARG
1	C	1075	LYS
1	C	1083	SER
1	C	1100	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	983	GLN
1	A	998	GLN
1	A	1002	ASN
1	B	911	ASN
1	C	1002	ASN
1	C	1040	GLN

5.3.3 RNA

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 monosaccharides 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	197/237 (83%)	-0.23	6 (3%) 50 40	7, 37, 82, 100	0
1	B	198/237 (83%)	-0.36	2 (1%) 82 77	12, 34, 71, 88	0
1	C	188/237 (79%)	-0.17	9 (4%) 30 21	17, 65, 93, 108	0
All	All	583/711 (81%)	-0.26	17 (2%) 51 41	7, 44, 88, 108	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1004	MET	4.0
1	C	1006	PRO	3.7
1	A	908	THR	3.5
1	B	908	THR	3.5
1	C	1004	MET	3.1
1	C	992	ARG	3.1
1	C	1102	GLN	3.1
1	A	1080	GLU	3.0
1	A	1006	PRO	2.7
1	C	1040	GLN	2.7
1	C	1078	SER	2.5
1	B	1061	SER	2.3
1	A	1079	PRO	2.3
1	C	1041	LEU	2.2
1	C	1079	PRO	2.2
1	A	1005	ALA	2.2
1	C	1077	HIS	2.0

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 (i)

There are no monosaccharides 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.