Full wwPDB X-ray Structure Validation Report ⓘ

Apr 27, 2024 – 10:43 am BST

PDB ID	:	4C95
Title	:	Crystal structure of the carboxy-terminal domain of yeast Ctf4 bound to Sld5
Authors	:	Simon, A.C.; Pellegrini, L.
Deposited on	:	2013-10-02
Resolution	:	2.69 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:

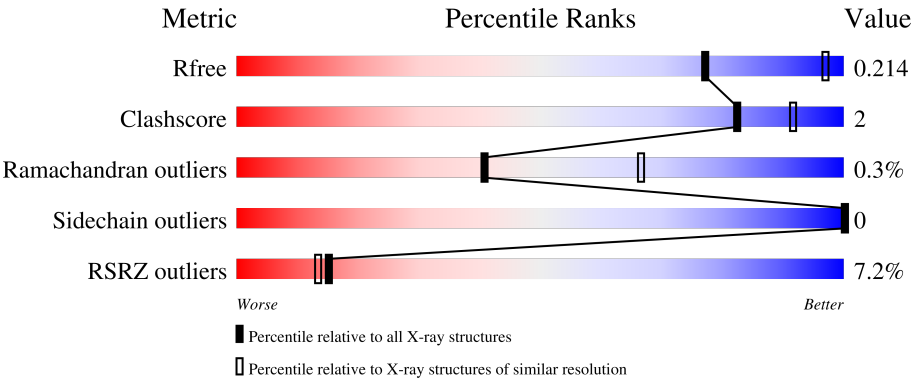
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 2.69 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 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	478	5% 82% 6% 11%
1	B	478	4% 83% 7% 10%
1	C	478	7% 58% 38%
2	D	19	37% 68% 32%
2	E	19	11% 68% 32%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 9684 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 DNA POLYMERASE ALPHA-BINDING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	424	Total	C	N	O	S	0	1	0
			3416	2193	566	642	15			
1	B	431	Total	C	N	O	S	0	1	0
			3472	2227	576	653	16			
1	C	296	Total	C	N	O	S	0	1	0
			2405	1562	392	440	11			

There are 63 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	450	MET	-	expression tag	UNP Q01454
A	451	GLY	-	expression tag	UNP Q01454
A	452	SER	-	expression tag	UNP Q01454
A	453	SER	-	expression tag	UNP Q01454
A	454	HIS	-	expression tag	UNP Q01454
A	455	HIS	-	expression tag	UNP Q01454
A	456	HIS	-	expression tag	UNP Q01454
A	457	HIS	-	expression tag	UNP Q01454
A	458	HIS	-	expression tag	UNP Q01454
A	459	HIS	-	expression tag	UNP Q01454
A	460	SER	-	expression tag	UNP Q01454
A	461	GLN	-	expression tag	UNP Q01454
A	462	ASP	-	expression tag	UNP Q01454
A	463	PRO	-	expression tag	UNP Q01454
A	464	GLU	-	expression tag	UNP Q01454
A	465	ASN	-	expression tag	UNP Q01454
A	466	LEU	-	expression tag	UNP Q01454
A	467	TYR	-	expression tag	UNP Q01454
A	468	PHE	-	expression tag	UNP Q01454
A	469	GLN	-	expression tag	UNP Q01454
A	470	GLY	-	expression tag	UNP Q01454
B	450	MET	-	expression tag	UNP Q01454
B	451	GLY	-	expression tag	UNP Q01454

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Chain	Residue	Modelled	Actual	Comment	Reference
B	452	SER	-	expression tag	UNP Q01454
B	453	SER	-	expression tag	UNP Q01454
B	454	HIS	-	expression tag	UNP Q01454
B	455	HIS	-	expression tag	UNP Q01454
B	456	HIS	-	expression tag	UNP Q01454
B	457	HIS	-	expression tag	UNP Q01454
B	458	HIS	-	expression tag	UNP Q01454
B	459	HIS	-	expression tag	UNP Q01454
B	460	SER	-	expression tag	UNP Q01454
B	461	GLN	-	expression tag	UNP Q01454
B	462	ASP	-	expression tag	UNP Q01454
B	463	PRO	-	expression tag	UNP Q01454
B	464	GLU	-	expression tag	UNP Q01454
B	465	ASN	-	expression tag	UNP Q01454
B	466	LEU	-	expression tag	UNP Q01454
B	467	TYR	-	expression tag	UNP Q01454
B	468	PHE	-	expression tag	UNP Q01454
B	469	GLN	-	expression tag	UNP Q01454
B	470	GLY	-	expression tag	UNP Q01454
C	450	MET	-	expression tag	UNP Q01454
C	451	GLY	-	expression tag	UNP Q01454
C	452	SER	-	expression tag	UNP Q01454
C	453	SER	-	expression tag	UNP Q01454
C	454	HIS	-	expression tag	UNP Q01454
C	455	HIS	-	expression tag	UNP Q01454
C	456	HIS	-	expression tag	UNP Q01454
C	457	HIS	-	expression tag	UNP Q01454
C	458	HIS	-	expression tag	UNP Q01454
C	459	HIS	-	expression tag	UNP Q01454
C	460	SER	-	expression tag	UNP Q01454
C	461	GLN	-	expression tag	UNP Q01454
C	462	ASP	-	expression tag	UNP Q01454
C	463	PRO	-	expression tag	UNP Q01454
C	464	GLU	-	expression tag	UNP Q01454
C	465	ASN	-	expression tag	UNP Q01454
C	466	LEU	-	expression tag	UNP Q01454
C	467	TYR	-	expression tag	UNP Q01454
C	468	PHE	-	expression tag	UNP Q01454
C	469	GLN	-	expression tag	UNP Q01454
C	470	GLY	-	expression tag	UNP Q01454

- Molecule 2 is a protein called DNA REPLICATION COMPLEX GINS PROTEIN SLD5.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
2	D	13	Total C N O 104 65 15 24	0	0	0
2	E	13	Total C N O 104 65 15 24	0	0	0

- Molecule 3 is water.

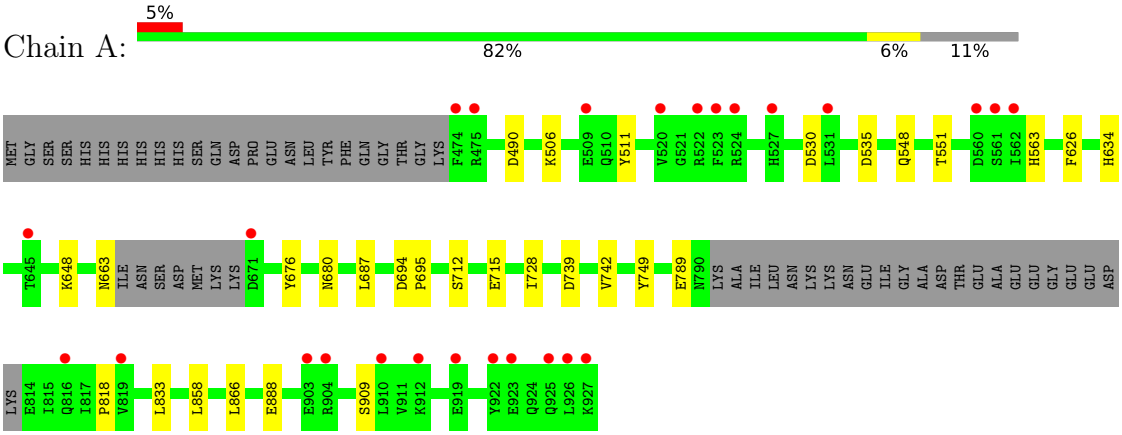
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	86	Total O 86 86	0	0
3	B	67	Total O 67 67	0	0
3	C	30	Total O 30 30	0	0

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.

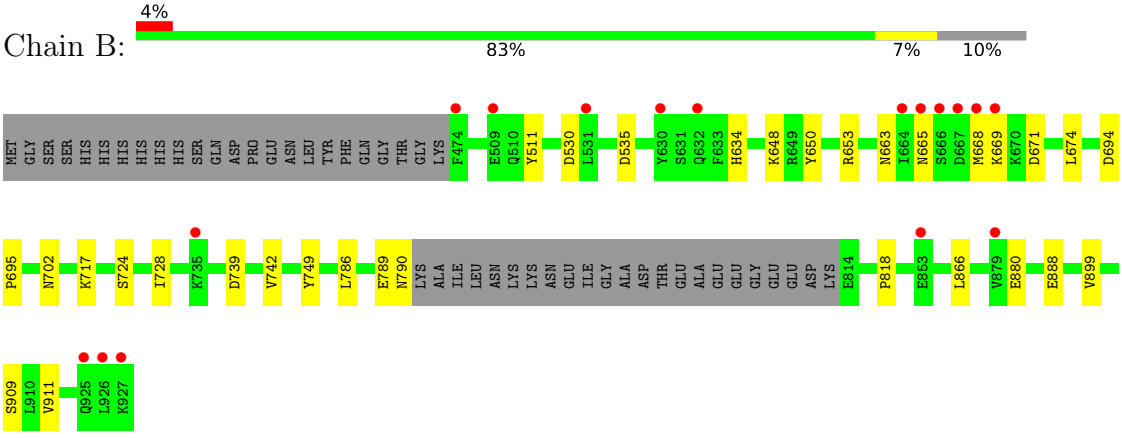
• Molecule 1: DNA POLYMERASE ALPHA-BINDING PROTEIN

Chain A:



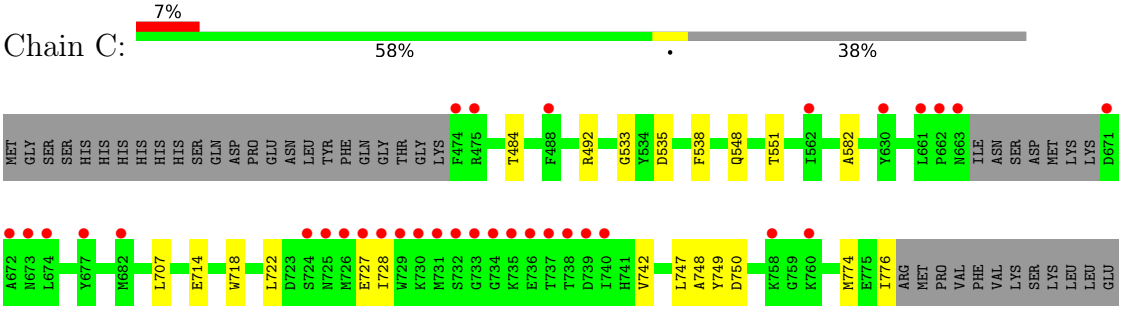
• Molecule 1: DNA POLYMERASE ALPHA-BINDING PROTEIN

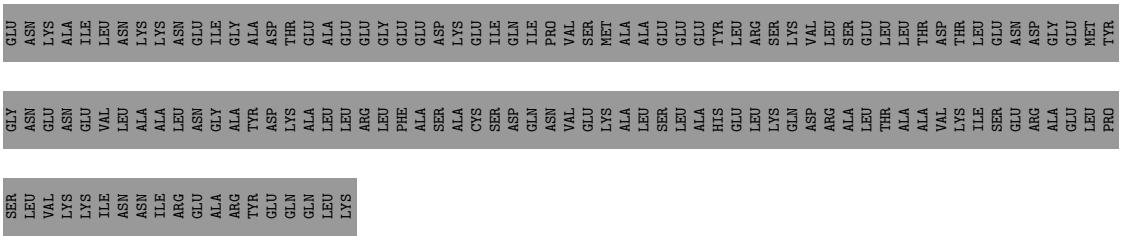
Chain B:



• Molecule 1: DNA POLYMERASE ALPHA-BINDING PROTEIN

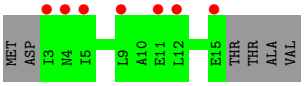
Chain C:





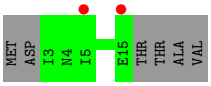
• Molecule 2: DNA REPLICATION COMPLEX GINS PROTEIN SLD5

Chain D:



• Molecule 2: DNA REPLICATION COMPLEX GINS PROTEIN SLD5

Chain E:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants a, b, c, α, β, γ	88.94Å 99.70Å 218.58Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.92 – 2.69 47.92 – 2.69	Depositor EDS
% Data completeness (in resolution range)	99.3 (47.92-2.69) 99.4 (47.92-2.69)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.25 (at 2.69Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.8.4_1496)	Depositor
R, R_{free}	0.179 , 0.214 0.178 , 0.214	Depositor DCC
R_{free} test set	2763 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å^2)	57.5	Xtriage
Anisotropy	0.333	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 48.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	9684	wwPDB-VP
Average B, all atoms (Å^2)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.11% 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	0.23	0/3501	0.39	0/4741
1	B	0.23	0/3558	0.39	0/4817
1	C	0.22	0/2481	0.38	0/3370
2	D	0.19	0/103	0.34	0/138
2	E	0.18	0/103	0.37	0/138
All	All	0.23	0/9746	0.39	0/13204

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	3416	0	3356	18	0
1	B	3472	0	3418	20	0
1	C	2405	0	2326	12	0
2	D	104	0	102	0	0
2	E	104	0	102	0	0
3	A	86	0	0	1	1
3	B	67	0	0	1	1
3	C	30	0	0	0	0
All	All	9684	0	9304	46	1

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 2.

All (46) 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:653:ARG:HE	1:C:714:GLU:HG3	1.58	0.68
1:A:728:ILE:HD11	1:A:742:VAL:HG23	1.81	0.63
1:A:563:HIS:ND1	1:B:880:GLU:OE1	2.30	0.59
1:C:747:LEU:HD11	1:C:776:ILE:HD11	1.85	0.58
1:A:511:TYR:HB2	1:A:530:ASP:HB3	1.87	0.57
1:B:909:SER:OG	3:B:2067:HOH:O	2.17	0.57
1:A:648:LYS:HB3	1:B:717:LYS:HD3	1.86	0.57
1:A:490:ASP:HB3	1:A:506:LYS:HB2	1.87	0.56
1:C:722:LEU:HD21	1:C:774:MET:HE2	1.89	0.54
1:C:533:GLY:O	1:C:548:GLN:NE2	2.43	0.52
1:C:748:ALA:O	1:C:750:ASP:N	2.42	0.52
1:B:669:LYS:HA	1:B:674:LEU:HD22	1.93	0.51
1:B:899:VAL:HG13	1:B:911:VAL:HG13	1.92	0.50
1:A:739:ASP:N	1:A:739:ASP:OD1	2.45	0.49
1:C:728:ILE:HD11	1:C:742:VAL:HG23	1.95	0.48
1:B:739:ASP:OD1	1:B:739:ASP:N	2.46	0.47
1:A:663:ASN:OD1	1:A:663:ASN:N	2.47	0.47
1:A:634:HIS:CE1	1:B:634:HIS:HA	2.49	0.47
1:B:789:GLU:HG3	1:B:818:PRO:HG3	1.97	0.47
1:B:702:ASN:HB3	1:B:724:SER:OG	2.15	0.47
1:B:665:ASN:H	1:B:668:MET:HG3	1.80	0.47
1:B:668:MET:HA	1:B:671:ASP:HB2	1.98	0.45
1:B:728:ILE:HD11	1:B:742:VAL:HG23	1.97	0.45
1:B:511:TYR:HB2	1:B:530:ASP:HB3	1.98	0.45
1:B:535:ASP:OD1	1:B:535:ASP:N	2.50	0.44
1:C:707:LEU:HD13	1:C:718:TRP:CE2	2.52	0.44
1:A:694:ASP:HA	1:A:695:PRO:HD3	1.88	0.44
1:C:538:PHE:CG	1:C:582:ALA:HA	2.53	0.43
1:A:676:TYR:O	1:A:680:ASN:N	2.50	0.43
1:A:712:SER:HB2	1:A:715:GLU:HB2	2.00	0.43
1:A:789:GLU:HG3	1:A:818:PRO:HG3	2.00	0.43
1:B:866:LEU:HD21	1:B:888:GLU:HB2	2.00	0.43
1:B:648:LYS:HE2	1:B:650:TYR:CZ	2.54	0.43
1:B:663:ASN:OD1	1:B:663:ASN:N	2.47	0.43
1:A:833:LEU:HB3	1:A:858:LEU:HD21	2.01	0.42
1:C:722:LEU:HD11	1:C:727:GLU:HG3	2.01	0.42
1:A:535:ASP:OD1	1:A:535:ASP:N	2.52	0.41
1:A:548:GLN:HG3	1:A:551:THR:H	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:694:ASP:HA	1:B:695:PRO:HD3	1.89	0.41
1:C:484:THR:O	1:C:492:ARG:HD2	2.21	0.41
1:A:909:SER:OG	3:A:2085:HOH:O	2.21	0.41
1:C:535:ASP:OD1	1:C:535:ASP:N	2.55	0.40
1:B:786:LEU:O	1:B:790:ASN:ND2	2.53	0.40
1:A:626:PHE:CE2	1:A:687:LEU:HD12	2.57	0.40
1:C:548:GLN:HG3	1:C:551:THR:H	1.87	0.40
1:A:866:LEU:HD21	1:A:888:GLU:HB2	2.04	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:2080:HOH:O	3:B:2038:HOH:O[3_554]	2.15	0.05

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	419/478 (88%)	403 (96%)	15 (4%)	1 (0%)	47	73
1	B	428/478 (90%)	414 (97%)	13 (3%)	1 (0%)	47	73
1	C	293/478 (61%)	276 (94%)	16 (6%)	1 (0%)	41	66
2	D	11/19 (58%)	11 (100%)	0	0	100	100
2	E	11/19 (58%)	11 (100%)	0	0	100	100
All	All	1162/1472 (79%)	1115 (96%)	44 (4%)	3 (0%)	41	66

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	749	TYR

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Mol	Chain	Res	Type
1	C	749	TYR
1	A	749	TYR

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	377/422 (89%)	377 (100%)	0	100	100
1	B	384/422 (91%)	384 (100%)	0	100	100
1	C	267/422 (63%)	267 (100%)	0	100	100
2	D	12/17 (71%)	12 (100%)	0	100	100
2	E	12/17 (71%)	12 (100%)	0	100	100
All	All	1052/1300 (81%)	1052 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

Mol	Chain	Res	Type
1	A	634	HIS
1	A	741	HIS
1	B	559	HIS

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 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	424/478 (88%)	0.14	26 (6%)	21	20	30, 50, 91, 119	0
1	B	431/478 (90%)	-0.00	17 (3%)	39	38	33, 52, 94, 125	0
1	C	296/478 (61%)	0.30	33 (11%)	5	4	36, 59, 110, 154	0
2	D	13/19 (68%)	1.87	7 (53%)	0	0	84, 92, 114, 118	0
2	E	13/19 (68%)	1.35	2 (15%)	2	1	67, 86, 102, 117	0
All	All	1177/1472 (79%)	0.16	85 (7%)	15	13	30, 53, 98, 154	0

All (85) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	733	GLY	6.8
1	C	474	PHE	6.3
1	C	734	GLY	6.2
1	C	729	TRP	5.9
1	C	736	GLU	5.8
1	C	737	THR	5.8
1	B	665	ASN	5.6
1	B	927	LYS	5.0
1	C	738	THR	5.0
1	C	732	SER	5.0
1	C	740	ILE	4.9
1	A	923	GLU	4.7
1	C	673	ASN	4.3
1	C	739	ASP	4.3
1	B	666	SER	4.3
1	B	474	PHE	4.3
1	B	668	MET	4.3
1	C	735	LYS	4.2
1	C	728	ILE	4.1
1	C	731	MET	4.0

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Mol	Chain	Res	Type	RSRZ
1	A	524	ARG	3.9
1	C	760	LYS	3.8
1	B	509	GLU	3.7
1	A	903	GLU	3.6
1	B	667	ASP	3.6
1	A	522	ARG	3.5
1	A	919	GLU	3.5
1	B	926	LEU	3.5
1	A	520	VAL	3.4
2	D	3	ILE	3.4
1	B	664	ILE	3.4
1	A	927	LYS	3.3
1	C	674	LEU	3.3
1	C	726	MET	3.3
2	D	9	LEU	3.0
1	C	677	TYR	3.0
1	A	925	GLN	3.0
1	A	912	LYS	3.0
1	C	662	PRO	2.9
1	C	724	SER	2.9
1	C	672	ALA	2.9
1	B	879	VAL	2.9
1	C	730	LYS	2.9
1	C	671	ASP	2.8
1	A	527	HIS	2.8
2	E	15	GLU	2.8
1	A	926	LEU	2.8
1	A	531	LEU	2.7
1	A	509	GLU	2.7
1	A	562	ILE	2.7
1	B	669	LYS	2.7
1	C	562	ILE	2.7
1	C	682	MET	2.6
1	A	910	LEU	2.6
1	C	663	ASN	2.6
1	A	816	GLN	2.6
2	D	4	ASN	2.5
1	A	475	ARG	2.5
1	A	523	PHE	2.5
1	C	727	GLU	2.4
2	D	11	GLU	2.4
1	A	922	TYR	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	488	PHE	2.4
1	A	645	THR	2.3
1	A	560	ASP	2.3
1	A	904	ARG	2.3
1	C	661	LEU	2.3
2	D	5	ILE	2.3
1	C	725	ASN	2.3
2	D	15	GLU	2.3
1	A	819	VAL	2.3
1	A	561	SER	2.3
1	B	735	LYS	2.3
2	E	5	ILE	2.2
1	C	758	LYS	2.1
1	B	853	GLU	2.1
1	C	630	TYR	2.1
2	D	12	LEU	2.1
1	B	925	GLN	2.1
1	B	632	GLN	2.1
1	C	475	ARG	2.1
1	B	531	LEU	2.1
1	B	630	TYR	2.1
1	A	671	ASP	2.0
1	A	474	PHE	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 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.