Full wwPDB X-ray Structure Validation Report ⓘ

Aug 20, 2020 – 08:59 AM BST

PDB ID	:	6LBR
Title	:	Crystal structure of yeast Cdc13 and ssDNA
Authors	:	Ge, Y.; Wu, Z.; Wu, J.; Lei, M.
Deposited on	:	2019-11-14
Resolution	:	2.50 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 following versions of software and data (see references ⓘ) were used in the production of this report:

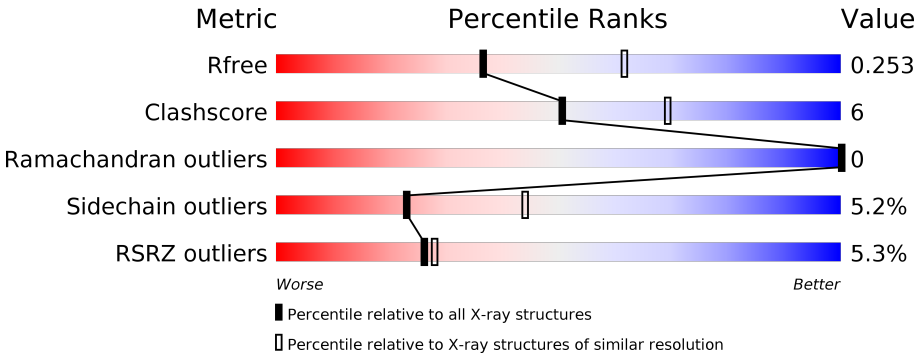
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.13
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13

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 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 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	551	4% 77% 15% • 6%
1	B	551	2% 32% 5% • 62%
2	C	25	12% 84% • 12%
2	D	25	16% 76% 16% 8%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7028 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 KLLA0F20922p.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	519	Total	C	N	O	S	0	0	0
			4190	2702	687	788	13			
1	B	208	Total	C	N	O	S	0	0	0
			1671	1078	280	307	6			

- Molecule 2 is a DNA chain called Telomere single-strand DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	22	Total	C	N	O	P	0	0	0
			460	219	84	135	22			
2	D	23	Total	C	N	O	P	0	0	0
			480	229	86	142	23			

- Molecule 3 is water.

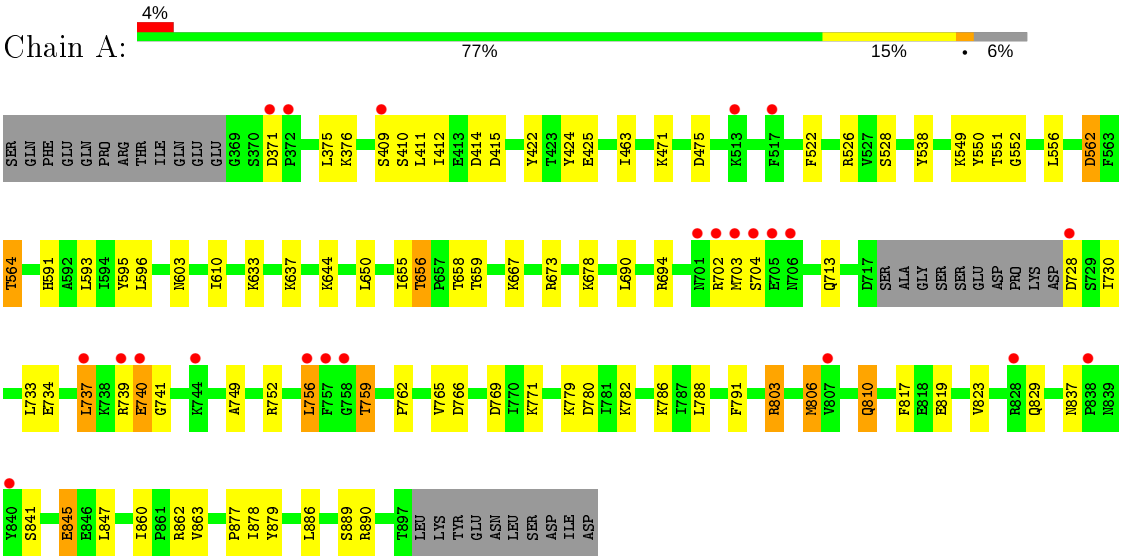
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	148	Total	O	0	0
			148	148		
3	B	35	Total	O	0	0
			35	35		
3	C	24	Total	O	0	0
			24	24		
3	D	20	Total	O	0	0
			20	20		

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.

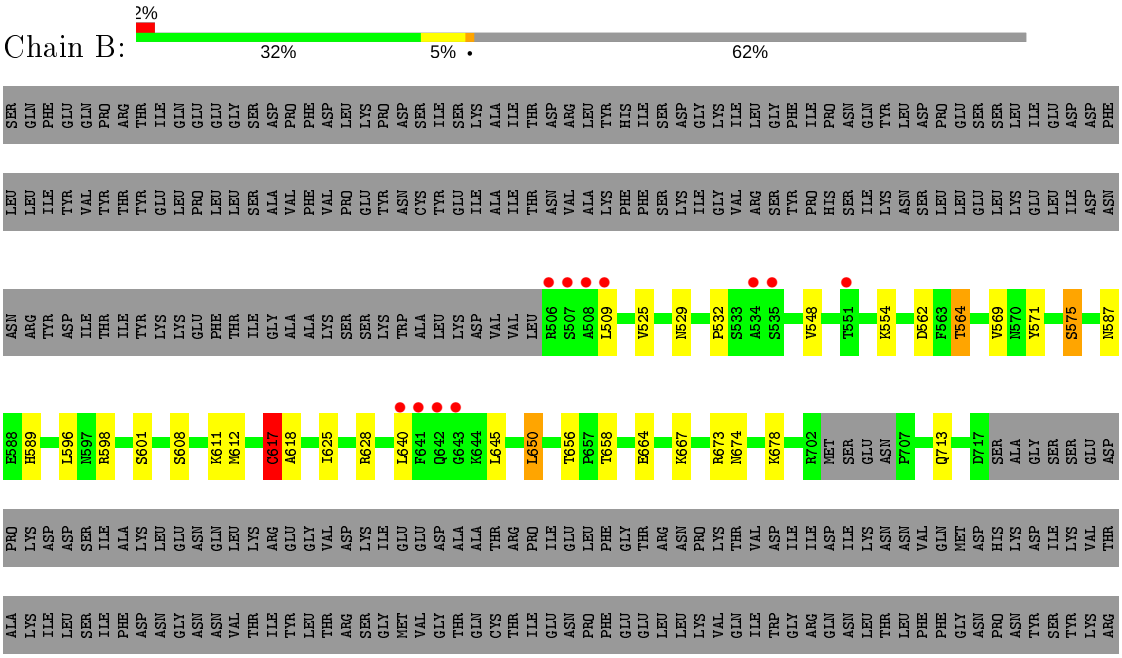
- Molecule 1: KLLA0F20922p

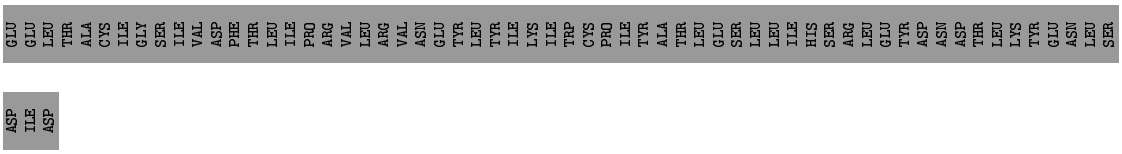
Chain A:



- Molecule 1: KLLA0F20922p

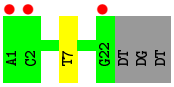
Chain B:





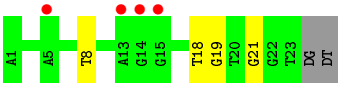
- Molecule 2: Telomere single-strand DNA

Chain C:



- Molecule 2: Telomere single-strand DNA

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	75.17Å 106.95Å 173.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.84 – 2.50 45.84 – 2.50	Depositor EDS
% Data completeness (in resolution range)	93.8 (45.84-2.50) 93.7 (45.84-2.50)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.65 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.15_3459	Depositor
R, R_{free}	0.202 , 0.252 0.203 , 0.253	Depositor DCC
R_{free} test set	2219 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å^2)	37.5	Xtriage
Anisotropy	0.136	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 53.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	7028	wwPDB-VP
Average B, all atoms (Å^2)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.19% 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	0.41	0/4278	0.69	8/5802 (0.1%)
1	B	0.41	0/1706	0.62	1/2310 (0.0%)
2	C	0.82	0/516	1.02	0/797
2	D	0.87	0/538	1.05	0/831
All	All	0.50	0/7038	0.74	9/9740 (0.1%)

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 (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	702	ARG	N-CA-C	14.85	151.10	111.00
1	A	703	MET	CB-CA-C	12.26	134.92	110.40
1	A	704	SER	N-CA-CB	-11.40	93.40	110.50
1	A	702	ARG	CB-CA-C	-8.14	94.11	110.40
1	A	740	GLU	CB-CA-C	-7.21	95.98	110.40
1	B	617	CYS	C-N-CA	6.47	137.89	121.70
1	A	703	MET	N-CA-CB	-5.92	99.94	110.60
1	A	704	SER	N-CA-C	5.72	126.44	111.00
1	A	741	GLY	N-CA-C	5.55	126.98	113.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	617	CYS	Peptide

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	4190	0	4252	53	0
1	B	1671	0	1719	23	0
2	C	460	0	251	1	0
2	D	480	0	263	6	0
3	A	148	0	0	2	0
3	B	35	0	0	0	0
3	C	24	0	0	0	0
3	D	20	0	0	0	0
All	All	7028	0	6485	76	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 (76) 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:656:THR:HG22	1:B:658:THR:H	1.31	0.94
1:A:759:THR:HG21	1:A:779:LYS:HA	1.64	0.78
1:A:562:ASP:HB3	1:A:564:THR:HB	1.68	0.76
1:A:656:THR:HG22	1:A:658:THR:H	1.51	0.74
1:A:860:ILE:HG23	1:A:878:ILE:HD11	1.70	0.72
1:A:765:VAL:HG13	1:A:769:ASP:HB2	1.71	0.71
1:B:617:CYS:N	1:B:618:ALA:HB3	2.07	0.70
1:A:810:GLN:OE1	2:D:19:DG:N1	2.22	0.67
1:B:617:CYS:O	1:B:628:ARG:HD2	1.95	0.66
1:A:803:ARG:NH1	1:A:819:GLU:OE1	2.29	0.66
1:A:656:THR:CG2	1:A:658:THR:H	2.08	0.65
1:A:656:THR:HG22	1:A:659:THR:H	1.62	0.64
1:A:633:LYS:HB2	1:A:655:ILE:HD11	1.79	0.64
1:B:618:ALA:H	1:B:625:ILE:HG22	1.62	0.62
1:A:823:VAL:HG13	1:A:877:PRO:HD3	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:617:CYS:H	1:B:618:ALA:HB3	1.62	0.61
1:B:656:THR:HG22	1:B:658:THR:N	2.11	0.61
1:A:656:THR:HG22	1:A:658:THR:N	2.17	0.60
1:A:737:LEU:O	1:A:740:GLU:O	2.20	0.60
1:A:471:LYS:NZ	1:A:475:ASP:OD2	2.35	0.59
1:A:528:SER:HB3	1:A:564:THR:HG23	1.86	0.57
1:A:803:ARG:NH2	1:A:806:MET:SD	2.73	0.57
1:A:837:ASN:ND2	1:A:841:SER:O	2.39	0.55
1:A:528:SER:H	1:A:564:THR:CG2	2.20	0.55
1:B:575:SER:OG	1:B:589:HIS:ND1	2.39	0.54
1:A:526:ARG:HB3	1:A:564:THR:HG21	1.91	0.52
1:A:730:ILE:O	1:A:734:GLU:HG2	2.10	0.51
1:B:618:ALA:N	1:B:625:ILE:HG22	2.24	0.51
1:A:656:THR:H	1:A:659:THR:HB	1.75	0.51
1:A:845:GLU:HA	1:B:608:SER:HB3	1.93	0.51
1:A:375:LEU:O	1:A:376:LYS:HD2	2.11	0.50
1:A:765:VAL:CG1	1:A:769:ASP:HB2	2.41	0.50
1:B:562:ASP:HB3	1:B:564:THR:OG1	2.11	0.50
1:A:771:LYS:HG3	1:A:817:PHE:O	2.12	0.49
1:A:591:HIS:CE1	1:A:593:LEU:HD21	2.47	0.49
1:A:409:SER:O	1:A:410:SER:C	2.50	0.49
1:A:759:THR:HG21	1:A:779:LYS:CA	2.38	0.48
1:A:728:ASP:N	3:A:1005:HOH:O	2.48	0.47
1:A:422:TYR:CE2	1:A:424:TYR:HA	2.51	0.46
1:B:569:VAL:O	1:B:587:ASN:HA	2.15	0.46
1:A:886:LEU:HD21	1:A:890:ARG:HH21	1.81	0.46
2:D:18:DT:H1'	2:D:19:DG:H5'	1.96	0.46
1:B:554:LYS:HD3	2:D:8:DT:H5"	1.97	0.46
1:A:610:ILE:HG22	1:A:694:ARG:HG2	1.98	0.46
1:A:791:PHE:HE1	2:D:21:DG:H5"	1.80	0.46
1:A:860:ILE:CG2	1:A:878:ILE:HD11	2.42	0.45
1:B:673:ARG:NH2	1:B:713:GLN:OE1	2.38	0.45
1:A:522:PHE:CD2	1:A:538:TYR:HB3	2.52	0.45
1:B:532:PRO:HB3	1:B:645:LEU:HD13	1.98	0.45
1:B:525:VAL:HB	1:B:529:ASN:HB2	1.99	0.45
1:B:674:ASN:O	1:B:678:LYS:HD3	2.16	0.45
1:A:759:THR:HG21	1:A:780:ASP:H	1.82	0.44
1:A:414:ASP:O	1:A:415:ASP:HB2	2.17	0.44
1:A:737:LEU:HD22	1:A:737:LEU:HA	1.72	0.44
1:B:628:ARG:NH2	2:D:19:DG:N7	2.65	0.44
1:A:788:LEU:HD21	1:A:806:MET:HE2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:673:ARG:NH2	1:A:713:GLN:OE1	2.43	0.43
1:A:749:ALA:O	1:A:862:ARG:NH1	2.52	0.43
1:A:803:ARG:O	1:A:803:ARG:HG2	2.18	0.43
1:B:611:LYS:HE2	2:D:21:DG:OP2	2.19	0.42
1:B:664:GLU:HA	1:B:667:LYS:HD3	2.01	0.42
1:B:598:ARG:HH12	1:B:650:LEU:HG	1.84	0.42
1:A:550:TYR:CE2	1:A:552:GLY:HA2	2.54	0.42
1:A:803:ARG:HE	1:A:806:MET:HB3	1.85	0.42
1:A:550:TYR:OH	1:A:596:LEU:HD11	2.19	0.42
1:A:762:PRO:HG2	1:A:782:LYS:HD2	2.01	0.42
1:A:528:SER:CB	1:A:564:THR:HG23	2.48	0.41
1:A:549:LYS:O	1:A:556:LEU:HD12	2.20	0.41
1:A:637:LYS:HE2	3:A:1021:HOH:O	2.19	0.41
1:B:548:VAL:HG23	1:B:625:ILE:HD13	2.02	0.41
1:B:596:LEU:HA	1:B:596:LEU:HD23	1.84	0.41
1:A:595:TYR:CZ	2:C:7:DT:H2'	2.56	0.41
1:A:412:ILE:HD11	1:A:463:ILE:HG23	2.03	0.40
1:A:756:LEU:HB3	1:A:879:TYR:CE1	2.55	0.40
1:A:786:LYS:HB2	1:A:786:LYS:HE3	1.88	0.40
1:B:571:TYR:O	1:B:589:HIS:ND1	2.55	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	515/551 (94%)	497 (96%)	18 (4%)	0	100	100
1	B	204/551 (37%)	198 (97%)	6 (3%)	0	100	100
All	All	719/1102 (65%)	695 (97%)	24 (3%)	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	477/507 (94%)	449 (94%)	28 (6%)	19 37
1	B	192/507 (38%)	185 (96%)	7 (4%)	35 61
All	All	669/1014 (66%)	634 (95%)	35 (5%)	23 44

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	371	ASP
1	A	411	LEU
1	A	425	GLU
1	A	551	THR
1	A	562	ASP
1	A	564	THR
1	A	603	ASN
1	A	644	LYS
1	A	650	LEU
1	A	656	THR
1	A	667	LYS
1	A	678	LYS
1	A	690	LEU
1	A	733	LEU
1	A	737	LEU
1	A	739	ARG
1	A	752	ARG
1	A	756	LEU
1	A	759	THR
1	A	766	ASP
1	A	803	ARG
1	A	806	MET
1	A	810	GLN
1	A	829	GLN
1	A	845	GLU
1	A	847	LEU
1	A	863	VAL

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Mol	Chain	Res	Type
1	A	889	SER
1	B	509	LEU
1	B	564	THR
1	B	575	SER
1	B	601	SER
1	B	612	MET
1	B	640	LEU
1	B	650	LEU

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

Mol	Chain	Res	Type
1	A	810	GLN

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 monosaccharides 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	519/551 (94%)	-0.11	23 (4%)	34	37	17, 34, 81, 143	0
1	B	208/551 (37%)	-0.04	11 (5%)	26	28	25, 40, 73, 107	0
2	C	22/25 (88%)	0.01	3 (13%)	3	2	30, 47, 100, 112	0
2	D	23/25 (92%)	0.46	4 (17%)	1	1	32, 60, 89, 120	0
All	All	772/1152 (67%)	-0.07	41 (5%)	26	28	17, 37, 80, 143	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	703	MET	10.1
1	A	704	SER	7.5
1	A	701	ASN	6.0
1	A	702	ARG	6.0
1	B	508	ALA	4.4
2	D	15	DG	4.4
1	B	507	SER	4.4
2	C	22	DG	4.2
1	B	534	ALA	4.2
1	B	535	SER	4.0
1	A	739	ARG	4.0
1	A	828	ARG	3.9
1	A	409	SER	3.7
1	A	807	VAL	3.6
1	A	706	ASN	3.5
1	A	758	GLY	3.4
1	A	756	LEU	3.3
1	A	371	ASP	3.3
1	B	506	ARG	3.2
2	D	14	DG	3.1
2	C	1	DA	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	551	THR	2.9
1	A	740	GLU	2.7
1	A	705	GLU	2.6
1	A	840	TYR	2.6
1	B	642	GLN	2.6
1	B	643	GLY	2.6
1	A	517	PHE	2.6
1	A	372	PRO	2.5
1	A	744	LYS	2.5
1	A	838	PRO	2.5
1	A	728	ASP	2.5
1	B	509	LEU	2.4
1	B	640	LEU	2.4
2	D	13	DA	2.4
1	A	757	PHE	2.4
1	B	641	PHE	2.2
2	D	5	DA	2.2
1	A	513	LYS	2.2
2	C	2	DC	2.2
1	A	737	LEU	2.1

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.