



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 05:37 AM UTC

PDB ID : 4C93 / pdb_00004c93
Title : Crystal structure of the carboxy-terminal domain of yeast Ctf4 bound to Pol alpha.
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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

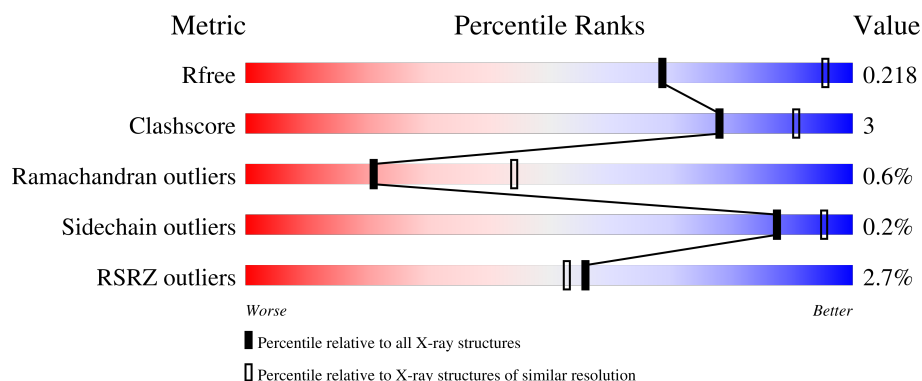
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

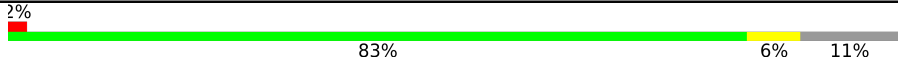
The reported resolution of this entry is 2.69 Å.

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}	180053	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (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 $\leq 5\%$. 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	
1	B	478	
1	C	478	
2	D	13	
2	E	13	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 9617 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 POLYMERASE ALPHA CATALYTIC SUBUNIT A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	10	Total	C	N	O	0	0	0
			82	53	10	19			
2	E	10	Total	C	N	O	0	0	0
			82	53	10	19			

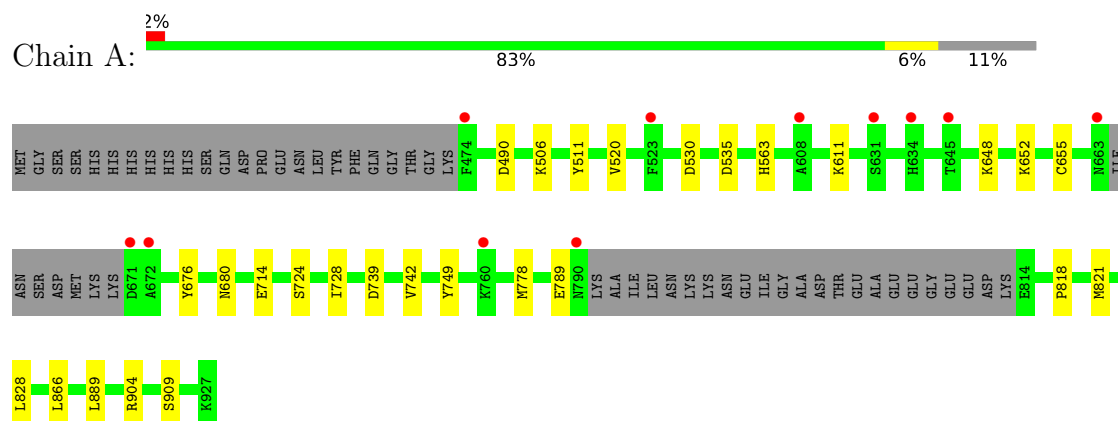
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	68	Total	O	0	0
			68	68		
3	B	64	Total	O	0	0
			64	64		
3	C	28	Total	O	0	0
			28	28		

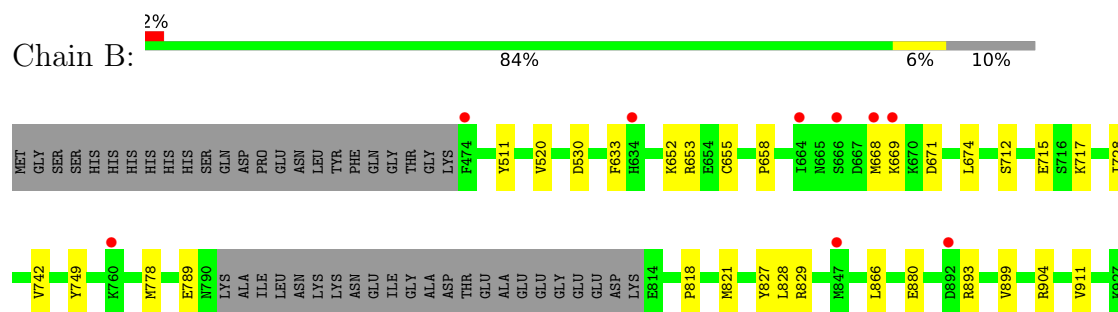
3 Residue-property plots [i](#)

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.

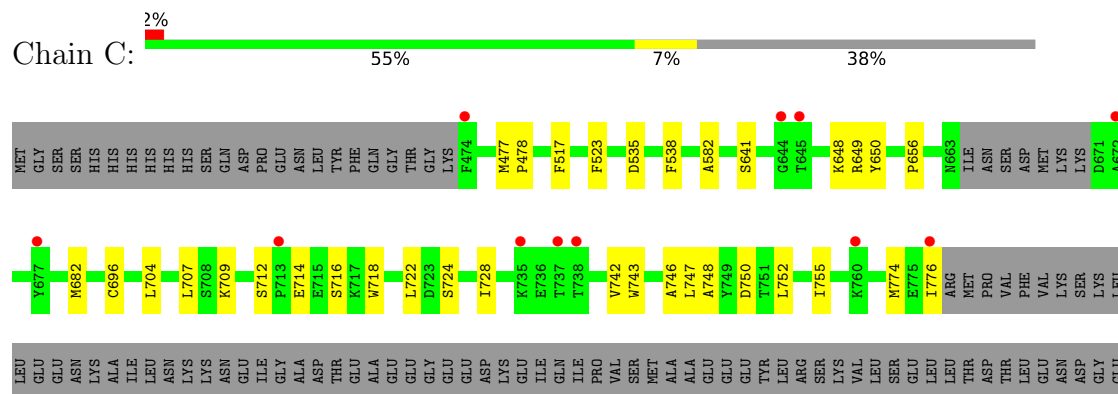
• Molecule 1: DNA POLYMERASE ALPHA-BINDING PROTEIN



• Molecule 1: DNA POLYMERASE ALPHA-BINDING PROTEIN



• Molecule 1: DNA POLYMERASE ALPHA-BINDING PROTEIN



LEU
PRO
SER
LEU
VAL
LYS
LYS
ILE
ASN
ASN
ILE
ARG
GLU
ALA
ARG
TYR
GLU
GLN
GLN
LEU
LYS

ILE	
ASP	
ASN	
F140	
D141	
D142	
S149	

ILE
ASP
ASN
F140
D141
D142
F147
E148
S149

4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2 ₁	Depositor
Cell constants a, b, c, α , β , γ	88.98Å 100.00Å 219.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.20 – 2.69 49.20 – 2.69	Depositor EDS
% Data completeness (in resolution range)	99.5 (49.20-2.69) 99.5 (49.20-2.69)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.23 (at 2.69Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.172 , 0.210 0.181 , 0.218	Depositor DCC
R_{free} test set	2763 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	54.3	Xtriage
Anisotropy	0.221	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 46.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9617	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 3.55% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.28	0/3501	0.68	0/4741
1	B	0.27	0/3558	0.68	0/4817
1	C	0.26	0/2481	0.67	2/3370 (0.1%)
2	D	0.20	0/83	0.58	0/110
2	E	0.23	0/83	0.68	0/110
All	All	0.27	0/9706	0.68	2/13148 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	712	SER	CA-C-N	5.10	124.71	119.05
1	C	712	SER	C-N-CA	5.10	124.71	119.05

There are no chirality outliers.

There are no planarity outliers.

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	3416	0	3356	18	0
1	B	3472	0	3418	19	0
1	C	2405	0	2326	21	0
2	D	82	0	67	1	0
2	E	82	0	67	2	0
3	A	68	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	64	0	0	0	0
3	C	28	0	0	0	0
All	All	9617	0	9234	52	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 3.

All (52) 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:789:GLU:HG3	1:B:818:PRO:HG3	1.79	0.64
1:A:904:ARG:NH1	2:D:142:ASP:OD1	2.37	0.58
1:A:648:LYS:HB3	1:B:717:LYS:HD3	1.86	0.57
1:A:778:MET:HG3	1:A:828:LEU:HB3	1.88	0.56
1:A:511:TYR:HB2	1:A:530:ASP:HB3	1.88	0.56
1:A:652:LYS:NZ	1:A:655:CYS:SG	2.64	0.55
1:B:904:ARG:NH1	2:E:142:ASP:OD1	2.40	0.55
1:A:789:GLU:HG3	1:A:818:PRO:HG3	1.90	0.53
1:B:653:ARG:HD2	1:C:714:GLU:HG2	1.89	0.53
1:B:893:ARG:NH2	2:E:147:PHE:O	2.41	0.53
1:A:490:ASP:HB3	1:A:506:LYS:HB2	1.90	0.53
1:B:778:MET:HG3	1:B:828:LEU:HB3	1.91	0.52
1:C:747:LEU:HD11	1:C:776:ILE:HD11	1.91	0.52
1:B:669:LYS:HA	1:B:674:LEU:HD22	1.92	0.52
1:C:722:LEU:HD21	1:C:774:MET:HE2	1.92	0.51
1:A:563:HIS:ND1	1:B:880:GLU:OE1	2.33	0.51
1:B:818:PRO:HG2	1:B:821:MET:HB3	1.92	0.51
1:C:535:ASP:OD1	1:C:535:ASP:N	2.44	0.51
1:C:728:ILE:HD11	1:C:742:VAL:HG23	1.93	0.51
1:B:899:VAL:HG13	1:B:911:VAL:HG13	1.94	0.50
1:A:611:LYS:NZ	1:B:658:PRO:O	2.39	0.49
1:C:704:LEU:HD22	1:C:752:LEU:HD13	1.95	0.48
1:C:724:SER:HB2	1:C:742:VAL:HG21	1.97	0.47
1:A:724:SER:HB2	1:A:742:VAL:HG21	1.96	0.47
1:B:712:SER:HB2	1:B:715:GLU:HB2	1.97	0.46
1:C:743:TRP:HB3	1:C:755:ILE:HB	1.98	0.46
1:C:648:LYS:HE2	1:C:650:TYR:CZ	2.51	0.46
1:A:739:ASP:OD1	1:A:739:ASP:N	2.47	0.45
1:B:652:LYS:NZ	1:B:655:CYS:SG	2.70	0.45
1:A:714:GLU:OE1	1:C:649:ARG:NE	2.45	0.45
1:C:538:PHE:CG	1:C:582:ALA:HA	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:477:MET:HE3	1:C:478:PRO:HD2	1.99	0.45
1:B:778:MET:HE3	1:B:829:ARG:HG3	1.99	0.44
1:A:866:LEU:HD23	1:A:889:LEU:HD23	2.00	0.44
1:A:728:ILE:HD11	1:A:742:VAL:HG23	2.01	0.43
1:A:818:PRO:HG2	1:A:821:MET:HB3	2.00	0.43
1:A:535:ASP:OD1	1:A:535:ASP:N	2.49	0.43
1:B:728:ILE:HD11	1:B:742:VAL:HG23	2.00	0.43
1:C:682:MET:HA	1:C:682:MET:HE2	2.00	0.43
1:A:909:SER:OG	3:A:2067:HOH:O	2.21	0.42
1:B:668:MET:HA	1:B:671:ASP:HB2	2.02	0.42
1:C:517:PHE:CG	1:C:523:PHE:HB2	2.55	0.42
1:C:746:ALA:O	1:C:752:LEU:HD12	2.20	0.42
1:A:676:TYR:O	1:A:680:ASN:N	2.53	0.41
1:B:633:PHE:CD1	1:C:656:PRO:HG3	2.55	0.41
1:C:696:CYS:HB3	1:C:704:LEU:HD11	2.01	0.41
1:C:707:LEU:HD13	1:C:718:TRP:CE2	2.56	0.41
1:C:748:ALA:O	1:C:750:ASP:N	2.53	0.41
1:B:511:TYR:HB2	1:B:530:ASP:HB3	2.02	0.41
1:B:827:TYR:CD1	1:B:866:LEU:HD13	2.57	0.40
1:C:641:SER:OG	1:C:648:LYS:HE3	2.21	0.40
1:C:709:LYS:O	1:C:716:SER:OG	2.37	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	155/478 (32%)	150 (97%)	4 (3%)	1 (1%)	21	44
1	B	128/478 (27%)	123 (96%)	4 (3%)	1 (1%)	16	37
1	C	48/478 (10%)	46 (96%)	2 (4%)	0	100	100
2	D	8/13 (62%)	8 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	E	8/13 (62%)	8 (100%)	0	0	100	100
All	All	347/1460 (24%)	335 (96%)	10 (3%)	2 (1%)	21	44

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	749	TYR
1	B	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%)	376 (100%)	1 (0%)	86	94
1	B	384/422 (91%)	383 (100%)	1 (0%)	86	94
1	C	267/422 (63%)	267 (100%)	0	100	100
2	D	9/12 (75%)	9 (100%)	0	100	100
2	E	9/12 (75%)	9 (100%)	0	100	100
All	All	1046/1290 (81%)	1044 (100%)	2 (0%)	87	95

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	520	VAL
1	B	520	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	510	GLN
1	A	634	HIS
1	A	877	GLN

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Mol	Chain	Res	Type
1	A	891	GLN
1	B	559	HIS
1	B	573	GLN
1	B	877	GLN
1	B	891	GLN
1	C	555	GLN
1	C	678	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 oligosaccharides 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, 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(Å ²)	Q<0.9
1	A	424/478 (88%)	-0.26	11 (2%) 57 54	19, 48, 93, 123	1 (0%)
1	B	431/478 (90%)	-0.26	9 (2%) 63 61	22, 50, 97, 142	1 (0%)
1	C	296/478 (61%)	0.01	11 (3%) 45 41	27, 59, 115, 157	1 (0%)
2	D	10/13 (76%)	0.55	0 100 100	81, 100, 116, 117	0
2	E	10/13 (76%)	1.40	1 (10%) 12 10	105, 118, 134, 139	0
All	All	1171/1460 (80%)	-0.17	32 (2%) 56 53	19, 52, 105, 157	3 (0%)

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	737	THR	4.0
1	B	474	PHE	3.6
1	A	645	THR	3.5
1	B	669	LYS	3.3
1	A	631	SER	3.2
1	B	666	SER	3.1
1	C	672	ALA	3.0
1	A	760	LYS	2.9
1	B	664	ILE	2.9
1	C	677	TYR	2.8
1	B	847	MET	2.7
1	C	474	PHE	2.7
1	B	668	MET	2.6
1	A	474	PHE	2.6
1	C	645	THR	2.6
1	C	735	LYS	2.6
1	A	608	ALA	2.6
1	B	634	HIS	2.6
1	A	634	HIS	2.5
1	A	523	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	713	PRO	2.5
1	C	644	GLY	2.4
1	B	760	LYS	2.4
1	C	760	LYS	2.2
2	E	149	SER	2.2
1	C	776	ILE	2.2
1	B	892	ASP	2.2
1	C	738	THR	2.2
1	A	671	ASP	2.1
1	A	663	ASN	2.1
1	A	672	ALA	2.1
1	A	790	ASN	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 oligosaccharides 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.