



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:44 AM UTC

PDB ID : 5NXQ / pdb_00005nxq
Title : Crystal structure of the carboxy-terminal domain of yeast Ctf4 bound to a stapled Sld5 CIP
Authors : Wu, Y.; Pellegrini, L.
Deposited on : 2017-05-10
Resolution : 2.41 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
Mogul : 2022.3.0, CSD as543be (2022)
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

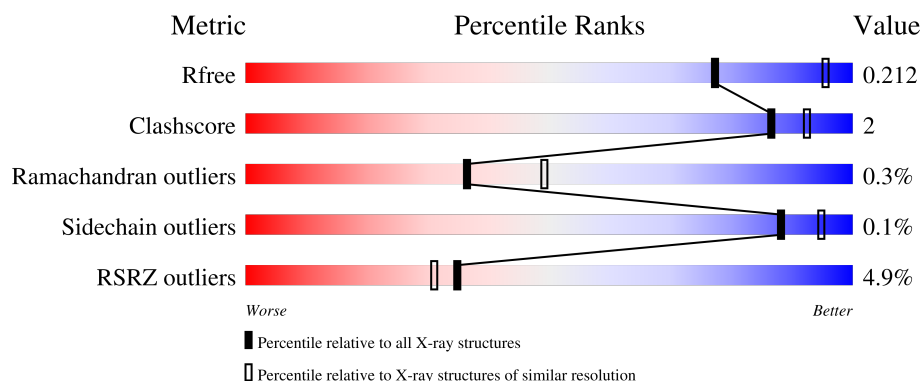
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.41 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	6062 (2.44-2.40)
Clashscore	190562	6562 (2.44-2.40)
Ramachandran outliers	187476	6481 (2.44-2.40)
Sidechain outliers	187428	6482 (2.44-2.40)
RSRZ outliers	180081	6066 (2.44-2.40)

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	479	4% 83% 6% 11%
1	B	479	4% 85% 5% 10%
1	C	479	4% 58% • 38%
2	D	19	11% 79% 21%
2	E	19	11% 74% 5% 21%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9931 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	3	0
			3434	2205	570	644	15			
1	B	431	Total	C	N	O	S	0	2	0
			3482	2233	579	654	16			
1	C	296	Total	C	N	O	S	0	1	0
			2405	1562	392	440	11			

There are 66 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	449	MET	-	initiating methionine	UNP Q01454
A	450	GLY	-	expression tag	UNP Q01454
A	451	SER	-	expression tag	UNP Q01454
A	452	SER	-	expression tag	UNP Q01454
A	453	HIS	-	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	SER	-	expression tag	UNP Q01454
A	460	GLN	-	expression tag	UNP Q01454
A	461	ASP	-	expression tag	UNP Q01454
A	462	PRO	-	expression tag	UNP Q01454
A	463	GLU	-	expression tag	UNP Q01454
A	464	ASN	-	expression tag	UNP Q01454
A	465	LEU	-	expression tag	UNP Q01454
A	466	TYR	-	expression tag	UNP Q01454
A	467	PHE	-	expression tag	UNP Q01454
A	468	GLN	-	expression tag	UNP Q01454
A	469	GLY	-	expression tag	UNP Q01454
A	470	SER	-	expression tag	UNP Q01454
B	449	MET	-	initiating methionine	UNP Q01454

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Chain	Residue	Modelled	Actual	Comment	Reference
B	450	GLY	-	expression tag	UNP Q01454
B	451	SER	-	expression tag	UNP Q01454
B	452	SER	-	expression tag	UNP Q01454
B	453	HIS	-	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	SER	-	expression tag	UNP Q01454
B	460	GLN	-	expression tag	UNP Q01454
B	461	ASP	-	expression tag	UNP Q01454
B	462	PRO	-	expression tag	UNP Q01454
B	463	GLU	-	expression tag	UNP Q01454
B	464	ASN	-	expression tag	UNP Q01454
B	465	LEU	-	expression tag	UNP Q01454
B	466	TYR	-	expression tag	UNP Q01454
B	467	PHE	-	expression tag	UNP Q01454
B	468	GLN	-	expression tag	UNP Q01454
B	469	GLY	-	expression tag	UNP Q01454
B	470	SER	-	expression tag	UNP Q01454
C	449	MET	-	initiating methionine	UNP Q01454
C	450	GLY	-	expression tag	UNP Q01454
C	451	SER	-	expression tag	UNP Q01454
C	452	SER	-	expression tag	UNP Q01454
C	453	HIS	-	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	SER	-	expression tag	UNP Q01454
C	460	GLN	-	expression tag	UNP Q01454
C	461	ASP	-	expression tag	UNP Q01454
C	462	PRO	-	expression tag	UNP Q01454
C	463	GLU	-	expression tag	UNP Q01454
C	464	ASN	-	expression tag	UNP Q01454
C	465	LEU	-	expression tag	UNP Q01454
C	466	TYR	-	expression tag	UNP Q01454
C	467	PHE	-	expression tag	UNP Q01454
C	468	GLN	-	expression tag	UNP Q01454
C	469	GLY	-	expression tag	UNP Q01454

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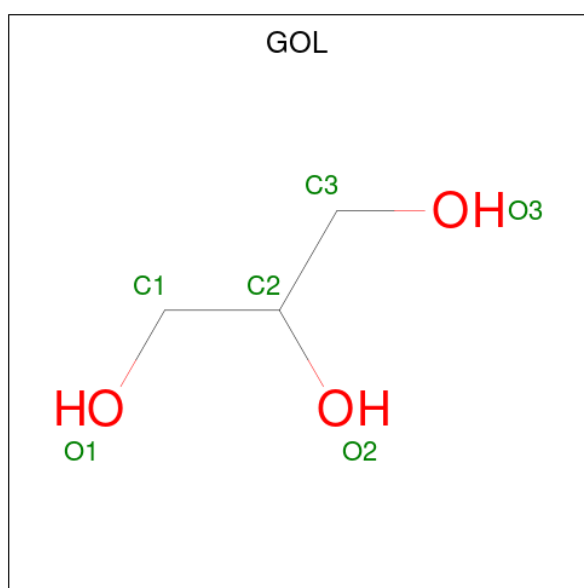
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Chain	Residue	Modelled	Actual	Comment	Reference
C	470	SER	-	expression tag	UNP Q01454

- Molecule 2 is a protein called MET-ASP-ILE-UA1-ILE-ASP-ASP-ILE-LEU-UA2-GLU-LEU-ASP-LYS-GLU.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	15	Total	C	N	O	S	0	0	0
			134	84	22	27	1			
2	E	15	Total	C	N	O	S	0	0	0
			134	84	22	27	1			

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	130	Total	O	0	0
			130	130		
4	B	121	Total	O	0	0
			121	121		
4	C	82	Total	O	0	0
			82	82		

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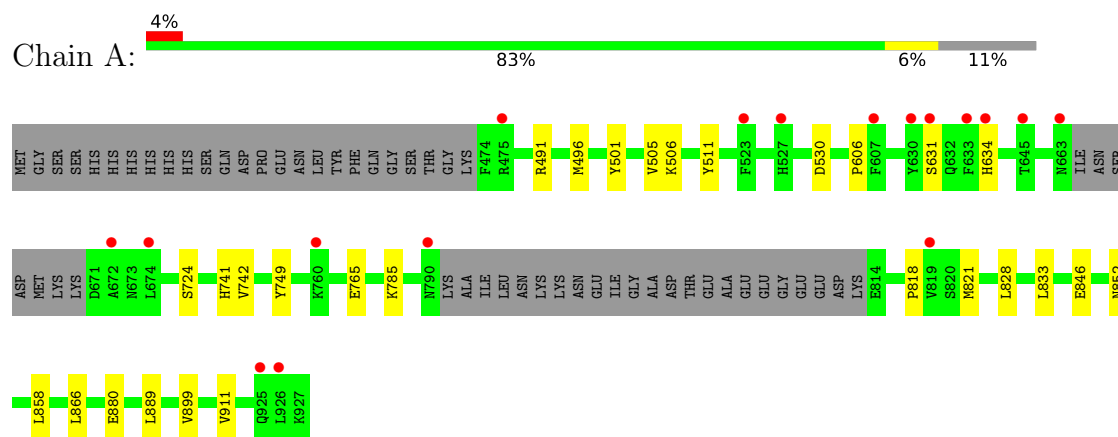
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	1	Total	O	0	0
			1	1		
4	E	2	Total	O	0	0
			2	2		

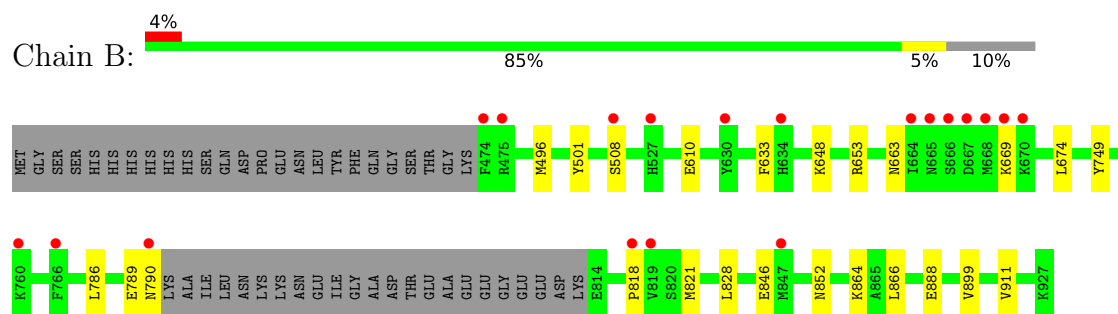
3 Residue-property plots [i](#)

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.

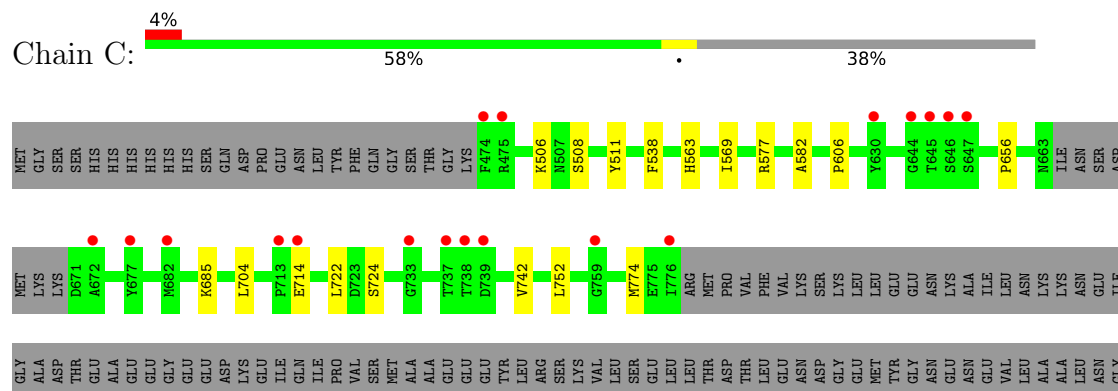
• Molecule 1: DNA polymerase alpha-binding protein



• Molecule 1: DNA polymerase alpha-binding protein



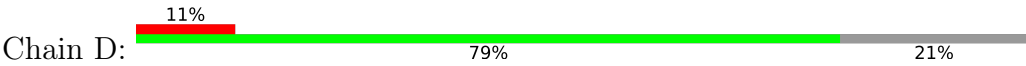
• Molecule 1: DNA polymerase alpha-binding protein



ALA
TYR
ASP
LYS
ALA
LEU
LEU
ARG
LEU
PHE
ALA
SER
ALA
CYS
SER
ASP
GLN
ASN
VAL
GLU
LYS
ALA
LEU
SER
LEU
ALA
HIS
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SER
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ALA
GLU
LEU
PRO
SER
LEU
VAL
LYS
ILE
ASN
THR
ARG
GLU
ALA

ARG
TYR
GLU
GLN
LEU
LYS

● Molecule 2: MET-ASP-ILE-UA1-ILE-ASP-ASP-ILE-LEU-UA2-GLU-LEU-ASP-LYS-GLU



●
●
MET
E15
THR
THR
ALA
VAL

● Molecule 2: MET-ASP-ILE-UA1-ILE-ASP-ASP-ILE-LEU-UA2-GLU-LEU-ASP-LYS-GLU



●
●
MET
L9
E15
THR
THR
ALA
VAL

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	88.68Å 100.29Å 219.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.21 – 2.41 49.21 – 2.41	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.21-2.41) 100.0 (49.21-2.41)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.44 (at 2.42Å)	Xtriage
Refinement program	PHENIX (1.11.1 _2575: ???)	Depositor
R, R_{free}	0.184 , 0.211 0.186 , 0.212	Depositor DCC
R_{free} test set	3806 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	59.7	Xtriage
Anisotropy	0.310	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 44.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9931	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.73% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 9FZ, GOL, 9G2

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	0.10	0/3520	0.31	0/4767
1	B	0.10	0/3569	0.31	0/4832
1	C	0.10	0/2481	0.31	0/3370
2	D	0.06	0/104	0.23	0/135
2	E	0.07	0/104	0.22	0/135
All	All	0.10	0/9778	0.31	0/13239

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 [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	3434	0	3372	18	0
1	B	3482	0	3424	15	0
1	C	2405	0	2326	13	0
2	D	134	0	107	0	0
2	E	134	0	107	1	0
3	B	6	0	8	0	0
4	A	130	0	0	2	0
4	B	121	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	82	0	0	2	0
4	D	1	0	0	0	0
4	E	2	0	0	0	0
All	All	9931	0	9344	39	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 2.

All (39) 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:846:GLU:OE2	1:B:852:ASN:ND2	2.18	0.76
1:A:785:LYS:NZ	4:A:1002:HOH:O	2.28	0.66
1:A:846:GLU:OE2	1:A:852:ASN:ND2	2.27	0.66
1:A:785:LYS:HE3	1:C:569:ILE:HD12	1.83	0.61
1:C:577:ARG:NH1	4:C:1001:HOH:O	2.34	0.59
1:B:899:VAL:HG13	1:B:911:VAL:HG13	1.87	0.55
1:C:685:LYS:NZ	4:C:1002:HOH:O	2.35	0.55
1:B:786:LEU:O	1:B:790:ASN:ND2	2.39	0.55
1:C:722:LEU:HD21	1:C:774:MET:HE2	1.90	0.54
1:B:669:LYS:HA	1:B:674:LEU:HD22	1.90	0.54
1:A:828[A]:LEU:HD11	1:C:606:PRO:HB2	1.91	0.53
1:B:866:LEU:HD21	1:B:888:GLU:HB2	1.90	0.52
1:B:864:LYS:HE3	2:E:9:LEU:HB3	1.92	0.52
1:A:899:VAL:HG13	1:A:911:VAL:HG13	1.91	0.51
1:B:653:ARG:NH2	1:C:714:GLU:HB2	2.26	0.51
1:A:506:LYS:HG2	1:A:511:TYR:CE1	2.46	0.50
1:A:741:HIS:ND1	4:A:1004:HOH:O	2.35	0.50
1:B:663:ASN:OD1	1:B:663:ASN:N	2.46	0.49
1:C:506:LYS:HG2	1:C:511:TYR:CE2	2.48	0.49
1:B:818:PRO:HG2	1:B:821:MET:HB3	1.95	0.48
1:B:653:ARG:CZ	1:C:714:GLU:HB2	2.43	0.48
1:A:496:MET:HG3	1:A:501:TYR:HB3	1.97	0.47
1:B:496:MET:HG3	1:B:501:TYR:HB3	1.97	0.46
1:B:789:GLU:HG3	1:B:818:PRO:HG3	1.97	0.46
1:C:724:SER:HB2	1:C:742:VAL:HG21	1.98	0.45
1:A:818:PRO:HG2	1:A:821:MET:HB3	1.98	0.45
1:A:833:LEU:HB3	1:A:858:LEU:HD21	1.99	0.45
1:A:511:TYR:HB2	1:A:530:ASP:HB3	1.99	0.45
1:A:724:SER:HB2	1:A:742:VAL:HG21	1.99	0.44
1:A:866:LEU:HD23	1:A:889:LEU:HD23	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:631:SER:HG	1:A:634:HIS:CE1	2.37	0.43
1:A:491:ARG:HB3	1:A:505:VAL:HG22	2.01	0.43
1:A:506:LYS:HG2	1:A:511:TYR:HE1	1.83	0.43
1:B:633:PHE:CD1	1:C:656:PRO:HG3	2.54	0.43
1:A:880:GLU:OE1	1:C:563:HIS:ND1	2.40	0.42
1:A:606:PRO:HB2	1:B:828:LEU:HD11	2.02	0.42
1:C:538:PHE:CG	1:C:582:ALA:HA	2.55	0.41
1:B:610:GLU:OE1	1:B:648:LYS:HD3	2.21	0.40
1:C:704:LEU:HD22	1:C:752:LEU:HD13	2.02	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	421/479 (88%)	406 (96%)	14 (3%)	1 (0%)	43	57
1	B	429/479 (90%)	416 (97%)	11 (3%)	2 (0%)	24	35
1	C	293/479 (61%)	279 (95%)	13 (4%)	1 (0%)	36	49
2	D	11/19 (58%)	11 (100%)	0	0	100	100
2	E	11/19 (58%)	11 (100%)	0	0	100	100
All	All	1165/1475 (79%)	1123 (96%)	38 (3%)	4 (0%)	36	49

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	508	SER
1	A	749	TYR
1	B	749	TYR
1	B	508	SER

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	379/423 (90%)	378 (100%)	1 (0%)	86	93
1	B	385/423 (91%)	385 (100%)	0	100	100
1	C	267/423 (63%)	267 (100%)	0	100	100
2	D	13/16 (81%)	13 (100%)	0	100	100
2	E	13/16 (81%)	13 (100%)	0	100	100
All	All	1057/1301 (81%)	1056 (100%)	1 (0%)	88	95

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	765	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	741	HIS
1	A	877	GLN
1	B	559	HIS
1	B	634	HIS
1	C	634	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

There are no oligosaccharides in this entry.

5.6 Ligand geometry

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	GOL	B	1001	-	5,5,5	0.38	0	5,5,5	0.28	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	B	1001	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	1001	GOL	O1-C1-C2-C3
3	B	1001	GOL	O1-C1-C2-O2

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

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	424/479 (88%)	0.12	17 (4%) 42 38	27, 60, 101, 127	3 (0%)
1	B	431/479 (89%)	0.14	19 (4%) 39 34	29, 61, 103, 160	2 (0%)
1	C	296/479 (61%)	0.34	18 (6%) 27 23	31, 66, 124, 161	1 (0%)
2	D	13/19 (68%)	0.90	2 (15%) 5 4	86, 97, 118, 123	0
2	E	13/19 (68%)	0.67	2 (15%) 5 4	80, 92, 120, 123	0
All	All	1177/1475 (79%)	0.20	58 (4%) 35 31	27, 62, 109, 161	6 (0%)

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	666	SER	5.3
1	A	634	HIS	5.2
1	B	668	MET	4.4
1	B	669	LYS	4.3
1	B	847	MET	3.8
1	C	677	TYR	3.7
1	A	631	SER	3.7
1	B	474	PHE	3.7
1	A	523	PHE	3.6
1	A	527[A]	HIS	3.5
1	A	672	ALA	3.4
1	C	713	PRO	3.3
1	B	766	PHE	3.3
1	A	630	TYR	3.3
1	C	474	PHE	3.2
1	B	664	ILE	3.2
1	B	790	ASN	3.0
1	C	645	THR	3.0
1	B	630	TYR	3.0
1	B	819	VAL	3.0

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Mol	Chain	Res	Type	RSRZ
1	C	682	MET	2.9
1	C	714	GLU	2.8
2	D	1	MET	2.8
1	A	645	THR	2.7
1	C	733	GLY	2.7
1	B	670	LYS	2.6
1	B	667	ASP	2.6
1	C	644	GLY	2.6
1	A	607	PHE	2.6
1	C	475	ARG	2.5
1	A	633	PHE	2.4
1	C	737	THR	2.4
1	C	738	THR	2.4
1	C	759	GLY	2.4
1	B	760	LYS	2.4
2	E	1	MET	2.3
1	A	760	LYS	2.3
1	C	647	SER	2.3
1	B	634	HIS	2.3
1	A	790	ASN	2.3
1	B	818	PRO	2.3
1	A	819	VAL	2.3
1	A	475	ARG	2.3
1	B	665	ASN	2.2
1	B	475	ARG	2.2
2	E	15	GLU	2.2
2	D	15	GLU	2.1
1	C	739	ASP	2.1
1	A	925	GLN	2.1
1	A	663	ASN	2.1
1	C	630	TYR	2.1
1	B	508	SER	2.1
1	C	646	SER	2.1
1	B	527[A]	HIS	2.1
1	A	926	LEU	2.0
1	C	776	ILE	2.0
1	A	674	LEU	2.0
1	C	672	ALA	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 oligosaccharides 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. 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	B-factors($\text{\AA}^2$)	Q<0.9
3	GOL	B	1001	6/6	0.83	0.22	80,87,94,96	0

6.5 Other polymers [i](#)

There are no such residues in this entry.