



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 09:48 PM UTC

PDB ID : 4OST / pdb_00004ost
Title : Crystal structure of the S505C mutant of TAL effector dHax3
Authors : Deng, D.; Wu, J.P.; Yan, C.Y.; Pan, X.J.; Yan, N.
Deposited on : 2014-02-13
Resolution : 2.00 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

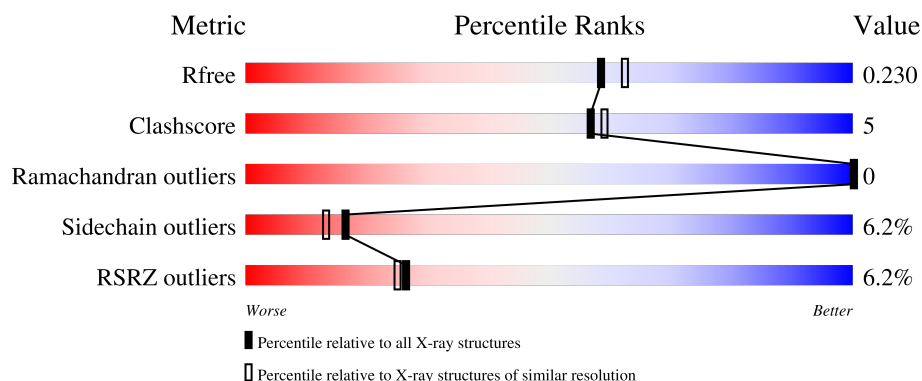
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	499	6% 86% 11% ..
1	B	499	6% 85% 10% ..
2	G	17	12% 76% 18% 6%
2	I	17	12% 82% 18%
3	H	17	12% 53% 41% 6%

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Mol	Chain	Length	Quality of chain
3	J	17	 71% 29%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9075 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 Hax3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	493	Total	C	N	O	S	0	6	0
			3618	2262	675	668	13			
1	B	488	Total	C	N	O	S	0	8	0
			3587	2239	667	667	14			

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	230	MET	-	expression tag	UNP Q3ZD72
A	300	HIS	ASN	engineered mutation	UNP Q3ZD72
A	301	ASP	ILE	engineered mutation	UNP Q3ZD72
A	368	HIS	ASN	engineered mutation	UNP Q3ZD72
A	369	ASP	ILE	engineered mutation	UNP Q3ZD72
A	402	ASN	HIS	engineered mutation	UNP Q3ZD72
A	403	GLY	ASP	engineered mutation	UNP Q3ZD72
A	436	ASN	HIS	engineered mutation	UNP Q3ZD72
A	437	GLY	ASP	engineered mutation	UNP Q3ZD72
A	470	ASN	HIS	engineered mutation	UNP Q3ZD72
A	471	GLY	ASP	engineered mutation	UNP Q3ZD72
A	505	CYS	SER	engineered mutation	UNP Q3ZD72
A	539	GLY	SER	engineered mutation	UNP Q3ZD72
A	572	HIS	ASN	engineered mutation	UNP Q3ZD72
A	573	ASP	SER	engineered mutation	UNP Q3ZD72
A	606	ASN	HIS	engineered mutation	UNP Q3ZD72
A	607	GLY	ASP	engineered mutation	UNP Q3ZD72
A	640	HIS	ASN	engineered mutation	UNP Q3ZD72
A	641	ASP	ILE	engineered mutation	UNP Q3ZD72
A	721	LEU	-	expression tag	UNP Q3ZD72
A	722	GLU	-	expression tag	UNP Q3ZD72
A	723	HIS	-	expression tag	UNP Q3ZD72
A	724	HIS	-	expression tag	UNP Q3ZD72
A	725	HIS	-	expression tag	UNP Q3ZD72
A	726	HIS	-	expression tag	UNP Q3ZD72

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Chain	Residue	Modelled	Actual	Comment	Reference
A	727	HIS	-	expression tag	UNP Q3ZD72
A	728	HIS	-	expression tag	UNP Q3ZD72
B	230	MET	-	expression tag	UNP Q3ZD72
B	300	HIS	ASN	engineered mutation	UNP Q3ZD72
B	301	ASP	ILE	engineered mutation	UNP Q3ZD72
B	368	HIS	ASN	engineered mutation	UNP Q3ZD72
B	369	ASP	ILE	engineered mutation	UNP Q3ZD72
B	402	ASN	HIS	engineered mutation	UNP Q3ZD72
B	403	GLY	ASP	engineered mutation	UNP Q3ZD72
B	436	ASN	HIS	engineered mutation	UNP Q3ZD72
B	437	GLY	ASP	engineered mutation	UNP Q3ZD72
B	470	ASN	HIS	engineered mutation	UNP Q3ZD72
B	471	GLY	ASP	engineered mutation	UNP Q3ZD72
B	505	CYS	SER	engineered mutation	UNP Q3ZD72
B	539	GLY	SER	engineered mutation	UNP Q3ZD72
B	572	HIS	ASN	engineered mutation	UNP Q3ZD72
B	573	ASP	SER	engineered mutation	UNP Q3ZD72
B	606	ASN	HIS	engineered mutation	UNP Q3ZD72
B	607	GLY	ASP	engineered mutation	UNP Q3ZD72
B	640	HIS	ASN	engineered mutation	UNP Q3ZD72
B	641	ASP	ILE	engineered mutation	UNP Q3ZD72
B	721	LEU	-	expression tag	UNP Q3ZD72
B	722	GLU	-	expression tag	UNP Q3ZD72
B	723	HIS	-	expression tag	UNP Q3ZD72
B	724	HIS	-	expression tag	UNP Q3ZD72
B	725	HIS	-	expression tag	UNP Q3ZD72
B	726	HIS	-	expression tag	UNP Q3ZD72
B	727	HIS	-	expression tag	UNP Q3ZD72
B	728	HIS	-	expression tag	UNP Q3ZD72

- Molecule 2 is a DNA chain called DNA (5'-D(*TP*GP*TP*CP*CP*CP*TP*TP*TP*AP*TP*CP*TP*CP*TP*CP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	16	Total	C	N	O	P	0	0	0
			314	154	44	101	15			
2	I	17	Total	C	N	O	P	0	0	0
			334	164	46	108	16			

- Molecule 3 is a DNA chain called DNA (5'-D(*AP*GP*AP*GP*AP*GP*AP*TP*AP*AP*AP*GP*GP*GP*AP*CP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	16	Total 339	C 159	N 75	O 89	P 16	0	0	0
3	J	17	Total 357	C 169	N 80	O 92	P 16	0	0	0

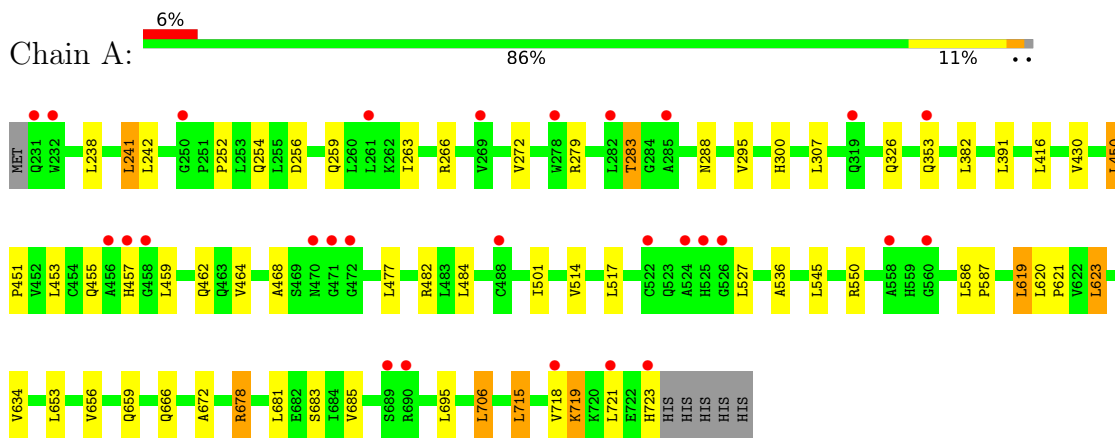
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	201	Total 201	O 201	0	0
4	B	195	Total 195	O 195	0	0
4	G	46	Total 46	O 46	0	0
4	H	19	Total 19	O 19	0	0
4	I	43	Total 43	O 43	0	0
4	J	22	Total 22	O 22	0	0

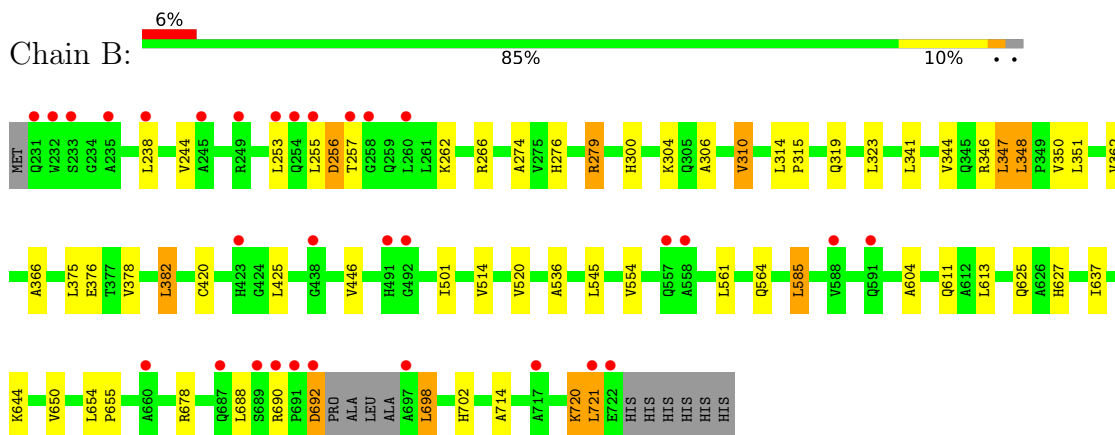
3 Residue-property plots [i](#)

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.

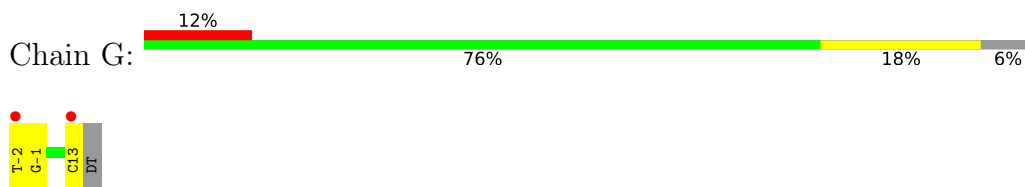
• Molecule 1: Hax3



• Molecule 1: Hax3



• Molecule 2: DNA (5'-D(*TP*GP*TP*CP*CP*CP*TP*TP*TP*AP*TP*CP*TP*CP*TP*CP*T)-3')



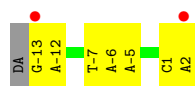
- Molecule 2: DNA (5'-D(*TP*GP*TP*CP*CP*CP*TP*TP*TP*AP*TP*CP*TP*CP*TP*CP*T)-3')

Chain I: 



- Molecule 3: DNA (5'-D(*AP*GP*AP*GP*AP*GP*AP*TP*AP*AP*AP*GP*GP*GP*AP*CP*A)-3')

Chain H: 



- Molecule 3: DNA (5'-D(*AP*GP*AP*GP*AP*GP*AP*TP*AP*AP*AP*GP*GP*GP*AP*CP*A)-3')

Chain J: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	81.12Å 87.02Å 87.91Å 90.00° 102.78° 90.00°	Depositor
Resolution (Å)	39.38 – 2.00 39.38 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.5 (39.38-2.00) 99.5 (39.38-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.89 (at 2.00Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.201 , 0.233 0.199 , 0.230	Depositor DCC
R_{free} test set	4036 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	27.9	Xtriage
Anisotropy	0.140	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 40.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9075	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.80% 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	0.50	0/3672	0.81	2/5016 (0.0%)
1	B	0.50	0/3637	0.79	2/4964 (0.0%)
2	G	0.33	0/347	1.03	0/532
2	I	0.32	0/369	0.93	0/566
3	H	0.27	0/384	0.82	0/592
3	J	0.27	0/405	0.84	0/625
All	All	0.47	0/8814	0.82	4/12295 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	678	ARG	CA-C-N	-5.33	114.18	119.56
1	A	678	ARG	C-N-CA	-5.33	114.18	119.56
1	B	678	ARG	CA-C-N	-5.26	114.33	119.64
1	B	678	ARG	C-N-CA	-5.26	114.33	119.64

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	3618	0	3758	29	0
1	B	3587	0	3719	37	0
2	G	314	0	186	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	I	334	0	198	3	0
3	H	339	0	178	5	0
3	J	357	0	190	4	0
4	A	201	0	0	1	0
4	B	195	0	0	1	0
4	G	46	0	0	0	0
4	H	19	0	0	0	0
4	I	43	0	0	0	0
4	J	22	0	0	0	0
All	All	9075	0	8229	75	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 (75) 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)
2:G:-2:DT:H3	3:H:2:DA:H2	1.17	0.91
1:B:720:LYS:O	1:B:720:LYS:HG3	1.88	0.73
1:B:256:ASP:OD1	1:B:256:ASP:N	2.22	0.72
1:B:692:ASP:OD2	1:B:692:ASP:N	2.25	0.69
1:A:468:ALA:HB2	1:A:477:LEU:HD11	1.74	0.68
1:A:451:PRO:O	1:A:455:GLN:HG2	1.99	0.63
1:A:653:LEU:HD13	1:A:685:VAL:HG21	1.82	0.62
1:B:306:ALA:O	1:B:310:VAL:HG13	2.01	0.60
1:B:266:ARG:HG2	1:B:300:HIS:HA	1.83	0.60
1:B:721:LEU:HD12	2:I:14:DT:H72	1.84	0.60
1:B:698:LEU:HG	1:B:702:HIS:CD2	2.38	0.59
1:A:450:LEU:HD13	1:A:464:VAL:HG11	1.84	0.59
3:J:1:DC:H2''	3:J:2:DA:C8	2.39	0.58
1:A:238:LEU:O	1:A:242:LEU:HG	2.04	0.57
1:B:720:LYS:NZ	1:B:720:LYS:HB3	2.21	0.56
1:B:274:ALA:HB2	1:B:304:LYS:HG3	1.88	0.55
1:B:425[A]:LEU:HD11	1:B:446:VAL:HG11	1.89	0.54
1:A:706:LEU:HD21	1:A:718:VAL:HG21	1.88	0.54
1:B:425[B]:LEU:HD11	1:B:446:VAL:HG11	1.90	0.54
1:A:619:LEU:HB3	1:A:623:LEU:HD22	1.88	0.54
1:A:672:ALA:HB2	1:A:681:LEU:HD11	1.90	0.53
1:A:721:LEU:HD13	1:B:714:ALA:HA	1.88	0.53
1:B:720:LYS:O	1:B:720:LYS:CG	2.56	0.53
2:I:-2:DT:H2''	2:I:-1:DG:C8	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:253:LEU:HD22	1:B:279:ARG:HB3	1.93	0.51
1:B:310:VAL:HG12	1:B:341:LEU:HD11	1.92	0.51
1:A:266:ARG:HG3	1:A:300:HIS:HA	1.93	0.51
1:B:501:ILE:HD13	1:B:514:VAL:HG21	1.94	0.50
1:B:611:GLN:HB3	1:B:644:LYS:HD2	1.94	0.50
1:B:720:LYS:O	2:I:14:DT:H3'	2.11	0.50
1:A:241:LEU:HD21	1:A:272:VAL:HG21	1.94	0.49
1:A:501:ILE:HD13	1:A:514:VAL:HG21	1.93	0.49
1:A:536:ALA:HB2	1:A:545:LEU:HD11	1.94	0.49
1:A:695:LEU:HD13	1:A:719:LYS:HG3	1.95	0.49
1:A:416:LEU:HD13	1:A:430:VAL:HG11	1.94	0.47
1:B:315:PRO:O	1:B:319:GLN:HB2	2.15	0.47
1:B:627:HIS:HB3	1:B:654:LEU:HD23	1.96	0.47
1:A:666:GLN:H	1:A:666:GLN:CD	2.22	0.47
1:B:262:LYS:HE3	3:H:-5:DA:OP1	2.15	0.47
1:A:252:PRO:HD2	1:A:279[A]:ARG:NE	2.29	0.46
3:J:-8:DA:H5'	3:J:-8:DA:C8	2.51	0.46
1:B:604:ALA:HB2	1:B:613:LEU:HD11	1.97	0.46
2:G:-2:DT:H2'	2:G:-1:DG:C8	2.51	0.46
3:J:-8:DA:H5'	3:J:-8:DA:H8	1.81	0.46
1:B:344:VAL:O	1:B:348:LEU:HB2	2.16	0.46
1:B:244:VAL:HG13	1:B:276:HIS:HB2	1.98	0.46
1:B:378:VAL:O	1:B:382:LEU:HB2	2.16	0.46
1:A:263:ILE:HD11	1:A:295:VAL:HG22	1.99	0.45
1:A:482:ARG:NE	4:A:844:HOH:O	2.39	0.45
1:B:654:LEU:HB3	1:B:655:PRO:HD3	1.98	0.45
3:H:-7:DT:H2''	3:H:-6:DA:C8	2.52	0.45
1:A:620:LEU:HD13	1:A:634:VAL:HG11	1.99	0.45
1:B:420[B]:CYS:HA	1:B:425[B]:LEU:O	2.16	0.45
1:B:348:LEU:HD23	1:B:362:VAL:HG11	1.99	0.44
1:B:637:ILE:HD13	1:B:650:VAL:HG21	2.00	0.43
1:A:723:HIS:O	2:G:13:DC:C6	2.71	0.43
1:B:346:ARG:NH1	1:B:376:GLU:OE2	2.51	0.43
1:B:366:ALA:HB2	1:B:375:LEU:HD11	2.01	0.43
3:J:-14:DA:H2''	3:J:-13:DG:C8	2.54	0.43
1:B:319:GLN:NE2	4:B:968:HOH:O	2.51	0.43
1:B:347:LEU:HD12	1:B:347:LEU:HA	1.87	0.43
1:A:256:ASP:OD2	1:A:259:GLN:HG3	2.19	0.42
1:B:536:ALA:HB2	1:B:545:LEU:HD11	2.01	0.42
3:H:1:DC:H2''	3:H:2:DA:C8	2.54	0.42
1:B:720:LYS:NZ	1:B:720:LYS:CB	2.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:585:LEU:HA	1:B:585:LEU:HD12	1.83	0.42
1:A:683:SER:HB3	1:A:715:LEU:HD23	2.03	0.41
1:A:620:LEU:HB3	1:A:621:PRO:HD3	2.02	0.41
1:A:450:LEU:HB3	1:A:451:PRO:HD3	2.02	0.41
1:A:457:HIS:HB3	1:A:484:LEU:CD2	2.51	0.41
3:H:-13:DG:H2"	3:H:-12:DA:H5"	2.02	0.41
1:A:586:LEU:N	1:A:587:PRO:HD2	2.35	0.40
1:A:283:THR:O	1:A:288:ASN:HA	2.22	0.40
1:B:314:LEU:HB3	1:B:315:PRO:HD3	2.03	0.40
1:A:391:LEU:HD21	1:A:416:LEU:HD21	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	497/499 (100%)	483 (97%)	14 (3%)	0	100	100
1	B	492/499 (99%)	472 (96%)	20 (4%)	0	100	100
All	All	989/998 (99%)	955 (97%)	34 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	381/383 (100%)	359 (94%)	22 (6%)	18	15
1	B	378/383 (99%)	354 (94%)	24 (6%)	16	13
All	All	759/766 (99%)	713 (94%)	46 (6%)	16	14

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	241	LEU
1	A	254	GLN
1	A	283	THR
1	A	307	LEU
1	A	326	GLN
1	A	353	GLN
1	A	382	LEU
1	A	450	LEU
1	A	453	LEU
1	A	459	LEU
1	A	462	GLN
1	A	517	LEU
1	A	527	LEU
1	A	550	ARG
1	A	619	LEU
1	A	623	LEU
1	A	656	VAL
1	A	659	GLN
1	A	678	ARG
1	A	706	LEU
1	A	715	LEU
1	A	719	LYS
1	B	238	LEU
1	B	255	LEU
1	B	256	ASP
1	B	257	THR
1	B	279	ARG
1	B	310	VAL
1	B	323	LEU
1	B	347	LEU
1	B	348	LEU
1	B	350	VAL
1	B	351	LEU
1	B	382	LEU
1	B	520	VAL

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Mol	Chain	Res	Type
1	B	554	VAL
1	B	561	LEU
1	B	564	GLN
1	B	585	LEU
1	B	625	GLN
1	B	688	LEU
1	B	690	ARG
1	B	692	ASP
1	B	698	LEU
1	B	720	LYS
1	B	721	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	339	GLN
1	A	389	HIS
1	A	407	GLN
1	A	423	HIS
1	A	441	GLN
1	A	470	ASN
1	A	543	GLN
1	A	572	HIS
1	A	577	GLN
1	A	611	GLN
1	A	640	HIS
1	A	645	GLN
1	A	661	HIS
1	A	702	HIS
1	A	723	HIS
1	B	288	ASN
1	B	339	GLN
1	B	373	GLN
1	B	407	GLN
1	B	457	HIS
1	B	475	GLN
1	B	509	GLN
1	B	525	HIS
1	B	538	ASN
1	B	572	HIS
1	B	577	GLN
1	B	611	GLN

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Mol	Chain	Res	Type
1	B	625	GLN
1	B	627	HIS
1	B	702	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 oligosaccharides 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, 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	493/499 (98%)	0.43	28 (5%)	29 28	10, 28, 57, 94	20 (4%)
1	B	488/499 (97%)	0.37	31 (6%)	25 24	12, 28, 58, 93	20 (4%)
2	G	16/17 (94%)	-0.33	2 (12%)	8 7	18, 21, 56, 56	0
2	I	17/17 (100%)	-0.23	2 (11%)	9 8	17, 21, 72, 105	0
3	H	16/17 (94%)	0.53	2 (12%)	8 7	31, 37, 76, 89	0
3	J	17/17 (100%)	0.78	0	100 100	25, 41, 85, 85	0
All	All	1047/1066 (98%)	0.39	65 (6%)	26 25	10, 28, 60, 105	40 (3%)

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	470	ASN	6.3
1	A	721	LEU	5.2
1	B	697	ALA	4.9
1	B	253	LEU	4.9
1	A	723	HIS	4.0
1	B	232	TRP	3.9
1	B	721	LEU	3.8
1	A	471	GLY	3.8
1	A	278[A]	TRP	3.8
1	B	492	GLY	3.7
1	A	231	GLN	3.7
1	A	524	ALA	3.5
1	B	722	GLU	3.5
1	B	692	ASP	3.5
1	A	525	HIS	3.3
1	B	255	LEU	3.3
1	B	423[A]	HIS	3.3
1	A	319	GLN	3.2
1	B	235	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	269[A]	VAL	3.0
3	H	-13	DG	3.0
1	B	257	THR	2.9
1	B	438	GLY	2.9
1	B	588	VAL	2.8
1	A	456	ALA	2.8
1	A	457	HIS	2.8
2	G	-2	DT	2.8
1	B	689	SER	2.7
1	B	249	ARG	2.7
1	A	232	TRP	2.7
2	G	13	DC	2.7
1	A	250	GLY	2.6
1	B	258	GLY	2.6
1	B	660	ALA	2.5
1	A	488	CYS	2.5
1	B	591	GLN	2.4
3	H	2	DA	2.4
1	A	526	GLY	2.4
1	B	687	GLN	2.4
1	A	718	VAL	2.4
1	B	254	GLN	2.4
2	I	-2	DT	2.4
1	B	260	LEU	2.4
1	A	458	GLY	2.4
1	A	282	LEU	2.3
1	A	285	ALA	2.3
1	A	689	SER	2.3
2	I	14	DT	2.3
1	B	690	ARG	2.2
1	A	472	GLY	2.2
1	B	691	PRO	2.2
1	B	231	GLN	2.2
1	A	522	CYS	2.2
1	A	560	GLY	2.2
1	B	245	ALA	2.2
1	A	261	LEU	2.2
1	A	690	ARG	2.1
1	B	717	ALA	2.1
1	B	233	SER	2.1
1	B	491	HIS	2.1
1	B	557	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	558	ALA	2.1
1	B	238	LEU	2.1
1	A	558	ALA	2.1
1	A	353	GLN	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.