



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:05 PM UTC

PDB ID : 4OSQ / pdb_00004osq
Title : Crystal structure of the S505R 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 : 2.26 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

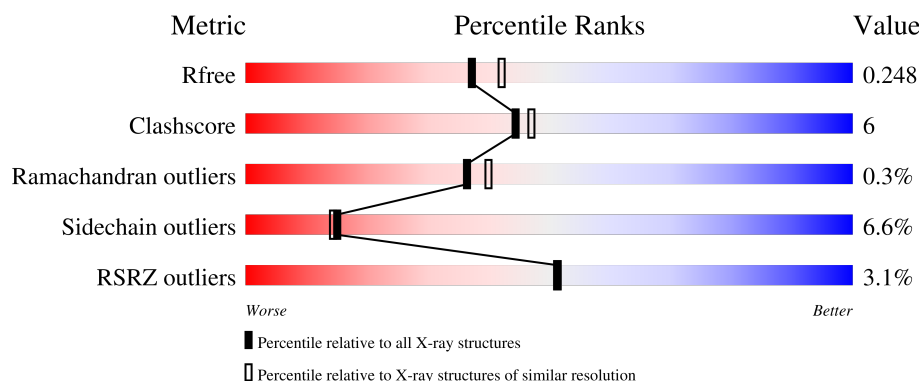
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.26 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	1898 (2.26-2.26)
Clashscore	190562	2005 (2.26-2.26)
Ramachandran outliers	187476	1965 (2.26-2.26)
Sidechain outliers	187428	1966 (2.26-2.26)
RSRZ outliers	180081	1898 (2.26-2.26)

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	4% 79% 17% ..
1	B	499	2% 82% 15% ..
2	G	17	6% 82% 18%
2	I	17	94% 6%
3	H	17	6% 71% 29%

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Mol	Chain	Length	Quality of chain
3	J	17	 53% 47%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8919 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	491	Total	C	N	O	S	0	3	0
			3577	2236	667	662	12			
1	B	487	Total	C	N	O	S	0	7	0
			3578	2234	668	663	13			

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	ARG	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	ARG	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*GP*TP*CP*TP*CP*TP*CP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	17	Total	C	N	O	P	0	0	0
			334	163	46	109	16			
2	I	17	Total	C	N	O	P	0	0	0
			335	164	46	109	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	17	Total	C	N	O	P	0	0	0
			357	169	80	92	16			
3	J	17	Total	C	N	O	P	0	0	0
			357	169	80	92	16			

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mg	0	0
			1	1		

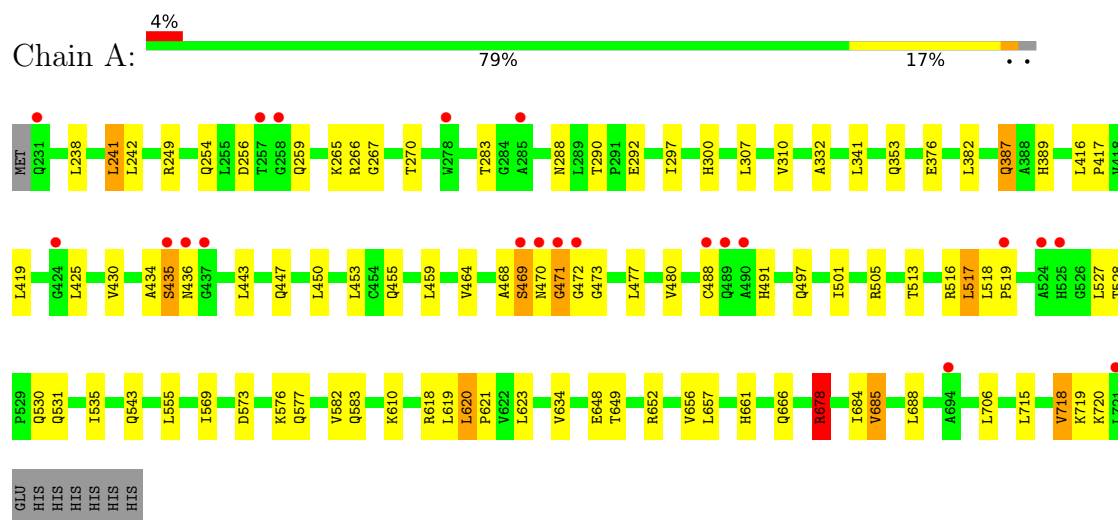
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	140	Total	O	0	0
			140	140		
5	B	144	Total	O	0	0
			144	144		
5	G	29	Total	O	0	0
			29	29		
5	H	21	Total	O	0	0
			21	21		
5	I	33	Total	O	0	0
			33	33		
5	J	13	Total	O	0	0
			13	13		

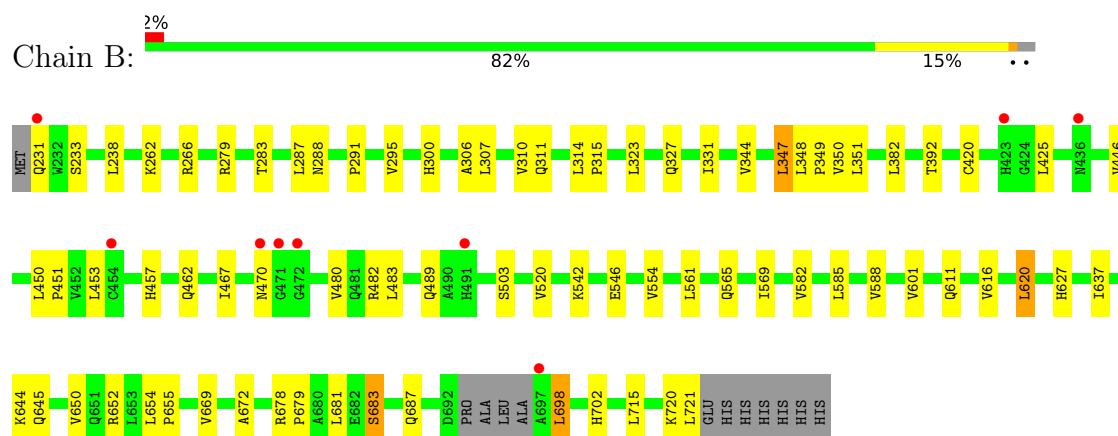
3 Residue-property plots [i](#)

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.

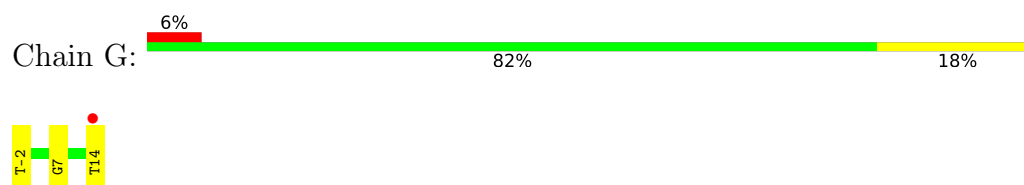
• Molecule 1: Hax3



• Molecule 1: Hax3



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



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

Chain I:  94% 6%



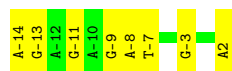
- Molecule 3: DNA (5'-D(*AP*GP*AP*GP*AP*GP*AP*TP*AP*AP*AP*GP*GP*GP*AP*CP*A)-3')

Chain H:  6% 71% 29%



- 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:  53% 47%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	81.76Å 87.58Å 88.16Å 90.00° 102.99° 90.00°	Depositor
Resolution (Å)	32.25 – 2.26 32.25 – 2.26	Depositor EDS
% Data completeness (in resolution range)	94.8 (32.25-2.26) 94.8 (32.25-2.26)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.50 (at 2.26Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.207 , 0.250 0.204 , 0.248	Depositor DCC
R_{free} test set	2746 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å ²)	34.5	Xtriage
Anisotropy	0.142	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 44.0	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	8919	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.18% 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: MG

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	0.54	0/3628	0.86	2/4955 (0.0%)
1	B	0.53	0/3628	0.84	1/4951 (0.0%)
2	G	0.37	0/369	0.94	0/566
2	I	0.39	0/370	0.98	0/568
3	H	0.33	0/405	0.97	0/625
3	J	0.31	0/405	0.90	1/625 (0.2%)
All	All	0.50	0/8805	0.87	4/12290 (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	-6.87	112.62	119.56
1	A	678	ARG	C-N-CA	-6.87	112.62	119.56
3	J	-3	DG	N9-C1'-C2'	-6.13	104.31	113.50
1	B	554	VAL	CB-CA-C	-5.42	105.03	111.97

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	3577	0	3731	54	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3578	0	3720	39	0
2	G	334	0	195	5	0
2	I	335	0	198	1	0
3	H	357	0	190	4	0
3	J	357	0	190	6	0
4	A	1	0	0	0	0
5	A	140	0	0	7	0
5	B	144	0	0	5	0
5	G	29	0	0	0	0
5	H	21	0	0	1	0
5	I	33	0	0	0	0
5	J	13	0	0	1	0
All	All	8919	0	8224	101	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 (101) 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:A:471:GLY:HA2	1:A:505:ARG:HG3	1.40	1.02
1:B:233:SER:OG	5:B:830:HOH:O	1.84	0.95
3:H:-13:DG:N7	5:H:107:HOH:O	2.06	0.88
2:G:7:DG:H1	3:H:-7:DT:H3	1.24	0.86
1:A:471:GLY:CA	1:A:505:ARG:HG3	2.07	0.83
3:J:2:DA:N6	5:J:108:HOH:O	2.11	0.82
2:I:7:DG:H1	3:J:-7:DT:H3	1.26	0.81
1:B:327:GLN:OE1	5:B:931:HOH:O	2.01	0.78
1:A:470:ASN:O	1:A:472:GLY:N	2.16	0.78
1:A:471:GLY:HA2	1:A:505:ARG:CG	2.18	0.70
1:A:530:GLN:O	5:A:925:HOH:O	2.09	0.70
1:A:516:ARG:NE	5:A:1021:HOH:O	2.22	0.69
1:A:706:LEU:HD21	1:A:718:VAL:HG21	1.72	0.69
1:A:469:SER:O	5:A:999:HOH:O	2.11	0.68
1:A:505:ARG:NH1	5:A:952:HOH:O	2.28	0.66
1:A:266:ARG:HG3	1:A:300:HIS:HA	1.77	0.65
1:B:453:LEU:HA	1:B:457:HIS:HB2	1.77	0.65
1:A:543:GLN:HB3	1:A:576:LYS:HD2	1.78	0.64
1:A:256:ASP:OD2	1:A:259:GLN:HG3	1.98	0.64
1:B:482:ARG:NE	5:B:855:HOH:O	2.28	0.63
1:B:467:ILE:HD13	1:B:480:VAL:HG21	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:471:GLY:HA3	1:A:505:ARG:N	2.19	0.57
1:B:425[B]:LEU:HD11	1:B:446:VAL:HG11	1.86	0.56
1:B:627:HIS:HB3	1:B:654:LEU:HD23	1.87	0.56
1:A:573:ASP:OD1	5:A:1033:HOH:O	2.18	0.56
1:B:420[B]:CYS:HA	1:B:425[B]:LEU:O	2.08	0.54
1:B:698:LEU:HG	1:B:702:HIS:CD2	2.42	0.54
1:A:434:ALA:HB2	1:A:443:LEU:HD11	1.88	0.54
1:B:331:ILE:HD13	1:B:344:VAL:HG21	1.89	0.53
1:A:376:GLU:OE1	5:A:962:HOH:O	2.18	0.53
1:A:416:LEU:HB3	1:A:417:PRO:HD3	1.91	0.53
1:B:611:GLN:HB3	1:B:644:LYS:HD2	1.91	0.53
2:G:-2:DT:H6	2:G:-2:DT:H5'	1.74	0.52
1:A:297:ILE:HD13	1:A:310:VAL:HG21	1.92	0.51
1:B:652:ARG:NE	5:B:839:HOH:O	2.10	0.51
1:A:491:HIS:ND1	1:A:518:LEU:HD22	2.26	0.51
1:A:569:ILE:HD13	1:A:582:VAL:HG21	1.92	0.51
1:A:649:THR:OG1	1:A:678:ARG:HD3	2.10	0.51
1:A:620:LEU:HD13	1:A:634:VAL:HG11	1.93	0.51
1:B:672:ALA:HB2	1:B:681:LEU:HD11	1.92	0.50
1:A:657:LEU:HD21	1:A:685:VAL:HG23	1.94	0.50
3:J:-9:DG:H2''	3:J:-8:DA:OP2	2.11	0.50
1:A:389:HIS:HB3	1:A:416:LEU:HD23	1.92	0.50
1:A:661:HIS:CD2	1:A:688:LEU:HB3	2.47	0.50
1:A:468:ALA:HB2	1:A:477:LEU:HD11	1.95	0.48
1:B:637:ILE:HD11	1:B:669:VAL:HG22	1.96	0.48
1:B:654:LEU:HB3	1:B:655:PRO:HD3	1.96	0.48
1:A:513:THR:O	1:A:517:LEU:HB2	2.14	0.47
1:A:256:ASP:OD2	1:A:259:GLN:CG	2.63	0.47
3:J:-14:DA:H2''	3:J:-13:DG:C8	2.50	0.47
1:A:435:SER:O	1:A:436:ASN:HB2	2.15	0.47
1:A:470:ASN:HD21	3:J:-11:DG:H2''	1.81	0.46
1:A:720:LYS:O	2:G:14:DT:H5''	2.15	0.46
1:A:292:GLU:O	5:A:943:HOH:O	2.21	0.46
3:H:1:DC:H2''	3:H:2:DA:C8	2.50	0.46
1:A:620:LEU:HB3	1:A:621:PRO:HD3	1.98	0.46
1:A:648:GLU:O	1:A:652[A]:ARG:HG3	2.15	0.46
1:A:470:ASN:HD21	3:J:-11:DG:C2'	2.29	0.46
1:B:679:PRO:O	1:B:683:SER:HB2	2.16	0.45
1:A:283:THR:O	1:A:288:ASN:HA	2.15	0.45
1:A:720:LYS:HA	2:G:14:DT:H3'	1.98	0.45
1:B:262:LYS:HE3	3:H:-5:DA:OP1	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:577:GLN:HB3	1:A:610:LYS:HD2	2.00	0.44
1:B:565:GLN:O	1:B:569:ILE:HG13	2.18	0.44
1:A:666:GLN:H	1:A:666:GLN:CD	2.26	0.44
1:B:392:THR:HG23	5:B:849:HOH:O	2.18	0.44
2:G:14:DT:H6	2:G:14:DT:H2'	1.63	0.44
1:B:307:LEU:O	1:B:311:GLN:HG3	2.18	0.43
1:A:416:LEU:HD13	1:A:430:VAL:HG11	1.99	0.43
1:B:348:LEU:HB3	1:B:349:PRO:HD3	2.00	0.43
1:B:425[A]:LEU:HD11	1:B:446:VAL:HG11	2.00	0.43
1:B:306:ALA:O	1:B:310:VAL:HG13	2.18	0.43
1:A:238:LEU:O	1:A:241:LEU:HB3	2.19	0.43
1:A:450:LEU:HD13	1:A:464:VAL:HG11	2.00	0.43
1:B:616:VAL:O	1:B:620:LEU:HB2	2.19	0.43
1:A:518:LEU:HB3	1:A:519:PRO:HD3	2.00	0.43
1:B:645:GLN:HB3	1:B:678:ARG:HD2	2.01	0.42
1:A:531:GLN:O	1:A:535:ILE:HG13	2.19	0.42
1:B:291:PRO:O	1:B:295:VAL:HG23	2.19	0.42
1:A:249:ARG:O	1:A:254:GLN:HG3	2.20	0.42
1:B:347:LEU:HD12	1:B:347:LEU:HA	1.73	0.42
1:A:265:LYS:HE2	1:A:265:LYS:HB3	1.93	0.42
1:B:283:THR:O	1:B:288:ASN:HA	2.19	0.42
1:B:569:ILE:HD11	1:B:601:VAL:HG22	2.02	0.42
1:A:267:GLY:HA2	1:A:300:HIS:O	2.20	0.41
1:B:314:LEU:HB3	1:B:315:PRO:HD3	2.02	0.41
1:B:542:LYS:O	1:B:546:GLU:HG3	2.20	0.41
1:B:344:VAL:O	1:B:348:LEU:HB2	2.21	0.41
1:B:483:LEU:HD23	1:B:483:LEU:HA	1.89	0.41
1:A:332:ALA:HB2	1:A:341:LEU:HD11	2.02	0.41
1:A:684:ILE:O	1:A:688:LEU:HG	2.20	0.41
1:A:472:GLY:HA3	1:A:473:GLY:HA2	1.79	0.41
1:A:497:GLN:O	1:A:501:ILE:HG13	2.20	0.41
1:B:266:ARG:HG2	1:B:300:HIS:HA	2.02	0.41
1:B:569:ILE:HD13	1:B:582:VAL:HG21	2.02	0.41
1:B:450:LEU:HB3	1:B:451:PRO:HD3	2.04	0.40
1:A:387:GLN:HB3	1:B:420[B]:CYS:O	2.21	0.40
1:A:555:LEU:HD21	1:A:583:GLN:HB2	2.02	0.40
1:B:470:ASN:ND2	1:B:503:SER:O	2.53	0.40
1:B:287:LEU:HD11	1:B:311:GLN:HA	2.03	0.40
1:A:419:LEU:HB3	1:A:425:LEU:HD12	2.02	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	492/499 (99%)	462 (94%)	27 (6%)	3 (1%)	21	21
1	B	490/499 (98%)	467 (95%)	23 (5%)	0	100	100
All	All	982/998 (98%)	929 (95%)	50 (5%)	3 (0%)	36	40

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	469	SER
1	A	471	GLY
1	A	488	CYS

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	377/383 (98%)	349 (93%)	28 (7%)	13	11
1	B	377/383 (98%)	355 (94%)	22 (6%)	18	19
All	All	754/766 (98%)	704 (93%)	50 (7%)	15	14

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	241	LEU
1	A	242	LEU
1	A	270[A]	THR

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Mol	Chain	Res	Type
1	A	270[B]	THR
1	A	290	THR
1	A	307	LEU
1	A	353	GLN
1	A	382	LEU
1	A	387	GLN
1	A	435	SER
1	A	447	GLN
1	A	453	LEU
1	A	455	GLN
1	A	459	LEU
1	A	480	VAL
1	A	517	LEU
1	A	527	LEU
1	A	528	THR
1	A	618	ARG
1	A	619	LEU
1	A	620	LEU
1	A	623	LEU
1	A	656	VAL
1	A	678	ARG
1	A	685	VAL
1	A	715	LEU
1	A	718	VAL
1	A	719	LYS
1	B	231	GLN
1	B	238	LEU
1	B	279	ARG
1	B	323	LEU
1	B	347	LEU
1	B	350	VAL
1	B	351	LEU
1	B	382	LEU
1	B	462	GLN
1	B	489	GLN
1	B	520	VAL
1	B	561	LEU
1	B	585	LEU
1	B	588	VAL
1	B	620	LEU
1	B	650	VAL
1	B	683	SER

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Mol	Chain	Res	Type
1	B	687	GLN
1	B	698	LEU
1	B	715	LEU
1	B	720	LYS
1	B	721	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	276	HIS
1	A	300	HIS
1	A	339	GLN
1	A	355	HIS
1	A	379	GLN
1	A	402	ASN
1	A	441	GLN
1	A	470	ASN
1	A	559	HIS
1	A	577	GLN
1	A	583	GLN
1	A	593	HIS
1	A	611	GLN
1	A	674	ASN
1	B	259	GLN
1	B	288	ASN
1	B	339	GLN
1	B	373	GLN
1	B	407	GLN
1	B	441	GLN
1	B	525	HIS
1	B	538	ASN
1	B	543	GLN
1	B	577	GLN
1	B	583	GLN
1	B	593	HIS
1	B	687	GLN
1	B	702	HIS

5.3.3 RNA ⓘ

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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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	491/499 (98%)	0.11	21 (4%) 40 39	16, 33, 71, 119	15 (3%)
1	B	487/499 (97%)	-0.02	9 (1%) 67 68	15, 32, 62, 103	17 (3%)
2	G	17/17 (100%)	-0.53	1 (5%) 28 26	20, 24, 63, 130	0
2	I	17/17 (100%)	-0.71	0 100 100	19, 22, 70, 106	0
3	H	17/17 (100%)	-0.06	1 (5%) 28 26	31, 37, 78, 112	0
3	J	17/17 (100%)	-0.04	0 100 100	31, 40, 79, 84	0
All	All	1046/1066 (98%)	0.02	32 (3%) 51 51	15, 33, 68, 130	32 (3%)

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	472	GLY	6.1
1	A	472	GLY	6.0
1	B	471	GLY	4.3
1	B	470	ASN	4.3
1	A	471	GLY	4.1
1	B	423[A]	HIS	3.6
1	A	437	GLY	3.4
2	G	14	DT	3.3
1	B	697	ALA	3.2
3	H	-14	DA	3.2
1	A	424	GLY	3.1
1	A	721	LEU	3.1
1	A	435	SER	3.1
1	A	470	ASN	3.0
1	B	436	ASN	2.8
1	A	524	ALA	2.7
1	A	278	TRP	2.7
1	A	258	GLY	2.6
1	A	525	HIS	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	285	ALA	2.5
1	A	436	ASN	2.5
1	A	469	SER	2.3
1	A	519	PRO	2.2
1	A	257	THR	2.2
1	B	454	CYS	2.2
1	A	488	CYS	2.2
1	B	491	HIS	2.2
1	A	231	GLN	2.1
1	A	490	ALA	2.1
1	A	694	ALA	2.0
1	A	489	GLN	2.0
1	B	231	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](#)

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
4	MG	A	801	1/1	0.82	0.16	72,72,72,72	0

6.5 Other polymers [i](#)

There are no such residues in this entry.