



Full wwPDB X-ray Structure Validation Report

Mar 1, 2014 – 01:03 AM GMT

PDB ID : 3PQ1
Title : Crystal structure of human mitochondrial poly(A) polymerase (PAPD1)
Authors : Bai, Y.; Srivastava, S.K.; Chang, J.H.; Tong, L.
Deposited on : 2010-11-25
Resolution : 3.10 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

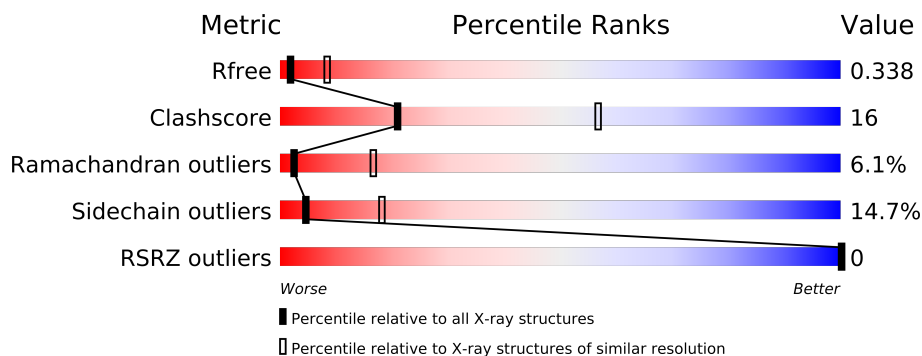
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 3.10 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}	66092	1007 (3.18-3.02)
Clashscore	79885	1078 (3.16-3.04)
Ramachandran outliers	78287	1044 (3.16-3.04)
Sidechain outliers	78261	1044 (3.16-3.04)
RSRZ outliers	66119	1008 (3.18-3.02)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	464	<div><div></div><div></div></div>
1	B	464	<div><div></div><div></div></div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 5351 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Poly(A) RNA polymerase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	355	Total	C	N	O	S	Se	0	0	0
			2793	1782	474	520	11	6			
1	B	321	Total	C	N	O	S	Se	0	0	0
			2558	1629	438	475	10	6			

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	23	MSE	-	EXPRESSION TAG	UNP Q9NVV4
A	24	GLY	-	EXPRESSION TAG	UNP Q9NVV4
A	25	SER	-	EXPRESSION TAG	UNP Q9NVV4
A	26	SER	-	EXPRESSION TAG	UNP Q9NVV4
A	27	HIS	-	EXPRESSION TAG	UNP Q9NVV4
A	28	HIS	-	EXPRESSION TAG	UNP Q9NVV4
A	29	HIS	-	EXPRESSION TAG	UNP Q9NVV4
A	30	HIS	-	EXPRESSION TAG	UNP Q9NVV4
A	31	HIS	-	EXPRESSION TAG	UNP Q9NVV4
A	32	HIS	-	EXPRESSION TAG	UNP Q9NVV4
A	33	SER	-	EXPRESSION TAG	UNP Q9NVV4
A	34	SER	-	EXPRESSION TAG	UNP Q9NVV4
A	35	GLY	-	EXPRESSION TAG	UNP Q9NVV4
A	36	LEU	-	EXPRESSION TAG	UNP Q9NVV4
A	37	VAL	-	EXPRESSION TAG	UNP Q9NVV4
A	38	PRO	-	EXPRESSION TAG	UNP Q9NVV4
A	39	ARG	-	EXPRESSION TAG	UNP Q9NVV4
A	40	GLY	-	EXPRESSION TAG	UNP Q9NVV4
A	41	SER	-	EXPRESSION TAG	UNP Q9NVV4
A	42	HIS	-	EXPRESSION TAG	UNP Q9NVV4
A	43	MSE	-	EXPRESSION TAG	UNP Q9NVV4
A	151	UNK	-	SEE REMARK 999	UNP Q9NVV4
A	152	UNK	-	SEE REMARK 999	UNP Q9NVV4
A	153	UNK	-	SEE REMARK 999	UNP Q9NVV4
A	154	UNK	-	SEE REMARK 999	UNP Q9NVV4

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Chain	Residue	Modelled	Actual	Comment	Reference
A	155	UNK	-	SEE REMARK 999	UNP Q9NVV4
A	156	UNK	-	SEE REMARK 999	UNP Q9NVV4
A	157	UNK	-	SEE REMARK 999	UNP Q9NVV4
A	325	ALA	ASP	ENGINEERED MUTATION	UNP Q9NVV4
A	464	UNK	-	SEE REMARK 999	UNP Q9NVV4
A	465	UNK	-	SEE REMARK 999	UNP Q9NVV4
A	466	UNK	-	SEE REMARK 999	UNP Q9NVV4
A	467	UNK	-	SEE REMARK 999	UNP Q9NVV4
A	468	UNK	-	SEE REMARK 999	UNP Q9NVV4
A	469	UNK	-	SEE REMARK 999	UNP Q9NVV4
A	470	UNK	-	SEE REMARK 999	UNP Q9NVV4
A	471	UNK	-	SEE REMARK 999	UNP Q9NVV4
A	472	UNK	-	SEE REMARK 999	UNP Q9NVV4
A	473	UNK	-	SEE REMARK 999	UNP Q9NVV4
A	474	UNK	-	SEE REMARK 999	UNP Q9NVV4
A	475	UNK	-	SEE REMARK 999	UNP Q9NVV4
A	476	UNK	-	SEE REMARK 999	UNP Q9NVV4
A	477	UNK	-	SEE REMARK 999	UNP Q9NVV4
A	478	UNK	-	SEE REMARK 999	UNP Q9NVV4
B	23	MSE	-	EXPRESSION TAG	UNP Q9NVV4
B	24	GLY	-	EXPRESSION TAG	UNP Q9NVV4
B	25	SER	-	EXPRESSION TAG	UNP Q9NVV4
B	26	SER	-	EXPRESSION TAG	UNP Q9NVV4
B	27	HIS	-	EXPRESSION TAG	UNP Q9NVV4
B	28	HIS	-	EXPRESSION TAG	UNP Q9NVV4
B	29	HIS	-	EXPRESSION TAG	UNP Q9NVV4
B	30	HIS	-	EXPRESSION TAG	UNP Q9NVV4
B	31	HIS	-	EXPRESSION TAG	UNP Q9NVV4
B	32	HIS	-	EXPRESSION TAG	UNP Q9NVV4
B	33	SER	-	EXPRESSION TAG	UNP Q9NVV4
B	34	SER	-	EXPRESSION TAG	UNP Q9NVV4
B	35	GLY	-	EXPRESSION TAG	UNP Q9NVV4
B	36	LEU	-	EXPRESSION TAG	UNP Q9NVV4
B	37	VAL	-	EXPRESSION TAG	UNP Q9NVV4
B	38	PRO	-	EXPRESSION TAG	UNP Q9NVV4
B	39	ARG	-	EXPRESSION TAG	UNP Q9NVV4
B	40	GLY	-	EXPRESSION TAG	UNP Q9NVV4
B	41	SER	-	EXPRESSION TAG	UNP Q9NVV4
B	42	HIS	-	EXPRESSION TAG	UNP Q9NVV4
B	43	MSE	-	EXPRESSION TAG	UNP Q9NVV4
B	151	UNK	-	SEE REMARK 999	UNP Q9NVV4
B	152	UNK	-	SEE REMARK 999	UNP Q9NVV4

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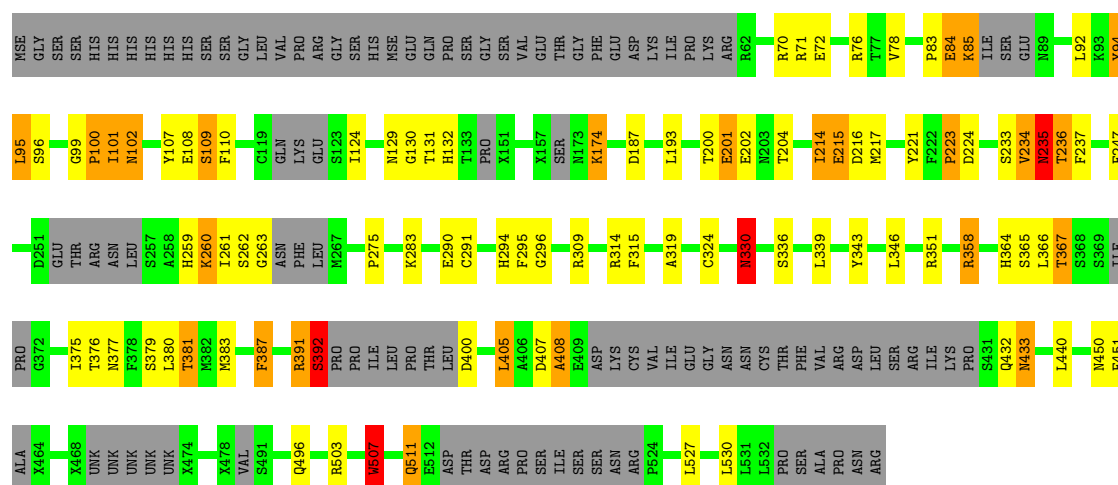
Chain	Residue	Modelled	Actual	Comment	Reference
B	153	UNK	-	SEE REMARK 999	UNP Q9NVV4
B	154	UNK	-	SEE REMARK 999	UNP Q9NVV4
B	155	UNK	-	SEE REMARK 999	UNP Q9NVV4
B	156	UNK	-	SEE REMARK 999	UNP Q9NVV4
B	157	UNK	-	SEE REMARK 999	UNP Q9NVV4
B	325	ALA	ASP	ENGINEERED MUTATION	UNP Q9NVV4
B	464	UNK	-	SEE REMARK 999	UNP Q9NVV4
B	465	UNK	-	SEE REMARK 999	UNP Q9NVV4
B	466	UNK	-	SEE REMARK 999	UNP Q9NVV4
B	467	UNK	-	SEE REMARK 999	UNP Q9NVV4
B	468	UNK	-	SEE REMARK 999	UNP Q9NVV4
B	469	UNK	-	SEE REMARK 999	UNP Q9NVV4
B	470	UNK	-	SEE REMARK 999	UNP Q9NVV4
B	471	UNK	-	SEE REMARK 999	UNP Q9NVV4
B	472	UNK	-	SEE REMARK 999	UNP Q9NVV4
B	473	UNK	-	SEE REMARK 999	UNP Q9NVV4
B	474	UNK	-	SEE REMARK 999	UNP Q9NVV4
B	475	UNK	-	SEE REMARK 999	UNP Q9NVV4
B	476	UNK	-	SEE REMARK 999	UNP Q9NVV4
B	477	UNK	-	SEE REMARK 999	UNP Q9NVV4
B	478	UNK	-	SEE REMARK 999	UNP Q9NVV4

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

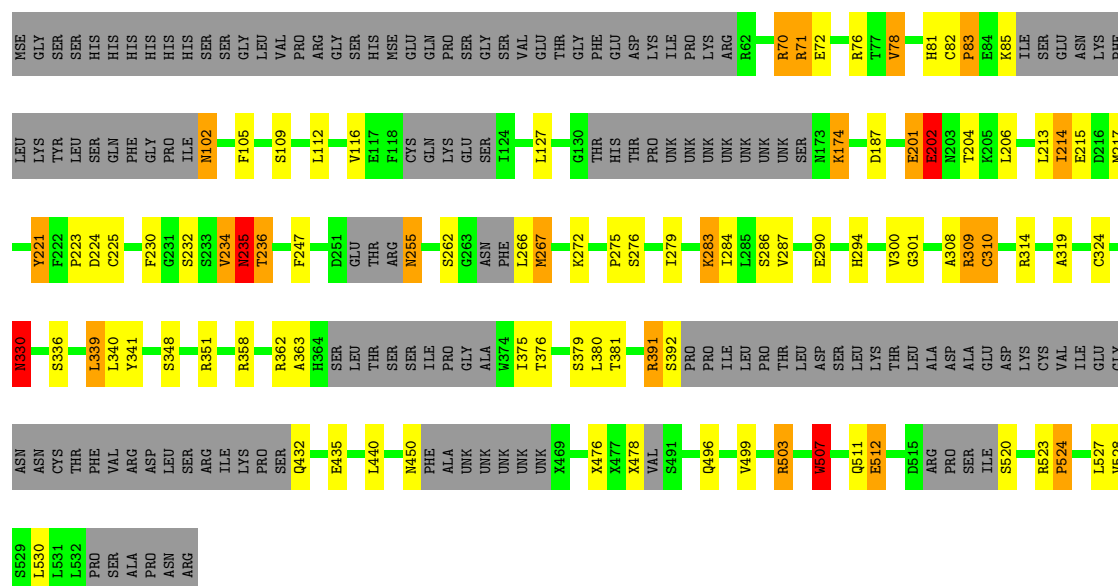
- Molecule 1: Poly(A) RNA polymerase

Chain A:



- Molecule 1: Poly(A) RNA polymerase

Chain B:



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	68.68Å 76.88Å 87.63Å 90.00° 103.39° 90.00°	Depositor
Resolution (Å)	28.91 – 3.10 28.91 – 2.98	Depositor EDS
% Data completeness (in resolution range)	91.7 (28.91-3.10) 92.6 (28.91-2.98)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.54 (at 3.00Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.5.2)	Depositor
R, R_{free}	0.247 , 0.328 0.260 , 0.338	Depositor DCC
R_{free} test set	834 reflections (4.94%)	DCC
Wilson B-factor (Å ²)	50.8	Xtriage
Anisotropy	0.261	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 27.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	1 of 33184 reflections (0.003%)	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	5351	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.05% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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	0.53	0/2750	0.69	3/3690 (0.1%)
1	B	0.50	0/2544	0.69	1/3413 (0.0%)
All	All	0.51	0/5294	0.69	4/7103 (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	A	0	1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	507	TRP	CA-CB-CG	10.60	133.84	113.70
1	A	507	TRP	CA-CB-CG	9.49	131.73	113.70
1	A	392	SER	N-CA-C	-5.20	96.96	111.00
1	A	507	TRP	N-CA-CB	-5.10	101.41	110.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	391	ARG	Peptide

5.2 Close contacts

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 hydrogens

added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2793	0	0	47	0
1	B	2558	0	0	45	0
All	All	5351	0	0	83	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 16.

All (83) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:507:TRP:CZ3	1:A:511:GLN:OE1	2.18	0.96
1:B:507:TRP:CZ3	1:B:511:GLN:OE1	2.18	0.96
1:A:107:TYR:OH	1:A:319:ALA:O	2.01	0.78
1:B:82:CYS:SG	1:B:112:LEU:O	2.45	0.74
1:A:364:HIS:O	1:A:366:LEU:N	2.27	0.67
1:B:511:GLN:O	1:B:512:GLU:C	2.31	0.66
1:B:527:LEU:O	1:B:530:LEU:N	2.30	0.65
1:A:527:LEU:O	1:A:530:LEU:N	2.33	0.61
1:A:392:SER:O	1:A:433:ASN:OD1	2.18	0.61
1:A:131:THR:CA	1:B:267:MSE:O	2.50	0.60
1:A:236:THR:O	1:A:351:ARG:NH2	2.36	0.58
1:A:84:GLU:O	1:A:85:LYS:CD	2.52	0.58
1:A:100:PRO:O	1:A:101:ILE:CB	2.52	0.58
1:B:236:THR:O	1:B:351:ARG:NH2	2.38	0.56
1:B:476:UNK:O	1:B:478:UNK:N	2.39	0.56
1:A:400:ASP:OD1	1:A:400:ASP:N	2.39	0.54
1:B:255:ASN:ND2	1:B:255:ASN:N	2.56	0.53
1:B:102:ASN:ND2	1:B:102:ASN:N	2.56	0.53
1:A:94:TYR:O	1:A:96:SER:N	2.42	0.53
1:B:78:VAL:N	1:B:116:VAL:O	2.42	0.53
1:B:391:ARG:CG	1:B:391:ARG:NH1	2.70	0.52
1:A:214:ILE:O	1:A:217:MSE:N	2.43	0.51
1:A:99:GLY:O	1:A:100:PRO:O	2.29	0.51
1:A:294:HIS:CD2	1:B:283:LYS:NZ	2.80	0.50
1:A:260:LYS:NZ	1:B:319:ALA:CB	2.75	0.49
1:B:330:ASN:O	1:B:330:ASN:ND2	2.46	0.49
1:A:72:GLU:OE2	1:A:76:ARG:NH1	2.46	0.49
1:B:380:LEU:O	1:B:381:THR:C	2.51	0.49
1:B:290:GLU:OE1	1:B:294:HIS:CE1	2.66	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:234:VAL:O	1:A:235:ASN:O	2.30	0.49
1:A:100:PRO:O	1:A:101:ILE:CG1	2.62	0.48
1:B:174:LYS:C	1:B:174:LYS:CD	2.82	0.48
1:A:174:LYS:C	1:A:174:LYS:CD	2.81	0.48
1:A:259:HIS:CB	1:B:213:LEU:CD2	2.93	0.47
1:B:72:GLU:OE2	1:B:76:ARG:NH1	2.47	0.47
1:A:71:ARG:NH1	1:A:215:GLU:OE2	2.48	0.46
1:A:200:THR:O	1:A:201:GLU:C	2.54	0.46
1:B:82:CYS:CB	1:B:83:PRO:CD	2.94	0.46
1:A:330:ASN:O	1:A:330:ASN:ND2	2.49	0.46
1:A:343:TYR:CE2	1:A:405:LEU:CD2	2.99	0.45
1:A:221:TYR:CE2	1:B:221:TYR:OH	2.69	0.45
1:B:105:PHE:CD1	1:B:202:GLU:CG	2.99	0.45
1:B:70:ARG:NH2	1:B:201:GLU:OE2	2.49	0.45
1:A:295:PHE:CZ	1:B:287:VAL:CB	3.00	0.45
1:B:300:VAL:O	1:B:301:GLY:C	2.55	0.45
1:A:214:ILE:O	1:A:216:ASP:N	2.51	0.44
1:A:237:PHE:O	1:A:358:ARG:NH2	2.50	0.44
1:B:310:CYS:SG	1:B:310:CYS:O	2.76	0.44
1:B:234:VAL:O	1:B:235:ASN:O	2.36	0.44
1:B:330:ASN:N	1:B:330:ASN:ND2	2.66	0.44
1:B:71:ARG:NH1	1:B:215:GLU:OE2	2.51	0.43
1:A:261:ILE:CG2	1:A:262:SER:N	2.81	0.43
1:A:92:LEU:O	1:A:96:SER:N	2.51	0.43
1:B:499:VAL:O	1:B:503:ARG:N	2.51	0.43
1:B:339:LEU:O	1:B:340:LEU:C	2.57	0.43
1:A:367:THR:OG1	1:A:377:ASN:OD1	2.37	0.43
1:A:290:GLU:OE1	1:A:294:HIS:CE1	2.72	0.43
1:A:383:MSE:O	1:A:387:PHE:N	2.51	0.43
1:A:315:PHE:N	1:A:315:PHE:CD2	2.86	0.43
1:A:407:ASP:O	1:A:408:ALA:CB	2.67	0.43
1:A:101:ILE:O	1:A:102:ASN:O	2.37	0.42
1:A:263:GLY:N	1:B:81:HIS:O	2.52	0.42
1:A:84:GLU:C	1:A:85:LYS:CD	2.88	0.42
1:B:283:LYS:O	1:B:284:ILE:C	2.58	0.42
1:B:339:LEU:O	1:B:341:TYR:N	2.53	0.42
1:A:129:ASN:ND2	1:A:129:ASN:N	2.68	0.42
1:A:296:GLY:O	1:B:272:LYS:CE	2.69	0.41
1:A:346:LEU:CD2	1:A:400:ASP:OD2	2.68	0.41
1:B:283:LYS:O	1:B:286:SER:N	2.53	0.41
1:B:230:PHE:CA	1:B:234:VAL:CG2	2.99	0.41
1:A:380:LEU:O	1:A:381:THR:C	2.57	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:367:THR:CG2	1:A:367:THR:O	2.68	0.41
1:A:130:GLY:O	1:B:267:MSE:CB	2.69	0.41
1:B:523:ARG:O	1:B:524:PRO:O	2.39	0.41
1:A:94:TYR:O	1:A:95:LEU:C	2.59	0.41
1:A:214:ILE:O	1:A:215:GLU:C	2.59	0.41
1:B:308:ALA:O	1:B:310:CYS:N	2.54	0.41
1:B:206:LEU:O	1:B:206:LEU:CD1	2.68	0.41
1:B:308:ALA:O	1:B:309:ARG:C	2.60	0.40
1:A:101:ILE:O	1:A:101:ILE:CG2	2.68	0.40
1:B:214:ILE:O	1:B:217:MSE:N	2.55	0.40
1:B:276:SER:OG	1:B:279:ILE:CG1	2.70	0.40
1:B:362:ARG:O	1:B:363:ALA:C	2.60	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	316/464 (68%)	241 (76%)	53 (17%)	22 (7%)	2	13
1	B	291/464 (63%)	232 (80%)	44 (15%)	15 (5%)	3	21
All	All	607/928 (65%)	473 (78%)	97 (16%)	37 (6%)	2	16

All (37) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	94	TYR
1	A	100	PRO
1	A	101	ILE
1	A	102	ASN
1	A	201	GLU
1	A	223	PRO
1	A	235	ASN
1	A	365	SER

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Mol	Chain	Res	Type
1	A	511	GLN
1	B	201	GLU
1	B	235	ASN
1	B	524	PRO
1	A	83	PRO
1	A	95	LEU
1	A	109	SER
1	A	330	ASN
1	A	387	PHE
1	A	408	ALA
1	B	83	PRO
1	B	109	SER
1	B	223	PRO
1	B	330	ASN
1	B	339	LEU
1	B	435	GLU
1	A	275	PRO
1	A	339	LEU
1	B	202	GLU
1	B	232	SER
1	B	275	PRO
1	B	309	ARG
1	B	512	GLU
1	A	84	GLU
1	A	215	GLU
1	A	260	LYS
1	A	405	LEU
1	A	381	THR
1	B	528	VAL

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	300/388 (77%)	257 (86%)	43 (14%)	5	19
1	B	278/388 (72%)	236 (85%)	42 (15%)	4	16
All	All	578/776 (74%)	493 (85%)	85 (15%)	4	18

All (85) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	70	ARG
1	A	78	VAL
1	A	85	LYS
1	A	108	GLU
1	A	109	SER
1	A	110	PHE
1	A	124	ILE
1	A	132	HIS
1	A	174	LYS
1	A	187	ASP
1	A	193	LEU
1	A	202	GLU
1	A	204	THR
1	A	214	ILE
1	A	223	PRO
1	A	224	ASP
1	A	233	SER
1	A	234	VAL
1	A	235	ASN
1	A	236	THR
1	A	247	PHE
1	A	283	LYS
1	A	291	CYS
1	A	309	ARG
1	A	314	ARG
1	A	324	CYS
1	A	330	ASN
1	A	336	SER
1	A	358	ARG
1	A	367	THR
1	A	375	ILE
1	A	376	THR
1	A	379	SER
1	A	391	ARG
1	A	392	SER
1	A	432	GLN
1	A	433	ASN
1	A	440	LEU
1	A	450	ASN
1	A	451	PHE
1	A	496	GLN
1	A	503	ARG

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Mol	Chain	Res	Type
1	A	507	TRP
1	B	70	ARG
1	B	71	ARG
1	B	78	VAL
1	B	85	LYS
1	B	102	ASN
1	B	127	LEU
1	B	174	LYS
1	B	187	ASP
1	B	202	GLU
1	B	204	THR
1	B	214	ILE
1	B	221	TYR
1	B	224	ASP
1	B	225	CYS
1	B	234	VAL
1	B	235	ASN
1	B	236	THR
1	B	247	PHE
1	B	255	ASN
1	B	262	SER
1	B	266	LEU
1	B	267	MSE
1	B	283	LYS
1	B	310	CYS
1	B	314	ARG
1	B	324	CYS
1	B	330	ASN
1	B	336	SER
1	B	348	SER
1	B	358	ARG
1	B	375	ILE
1	B	376	THR
1	B	379	SER
1	B	391	ARG
1	B	392	SER
1	B	432	GLN
1	B	440	LEU
1	B	450	ASN
1	B	496	GLN
1	B	503	ARG
1	B	507	TRP

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Mol	Chain	Res	Type
1	B	520	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates 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	338/464 (72%)	-0.24	0 100 100	17, 43, 83, 108	0
1	B	311/464 (67%)	-0.19	0 100 100	17, 46, 85, 119	0
All	All	649/928 (69%)	-0.22	0 100 100	17, 44, 84, 119	0

There are no RSRZ outliers to report.

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 ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.