



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 09:13 PM UTC

PDB ID : 3SAH / pdb_00003sah
Title : Crystal structure of the human RRP6 catalytic domain with Y436A mutation in the catalytic site
Authors : Januszyk, K.; Liu, Q.; Lima, C.D.
Deposited on : 2011-06-02
Resolution : 2.65 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

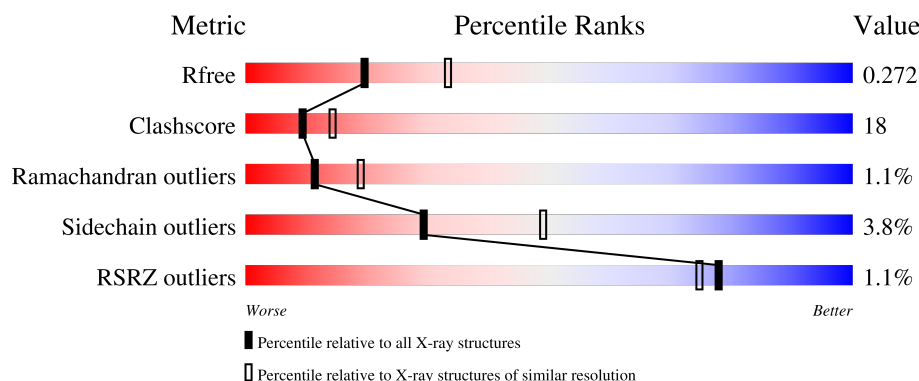
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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	1110 (2.66-2.66)
Clashscore	190562	1141 (2.66-2.66)
Ramachandran outliers	187476	1126 (2.66-2.66)
Sidechain outliers	187428	1126 (2.66-2.66)
RSRZ outliers	180081	1110 (2.66-2.66)

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	428	54% 29% • 12%
1	B	428	58% 28% • 11%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6506 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 Exosome component 10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	377	Total	C	N	O	S	0	0	0
			3133	2006	540	569	18			
1	B	382	Total	C	N	O	S	0	0	0
			3166	2026	548	574	18			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	179	SER	-	expression tag	UNP Q01780
A	436	ALA	TYR	engineered mutation	UNP Q01780
B	179	SER	-	expression tag	UNP Q01780
B	436	ALA	TYR	engineered mutation	UNP Q01780

- Molecule 2 is YTTRIUM (III) ION (CCD ID: YT3) (formula: Y).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Y	0	0
			2	2		
2	B	1	Total	Y	0	0
			1	1		

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	Mg	0	0
			2	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	68	Total	O	0	0
			68	68		

Continued on next page...

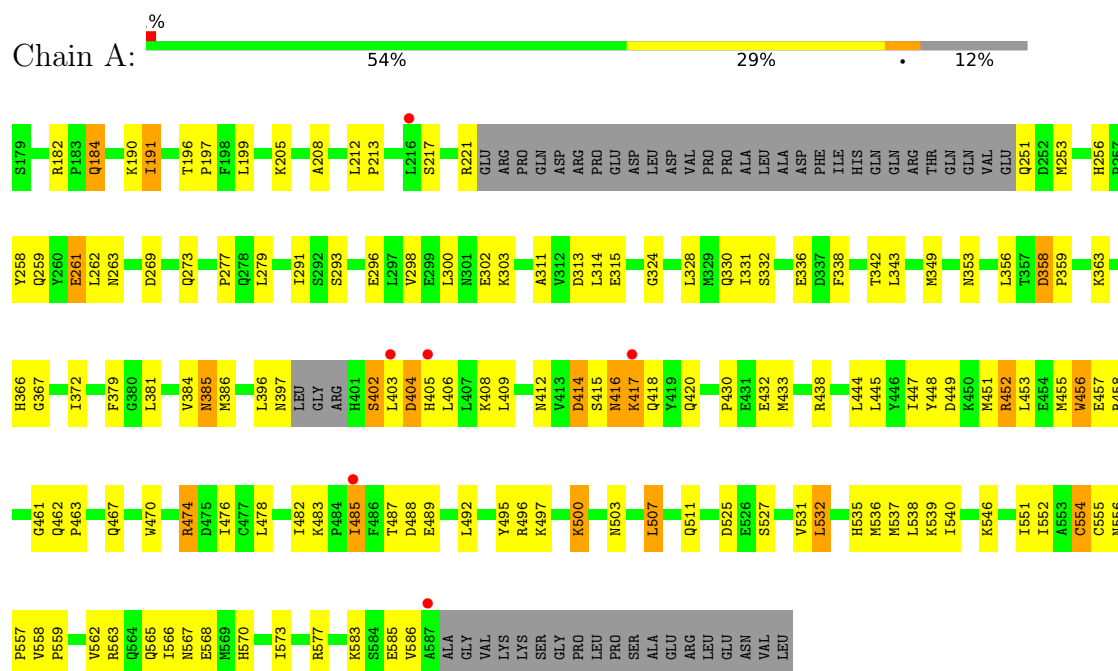
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	134	Total 134	O 134	0	0

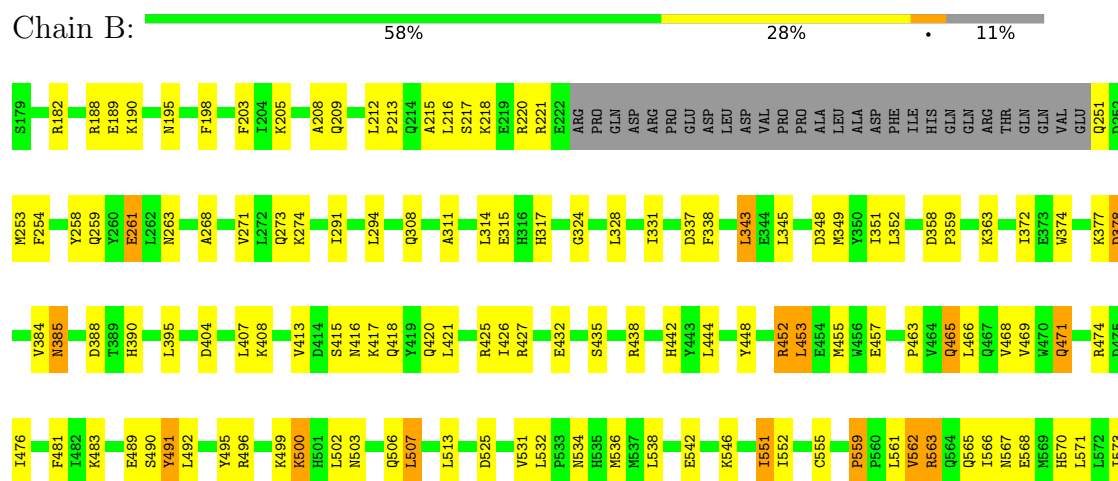
3 Residue-property plots

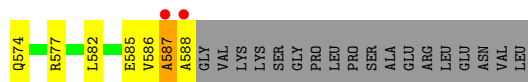
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Exosome component 10



• Molecule 1: Exosome component 10





4 Data and refinement statistics

Property	Value	Source
Space group	P 4	Depositor
Cell constants a, b, c, α , β , γ	141.00Å 141.00Å 58.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.99 – 2.65 24.99 – 2.65	Depositor EDS
% Data completeness (in resolution range)	99.6 (24.99-2.65) 99.5 (24.99-2.65)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.60 (at 2.64Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, R_{free}	0.215 , 0.265 0.212 , 0.272	Depositor DCC
R_{free} test set	1683 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	56.4	Xtriage
Anisotropy	0.644	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 51.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.022 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6506	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 5.62% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: YT3, 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	0.43	0/3208	0.90	13/4343 (0.3%)
1	B	0.45	0/3242	0.92	10/4390 (0.2%)
All	All	0.44	0/6450	0.91	23/8733 (0.3%)

There are no bond length outliers.

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	209	GLN	N-CA-C	-9.28	102.46	113.88
1	A	324	GLY	N-CA-C	-8.53	103.85	111.95
1	A	444	LEU	N-CA-C	6.50	118.37	111.28
1	B	308	GLN	N-CA-C	-6.18	105.57	113.23
1	A	537	MET	N-CA-C	-6.12	104.30	110.97
1	A	343	LEU	N-CA-C	-5.88	103.58	112.04
1	A	456	TRP	N-CA-C	-5.69	105.06	112.23
1	A	358	ASP	CA-C-N	5.60	125.31	119.82
1	A	358	ASP	C-N-CA	5.60	125.31	119.82
1	B	551	ILE	N-CA-C	-5.52	105.34	110.53
1	B	378	ASP	N-CA-C	5.49	120.10	113.41
1	B	324	GLY	N-CA-C	-5.44	106.08	111.85
1	B	562	VAL	N-CA-C	-5.29	105.38	110.72
1	B	452	ARG	N-CA-C	-5.28	105.60	111.36
1	A	256	HIS	CA-C-N	5.28	125.33	119.32
1	A	256	HIS	C-N-CA	5.28	125.33	119.32
1	A	402	SER	N-CA-C	5.23	115.75	108.00
1	B	559	PRO	CA-C-N	5.18	125.47	119.47
1	B	559	PRO	C-N-CA	5.18	125.47	119.47
1	B	343	LEU	N-CA-C	-5.17	105.26	112.45
1	A	404	ASP	N-CA-C	-5.09	105.74	111.28
1	A	452	ARG	N-CA-C	-5.06	106.62	112.89

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	497	LYS	N-CA-C	-5.04	105.23	111.33

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-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 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	3133	0	3123	125	0
1	B	3166	0	3158	101	0
2	A	2	0	0	0	0
2	B	1	0	0	0	0
3	B	2	0	0	0	0
4	A	68	0	0	4	0
4	B	134	0	0	4	0
All	All	6506	0	6281	226	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 18.

All (226) 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:586:VAL:HG23	1:B:587:ALA:H	1.29	0.96
1:A:536:MET:HE3	1:A:555:CYS:HB3	1.50	0.92
1:A:417:LYS:HE3	1:A:420:GLN:OE1	1.69	0.90
1:A:366:HIS:CE1	1:A:402:SER:HB3	2.08	0.89
1:B:188:ARG:HA	1:B:188:ARG:NE	1.91	0.86
1:A:258:TYR:HD1	1:A:261:GLU:HG3	1.43	0.83
1:A:293:SER:OG	1:A:296:GLU:HG2	1.79	0.82
1:A:366:HIS:HE1	1:A:402:SER:HB3	1.47	0.80
1:A:291:ILE:HG23	1:A:296:GLU:HB2	1.63	0.79
1:A:552:ILE:HD13	1:A:563:ARG:CZ	2.16	0.76
1:A:495:TYR:O	1:A:500:LYS:HB2	1.86	0.74
1:A:536:MET:HE1	1:A:559:PRO:HD3	1.67	0.74

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:462:GLN:NE2	1:A:463:PRO:HD2	2.02	0.74
1:A:488:ASP:OD2	1:A:511:GLN:HG2	1.88	0.74
1:A:403:LEU:HA	1:A:406:LEU:HB2	1.71	0.73
1:A:536:MET:HE3	1:A:555:CYS:CB	2.19	0.72
1:B:188:ARG:HA	1:B:188:ARG:HE	1.54	0.71
1:B:586:VAL:HG23	1:B:587:ALA:N	2.05	0.70
1:B:536:MET:HE3	1:B:555:CYS:SG	2.33	0.69
1:B:463:PRO:HG2	1:B:466:LEU:HD22	1.74	0.68
1:B:552:ILE:HD13	1:B:563:ARG:NH2	2.09	0.68
1:A:552:ILE:HG23	1:A:558:VAL:HG21	1.77	0.67
1:B:205:LYS:HG2	1:B:208:ALA:HB2	1.76	0.67
1:A:474:ARG:HH11	1:A:474:ARG:HG2	1.60	0.66
1:A:539:LYS:HG3	1:A:554:CYS:SG	2.34	0.66
1:B:317:HIS:CD2	1:B:425:ARG:HD3	2.31	0.66
1:B:586:VAL:C	1:B:588:ALA:H	2.02	0.66
1:A:191:ILE:H	1:A:191:ILE:HD12	1.61	0.66
1:B:492:LEU:O	1:B:496:ARG:HB2	1.95	0.66
1:A:191:ILE:HD12	1:A:191:ILE:N	2.11	0.65
1:B:315:GLU:OE1	1:B:315:GLU:HA	1.98	0.64
1:A:453:LEU:O	1:A:457:GLU:HG3	1.98	0.63
1:A:540:ILE:HD13	1:A:551:ILE:HG23	1.81	0.63
1:B:536:MET:HE1	1:B:559:PRO:CD	2.29	0.63
1:B:217:SER:HB3	1:B:220:ARG:HB2	1.80	0.62
1:A:396:LEU:HA	1:A:458:ARG:HH12	1.64	0.62
1:A:503:ASN:HB2	1:A:585:GLU:OE1	2.00	0.62
1:B:586:VAL:CG2	1:B:587:ALA:H	2.10	0.62
1:A:496:ARG:HH21	1:A:500:LYS:HE3	1.64	0.61
1:A:495:TYR:CE1	1:A:538:LEU:HD22	2.35	0.61
1:B:536:MET:HE3	1:B:555:CYS:CB	2.30	0.61
1:B:351:ILE:HG13	1:B:352:LEU:N	2.15	0.61
1:B:198:PHE:HB2	1:B:483:LYS:HG2	1.81	0.61
1:A:402:SER:HB2	4:A:164:HOH:O	2.01	0.61
1:A:269:ASP:O	1:A:273:GLN:HG3	2.00	0.61
1:A:196:THR:O	1:A:483:LYS:HD2	2.00	0.60
1:A:559:PRO:HG2	1:A:562:VAL:CG2	2.32	0.60
1:A:205:LYS:HG2	1:A:208:ALA:HB2	1.84	0.60
1:A:463:PRO:O	1:A:467:GLN:HG3	2.02	0.60
1:B:448:TYR:CE1	1:B:452:ARG:HD2	2.36	0.60
1:A:462:GLN:HE21	1:A:463:PRO:HD2	1.67	0.59
1:A:315:GLU:HB2	1:A:328:LEU:HB3	1.84	0.59
1:A:291:ILE:HG23	1:A:296:GLU:CB	2.29	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:496:ARG:O	1:B:499:LYS:HD2	2.04	0.58
1:A:313:ASP:C	1:A:314:LEU:HD12	2.29	0.58
1:B:216:LEU:HA	1:B:221:ARG:HH21	1.68	0.58
1:A:261:GLU:CD	1:A:261:GLU:H	2.12	0.58
1:B:552:ILE:HD13	1:B:563:ARG:HH21	1.68	0.58
1:B:416:ASN:HB3	4:B:76:HOH:O	2.03	0.58
1:A:217:SER:O	1:A:221:ARG:HG3	2.04	0.57
1:A:492:LEU:HD22	1:A:507:LEU:HD11	1.86	0.57
1:A:536:MET:CE	1:A:555:CYS:HB3	2.31	0.57
1:A:448:TYR:O	1:A:452:ARG:HD3	2.04	0.57
1:A:448:TYR:CE1	1:A:452:ARG:HD2	2.40	0.57
1:B:190:LYS:HA	4:B:75:HOH:O	2.04	0.56
1:B:491:TYR:HE2	1:B:534:ASN:ND2	2.03	0.56
1:A:568:GLU:HB2	4:A:176:HOH:O	2.06	0.56
1:A:438:ARG:HD3	4:A:42:HOH:O	2.05	0.56
1:A:342:THR:HG22	1:A:349:MET:HE2	1.87	0.56
1:B:559:PRO:HG2	1:B:562:VAL:CG2	2.36	0.56
1:A:546:LYS:HG3	1:A:577:ARG:NH1	2.21	0.55
1:B:343:LEU:HD12	1:B:427:ARG:HH12	1.72	0.55
1:A:313:ASP:O	1:A:314:LEU:HD12	2.06	0.55
1:A:485:ILE:HD12	1:A:485:ILE:O	2.06	0.55
1:A:353:ASN:HB2	4:A:93:HOH:O	2.07	0.54
1:B:491:TYR:CD1	1:B:491:TYR:N	2.75	0.54
1:B:465:GLN:CD	1:B:465:GLN:H	2.14	0.54
1:B:212:LEU:HD12	1:B:213:PRO:HD2	1.88	0.54
1:A:474:ARG:HH11	1:A:474:ARG:CG	2.20	0.54
1:B:182:ARG:NH2	1:B:525:ASP:O	2.41	0.54
1:B:216:LEU:CA	1:B:221:ARG:HH21	2.21	0.54
1:A:536:MET:HE3	1:A:555:CYS:SG	2.47	0.54
1:B:395:LEU:HD11	1:B:468:VAL:HG12	1.89	0.54
1:B:253:MET:HG3	1:B:254:PHE:CD1	2.43	0.53
1:B:465:GLN:O	1:B:469:VAL:HG23	2.08	0.53
1:B:536:MET:HE3	1:B:555:CYS:HB3	1.89	0.53
1:B:582:LEU:HB2	1:B:585:GLU:HG3	1.89	0.53
1:A:182:ARG:NH2	1:A:525:ASP:O	2.42	0.53
1:B:311:ALA:O	1:B:331:ILE:HA	2.09	0.53
1:A:405:HIS:NE2	1:A:409:LEU:HD22	2.24	0.53
1:B:536:MET:HE1	1:B:559:PRO:HD3	1.91	0.52
1:B:565:GLN:NE2	1:B:568:GLU:OE1	2.42	0.52
1:A:546:LYS:HG3	1:A:577:ARG:HH12	1.75	0.52
1:B:258:TYR:HD1	1:B:261:GLU:HG3	1.75	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:294:LEU:HD13	1:B:348:ASP:HB3	1.92	0.52
1:B:317:HIS:HB2	4:B:11:HOH:O	2.09	0.52
1:B:570:HIS:NE2	1:B:574:GLN:OE1	2.43	0.52
1:B:345:LEU:O	1:B:349:MET:HG2	2.10	0.52
1:A:396:LEU:HA	1:A:458:ARG:NH1	2.25	0.52
1:A:546:LYS:HD2	1:A:577:ARG:HH22	1.75	0.52
1:A:482:ILE:N	1:A:482:ILE:HD12	2.25	0.52
1:A:453:LEU:C	1:A:455:MET:H	2.17	0.51
1:A:303:LYS:NZ	1:A:336:GLU:OE2	2.41	0.51
1:B:404:ASP:OD1	1:B:408:LYS:HE3	2.11	0.51
1:A:552:ILE:HG13	1:A:566:ILE:HD13	1.92	0.51
1:B:259:GLN:HE21	1:B:263:ASN:HD21	1.57	0.51
1:A:451:MET:O	1:A:455:MET:HB2	2.11	0.51
1:A:291:ILE:CD1	1:A:300:LEU:HD22	2.41	0.51
1:A:356:LEU:HD12	1:A:381:LEU:HD22	1.93	0.51
1:A:262:LEU:O	1:A:474:ARG:HD3	2.11	0.50
1:A:384:VAL:O	1:A:385:ASN:HB3	2.10	0.50
1:A:566:ILE:HG23	1:A:567:ASN:N	2.26	0.50
1:A:583:LYS:O	1:A:586:VAL:HG22	2.11	0.50
1:A:300:LEU:HD13	1:A:338:PHE:CD2	2.46	0.50
1:B:213:PRO:HB3	1:B:251:GLN:HB3	1.94	0.50
1:B:432:GLU:CD	1:B:432:GLU:H	2.20	0.49
1:B:420:GLN:O	1:B:421:LEU:HD23	2.13	0.49
1:A:503:ASN:HB2	1:A:585:GLU:CD	2.38	0.49
1:B:377:LYS:HE2	1:B:481:PHE:CZ	2.47	0.49
1:A:408:LYS:HE3	1:A:414:ASP:HB3	1.95	0.49
1:A:536:MET:HE1	1:A:559:PRO:CD	2.40	0.49
1:B:586:VAL:C	1:B:588:ALA:N	2.70	0.48
1:A:366:HIS:CE1	1:A:403:LEU:H	2.31	0.48
1:A:445:LEU:O	1:A:448:TYR:HB3	2.13	0.48
1:B:315:GLU:HB2	1:B:328:LEU:HB3	1.96	0.48
1:A:182:ARG:HB3	1:A:184:GLN:NE2	2.28	0.48
1:A:298:VAL:O	1:A:302:GLU:HG2	2.14	0.48
1:B:217:SER:O	1:B:221:ARG:HG2	2.14	0.48
1:A:366:HIS:CD2	1:A:403:LEU:HB2	2.49	0.48
1:B:261:GLU:H	1:B:261:GLU:CD	2.21	0.47
1:B:448:TYR:CD1	1:B:452:ARG:HD2	2.50	0.47
1:A:430:PRO:HG2	1:A:433:MET:HG3	1.97	0.47
1:B:216:LEU:HD22	1:B:221:ARG:HH22	1.80	0.47
1:A:212:LEU:HD12	1:A:213:PRO:HD2	1.97	0.47
1:A:311:ALA:O	1:A:331:ILE:HA	2.15	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:471:GLN:O	1:B:474:ARG:HG3	2.15	0.47
1:B:551:ILE:HD11	1:B:570:HIS:HA	1.97	0.47
1:A:402:SER:O	1:A:405:HIS:N	2.48	0.47
1:A:363:LYS:HE2	1:A:385:ASN:O	2.15	0.47
1:A:258:TYR:CD1	1:A:261:GLU:HG3	2.34	0.47
1:B:273:GLN:O	1:B:274:LYS:C	2.58	0.47
1:B:363:LYS:HE2	1:B:385:ASN:O	2.15	0.47
1:A:196:THR:CG2	1:A:197:PRO:HD2	2.45	0.46
1:B:337:ASP:OD2	1:B:442:HIS:ND1	2.43	0.46
1:B:377:LYS:HB2	1:B:481:PHE:CD2	2.50	0.46
1:A:372:ILE:HG13	1:A:476:ILE:HG22	1.98	0.46
1:A:496:ARG:HA	1:A:500:LYS:HB2	1.97	0.46
1:A:532:LEU:HD23	1:A:536:MET:HE2	1.98	0.46
1:B:343:LEU:HD12	1:B:427:ARG:NH1	2.30	0.46
1:B:538:LEU:O	1:B:542:GLU:HG3	2.16	0.46
1:A:495:TYR:C	1:A:500:LYS:HB2	2.40	0.46
1:B:358:ASP:OD2	1:B:358:ASP:C	2.59	0.46
1:B:546:LYS:HE2	1:B:577:ARG:NH2	2.31	0.46
1:B:404:ASP:O	1:B:408:LYS:HG3	2.16	0.46
1:A:573:ILE:O	1:A:577:ARG:HG3	2.16	0.45
1:A:474:ARG:CG	1:A:474:ARG:NH1	2.77	0.45
1:A:184:GLN:H	1:A:184:GLN:HE21	1.65	0.45
1:A:199:LEU:CD1	1:A:253:MET:HE3	2.46	0.45
1:B:216:LEU:HD22	1:B:221:ARG:NH2	2.31	0.45
1:A:496:ARG:HB2	1:A:496:ARG:CZ	2.45	0.45
1:A:213:PRO:HB3	1:A:251:GLN:HB3	1.97	0.45
1:A:396:LEU:O	1:A:397:ASN:HB2	2.16	0.45
1:B:291:ILE:HD11	1:B:338:PHE:HD2	1.82	0.45
1:A:535:HIS:NE2	1:A:536:MET:HG3	2.32	0.44
1:A:565:GLN:HA	1:A:565:GLN:HE21	1.83	0.44
1:B:374:TRP:O	1:B:378:ASP:HB2	2.17	0.44
1:B:418:GLN:O	1:B:418:GLN:HG2	2.17	0.44
1:A:300:LEU:HD13	1:A:338:PHE:CE2	2.52	0.44
1:A:184:GLN:NE2	1:A:184:GLN:H	2.15	0.44
1:A:559:PRO:HG2	1:A:562:VAL:HB	2.00	0.44
1:B:395:LEU:HD12	1:B:469:VAL:HG22	1.98	0.44
1:B:502:LEU:HA	1:B:506:GLN:OE1	2.17	0.44
1:A:500:LYS:NZ	1:A:500:LYS:HB3	2.33	0.44
1:B:215:ALA:HA	1:B:220:ARG:HG2	2.00	0.44
1:A:262:LEU:HB2	1:A:478:LEU:HD21	1.99	0.44
1:A:363:LYS:HD3	1:A:363:LYS:N	2.33	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:363:LYS:O	1:A:386:MET:HG2	2.18	0.44
1:A:551:ILE:O	1:A:554:CYS:HB3	2.18	0.43
1:B:203:PHE:HD1	1:B:218:LYS:HG2	1.82	0.43
1:B:388:ASP:OD1	1:B:390:HIS:HB3	2.19	0.43
1:A:205:LYS:O	1:A:208:ALA:HB2	2.19	0.43
1:B:268:ALA:O	1:B:271:VAL:HG22	2.18	0.43
1:B:536:MET:CE	1:B:555:CYS:HB3	2.48	0.43
1:B:551:ILE:HB	1:B:566:ILE:HD11	1.99	0.43
1:B:435:SER:O	1:B:438:ARG:HG2	2.19	0.43
1:A:432:GLU:OE2	1:A:432:GLU:N	2.47	0.43
1:B:502:LEU:HB2	1:B:507:LEU:CD1	2.49	0.43
1:B:571:LEU:HB3	4:B:149:HOH:O	2.19	0.43
1:B:384:VAL:O	1:B:385:ASN:HB3	2.19	0.42
1:A:358:ASP:HA	1:A:359:PRO:HD2	1.88	0.42
1:A:551:ILE:HD11	1:A:570:HIS:HA	2.00	0.42
1:B:455:MET:HE1	1:B:469:VAL:HG21	2.01	0.42
1:B:531:VAL:HG22	1:B:561:LEU:HD12	2.01	0.42
1:B:491:TYR:HD1	1:B:491:TYR:H	1.66	0.42
1:A:565:GLN:HA	1:A:565:GLN:NE2	2.34	0.42
1:A:353:ASN:CG	1:A:381:LEU:HD23	2.45	0.42
1:B:513:LEU:HD21	1:B:573:ILE:HD11	2.02	0.42
1:A:199:LEU:HD11	1:A:253:MET:HE3	2.02	0.41
1:A:277:PRO:HA	1:A:449:ASP:HB3	2.02	0.41
1:B:453:LEU:O	1:B:457:GLU:HG3	2.20	0.41
1:B:372:ILE:HG13	1:B:476:ILE:HG22	2.01	0.41
1:B:495:TYR:HB3	1:B:500:LYS:HB2	2.01	0.41
1:B:503:ASN:OD1	1:B:506:GLN:HG3	2.20	0.41
1:A:485:ILE:HD12	1:A:485:ILE:H	1.85	0.41
1:A:311:ALA:HB3	1:A:332:SER:HB2	2.03	0.41
1:B:407:LEU:CD1	1:B:415:SER:HB3	2.50	0.41
1:A:447:ILE:O	1:A:451:MET:HG3	2.21	0.41
1:B:358:ASP:HA	1:B:359:PRO:HD2	1.89	0.41
1:A:556:ASN:HA	1:A:557:PRO:HA	1.88	0.41
1:B:408:LYS:HG2	1:B:413:VAL:O	2.20	0.41
1:A:291:ILE:HD12	1:A:300:LEU:HD22	2.01	0.41
1:B:417:LYS:HE2	1:B:420:GLN:HG2	2.03	0.41
1:B:426:ILE:O	1:B:426:ILE:HG23	2.21	0.41
1:A:259:GLN:O	1:A:263:ASN:ND2	2.54	0.41
1:A:496:ARG:NH2	1:A:500:LYS:HE3	2.35	0.41
1:A:527:SER:O	1:A:531:VAL:HG23	2.21	0.41
1:B:420:GLN:C	1:B:421:LEU:HD23	2.46	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:190:LYS:HG3	1:A:191:ILE:N	2.36	0.40
1:B:489:GLU:O	1:B:490:SER:C	2.64	0.40
1:B:566:ILE:HG23	1:B:567:ASN:N	2.36	0.40
1:B:573:ILE:O	1:B:577:ARG:HG3	2.21	0.40
1:A:456:TRP:CE2	1:A:461:GLY:HA2	2.57	0.40
1:A:487:THR:HB	1:A:489:GLU:OE1	2.21	0.40
1:A:342:THR:HB	1:A:379:PHE:CZ	2.57	0.40
1:A:402:SER:HB3	1:A:403:LEU:H	1.69	0.40
1:A:416:ASN:C	1:A:418:GLN:H	2.29	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	371/428 (87%)	338 (91%)	27 (7%)	6 (2%)	7	12
1	B	378/428 (88%)	358 (95%)	18 (5%)	2 (0%)	24	39
All	All	749/856 (88%)	696 (93%)	45 (6%)	8 (1%)	11	19

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	417	LYS
1	A	385	ASN
1	B	587	ALA
1	A	416	ASN
1	A	554	CYS
1	B	385	ASN
1	A	415	SER
1	A	367	GLY

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	350/394 (89%)	336 (96%)	14 (4%)	28	47
1	B	352/394 (89%)	339 (96%)	13 (4%)	30	50
All	All	702/788 (89%)	675 (96%)	27 (4%)	29	49

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	184	GLN
1	A	191	ILE
1	A	261	GLU
1	A	279	LEU
1	A	330	GLN
1	A	404	ASP
1	A	412	ASN
1	A	414	ASP
1	A	470	TRP
1	A	474	ARG
1	A	485	ILE
1	A	500	LYS
1	A	507	LEU
1	A	532	LEU
1	B	189	GLU
1	B	195	ASN
1	B	261	GLU
1	B	314	LEU
1	B	444	LEU
1	B	453	LEU
1	B	465	GLN
1	B	471	GLN
1	B	491	TYR
1	B	500	LYS
1	B	507	LEU
1	B	532	LEU
1	B	563	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	184	GLN
1	A	209	GLN
1	A	251	GLN
1	A	263	ASN
1	A	278	GLN
1	A	316	HIS
1	A	412	ASN
1	A	418	GLN
1	A	462	GLN
1	A	498	GLN
1	A	511	GLN
1	A	564	GLN
1	A	565	GLN
1	A	570	HIS
1	B	263	ASN
1	B	278	GLN
1	B	412	ASN
1	B	418	GLN
1	B	467	GLN
1	B	505	GLN
1	B	549	GLN
1	B	564	GLN
1	B	565	GLN

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

Of 5 ligands modelled in this entry, 5 are 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

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	377/428 (88%)	0.09	6 (1%) 70 66	46, 74, 105, 120	0
1	B	382/428 (89%)	-0.25	2 (0%) 87 85	37, 58, 96, 116	0
All	All	759/856 (88%)	-0.08	8 (1%) 78 75	37, 66, 104, 120	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	403	LEU	4.2
1	B	588	ALA	3.4
1	B	587	ALA	3.0
1	A	417	LYS	2.7
1	A	405	HIS	2.4
1	A	485	ILE	2.3
1	A	587	ALA	2.3
1	A	216	LEU	2.1

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(Å ²)	Q<0.9
3	MG	B	2	1/1	0.76	0.16	62,62,62,62	0
3	MG	B	1	1/1	0.80	0.18	74,74,74,74	0
2	YT3	A	1	1/1	0.95	0.06	100,100,100,100	0
2	YT3	A	3	1/1	0.99	0.06	75,75,75,75	0
2	YT3	B	607	1/1	1.00	0.03	59,59,59,59	0

6.5 Other polymers [i](#)

There are no such residues in this entry.