



Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 08:27 am BST

PDB ID : 3APM
Title : Crystal structure of the human SNP PAD4 protein
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Deposited on : 2010-10-19
Resolution : 2.50 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

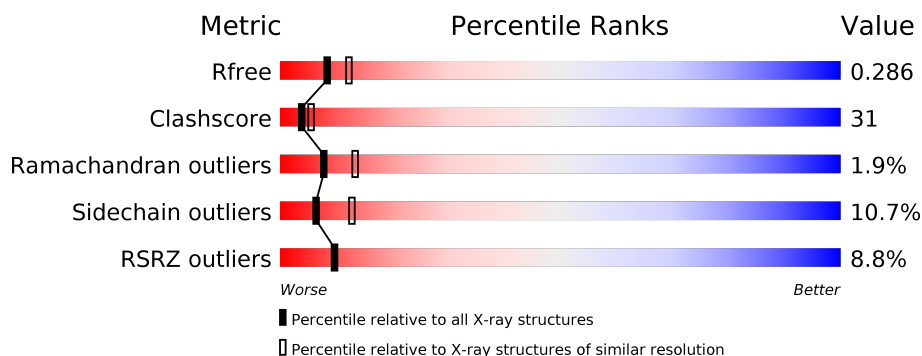
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 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	666	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 4383 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 Protein-arginine deiminase type-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	559	Total	C	N	O	S	0	0	0
			4383	2806	738	809	30			

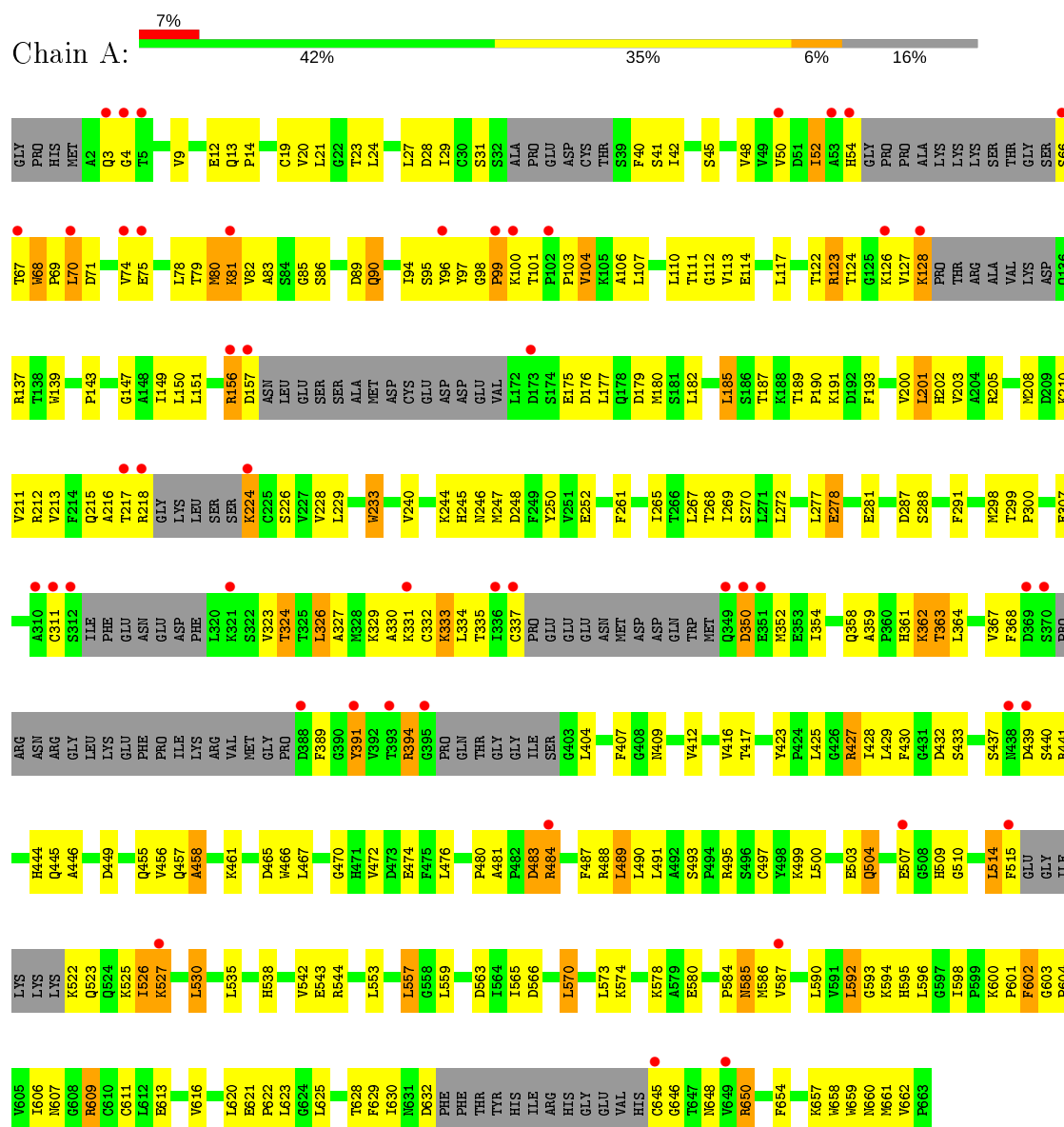
There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	EXPRESSION TAG	UNP Q9UM07
A	-1	PRO	-	EXPRESSION TAG	UNP Q9UM07
A	0	HIS	-	EXPRESSION TAG	UNP Q9UM07

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Protein-arginine deiminase type-4



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	145.56Å 61.24Å 113.47Å 90.00° 123.85° 90.00°	Depositor
Resolution (Å)	30.00 – 2.50 28.20 – 2.50	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-2.50) 99.8 (28.20-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.18 (at 2.51Å)	Xtriage
Refinement program	CNS 1.21	Depositor
R, R_{free}	0.260 , 0.287 0.261 , 0.286	Depositor DCC
R_{free} test set	1469 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	54.6	Xtriage
Anisotropy	0.528	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 41.3	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	0.92	EDS
Total number of atoms	4383	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.58% 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	0.44	0/4479	0.69	0/6069

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	4383	0	4390	270	0
All	All	4383	0	4390	270	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 31.

All (270) 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:96:TYR:HB2	1:A:104:VAL:HG12	1.33	1.10
1:A:52:ILE:HG23	1:A:66:SER:HA	1.39	1.05
1:A:488:ARG:HH21	1:A:623:LEU:HD21	1.19	1.05
1:A:354:ILE:HG21	1:A:650:ARG:HG2	1.43	1.00
1:A:45:SER:HB2	1:A:90:GLN:HG3	1.44	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:609:ARG:HH11	1:A:609:ARG:HG2	1.29	0.94
1:A:650:ARG:HH11	1:A:650:ARG:HG3	1.31	0.92
1:A:81:LYS:HG3	1:A:82:VAL:HG23	1.53	0.89
1:A:333:LYS:HG3	1:A:334:LEU:N	1.87	0.88
1:A:20:VAL:O	1:A:23:THR:HG22	1.77	0.84
1:A:48:VAL:HG23	1:A:90:GLN:HG2	1.60	0.83
1:A:27:LEU:HD22	1:A:78:LEU:HD11	1.60	0.82
1:A:42:ILE:HG21	1:A:50:VAL:HG11	1.63	0.81
1:A:404:LEU:HD13	1:A:432:ASP:HA	1.62	0.81
1:A:54:HIS:CD2	1:A:67:THR:HG21	2.15	0.81
1:A:277:LEU:HD12	1:A:277:LEU:H	1.47	0.78
1:A:151:LEU:HD21	1:A:359:ALA:HB2	1.66	0.77
1:A:45:SER:CB	1:A:90:GLN:HG3	2.14	0.76
1:A:128:LYS:HE2	1:A:128:LYS:H	1.50	0.75
1:A:609:ARG:HH11	1:A:609:ARG:CG	1.99	0.74
1:A:19:CYS:HB2	1:A:80:MET:CE	2.17	0.74
1:A:445:GLN:HE21	1:A:449:ASP:CG	1.91	0.73
1:A:585:ASN:HD21	1:A:587:VAL:HG12	1.52	0.73
1:A:96:TYR:CB	1:A:104:VAL:HG12	2.16	0.72
1:A:52:ILE:HG23	1:A:66:SER:CA	2.17	0.72
1:A:590:LEU:HD21	1:A:592:LEU:HD13	1.71	0.72
1:A:298:MET:HB3	1:A:412:VAL:HG21	1.71	0.72
1:A:416:VAL:HG21	1:A:557:LEU:O	1.90	0.72
1:A:484:ARG:HB2	1:A:488:ARG:HH12	1.54	0.71
1:A:488:ARG:NH2	1:A:623:LEU:HD21	2.03	0.71
1:A:179:ASP:CG	1:A:362:LYS:HZ1	1.94	0.70
1:A:488:ARG:HH21	1:A:623:LEU:CD2	2.02	0.70
1:A:52:ILE:CG2	1:A:66:SER:HA	2.20	0.70
1:A:585:ASN:ND2	1:A:587:VAL:HG12	2.06	0.69
1:A:137:ARG:NE	1:A:137:ARG:HA	2.08	0.68
1:A:201:LEU:HD13	1:A:229:LEU:CD1	2.23	0.68
1:A:350:ASP:OD1	1:A:646:GLY:HA2	1.94	0.68
1:A:216:ALA:HB3	1:A:248:ASP:HB2	1.77	0.67
1:A:650:ARG:HH11	1:A:650:ARG:CG	2.07	0.67
1:A:361:HIS:O	1:A:362:LYS:HB2	1.96	0.66
1:A:311:CYS:HA	1:A:337:CYS:SG	2.36	0.66
1:A:298:MET:CE	1:A:428:ILE:HD12	2.25	0.66
1:A:54:HIS:HD2	1:A:67:THR:HG21	1.58	0.66
1:A:499:LYS:O	1:A:503:GLU:HG3	1.95	0.65
1:A:150:LEU:HG	1:A:291:PHE:HB3	1.79	0.65
1:A:215:GLN:HE21	1:A:228:VAL:HG11	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:68:TRP:HD1	1:A:97:TYR:OH	1.80	0.65
1:A:596:LEU:HD21	1:A:625:LEU:HD12	1.78	0.65
1:A:67:THR:C	1:A:68:TRP:HE3	2.00	0.65
1:A:538:HIS:HD2	1:A:573:LEU:H	1.43	0.65
1:A:211:VAL:HB	1:A:265:ILE:HD13	1.80	0.64
1:A:122:THR:OG1	1:A:124:THR:HG22	1.97	0.64
1:A:128:LYS:N	1:A:128:LYS:HE2	2.14	0.63
1:A:48:VAL:HG23	1:A:90:GLN:CG	2.28	0.63
1:A:620:LEU:O	1:A:623:LEU:HB2	2.00	0.62
1:A:13:GLN:HB2	1:A:14:PRO:HD2	1.81	0.61
1:A:404:LEU:CD1	1:A:432:ASP:HA	2.29	0.61
1:A:68:TRP:CD1	1:A:97:TYR:OH	2.53	0.61
1:A:601:PRO:O	1:A:603:GLY:N	2.34	0.61
1:A:334:LEU:HD13	1:A:335:THR:N	2.15	0.61
1:A:484:ARG:HB2	1:A:488:ARG:NH1	2.16	0.61
1:A:650:ARG:HG3	1:A:650:ARG:NH1	2.10	0.60
1:A:268:THR:HA	1:A:288:SER:HB3	1.83	0.60
1:A:590:LEU:CD2	1:A:592:LEU:HD13	2.32	0.60
1:A:298:MET:HE1	1:A:428:ILE:HD12	1.84	0.60
1:A:85:GLY:N	1:A:89:ASP:OD1	2.35	0.59
1:A:201:LEU:HD13	1:A:229:LEU:HD12	1.85	0.59
1:A:126:LYS:NZ	1:A:126:LYS:HB3	2.17	0.59
1:A:86:SER:O	1:A:89:ASP:OD2	2.20	0.59
1:A:613:GLU:HG3	1:A:629:PHE:CE1	2.37	0.59
1:A:19:CYS:HB2	1:A:80:MET:HE1	1.84	0.59
1:A:481:ALA:HB3	1:A:487:PHE:N	2.19	0.58
1:A:493:SER:HB2	1:A:566:ASP:HB3	1.86	0.58
1:A:52:ILE:HD13	1:A:52:ILE:C	2.23	0.58
1:A:609:ARG:NH1	1:A:609:ARG:CG	2.64	0.58
1:A:277:LEU:HD12	1:A:277:LEU:N	2.17	0.58
1:A:368:PHE:CD2	1:A:407:PHE:HE1	2.22	0.58
1:A:203:VAL:HG22	1:A:267:LEU:HD23	1.86	0.58
1:A:156:ARG:C	1:A:156:ARG:HD2	2.24	0.58
1:A:441:ARG:HH11	1:A:441:ARG:HG3	1.69	0.58
1:A:444:HIS:HD2	1:A:446:ALA:HB3	1.69	0.57
1:A:114:GLU:O	1:A:187:THR:HA	2.04	0.57
1:A:553:LEU:O	1:A:557:LEU:HB2	2.05	0.57
1:A:137:ARG:HE	1:A:137:ARG:HA	1.68	0.57
1:A:19:CYS:HB2	1:A:80:MET:HE2	1.86	0.57
1:A:327:ALA:O	1:A:330:ALA:HB3	2.04	0.57
1:A:466:TRP:CZ3	1:A:542:VAL:HG13	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:201:LEU:HD13	1:A:229:LEU:HD11	1.87	0.56
1:A:489:LEU:HD12	1:A:559:LEU:CD1	2.35	0.56
1:A:354:ILE:CG2	1:A:650:ARG:HG2	2.26	0.56
1:A:445:GLN:NE2	1:A:449:ASP:OD1	2.38	0.56
1:A:326:LEU:HD13	1:A:592:LEU:HD23	1.88	0.55
1:A:278:GLU:HA	1:A:278:GLU:OE1	2.06	0.55
1:A:428:ILE:HG12	1:A:457:GLN:HB3	1.88	0.55
1:A:71:ASP:O	1:A:74:VAL:HG12	2.06	0.55
1:A:661:MET:HG2	1:A:662:VAL:H	1.72	0.55
1:A:139:TRP:CD1	1:A:147:GLY:HA3	2.42	0.55
1:A:514:LEU:HD22	1:A:515:PHE:CD1	2.42	0.54
1:A:362:LYS:HE3	1:A:364:LEU:HB2	1.89	0.54
1:A:52:ILE:HD12	1:A:67:THR:N	2.23	0.54
1:A:3:GLN:HG3	1:A:4:GLY:N	2.23	0.54
1:A:467:LEU:HD13	1:A:474:GLU:HB2	1.89	0.53
1:A:594:LYS:HG2	1:A:595:HIS:HD2	1.73	0.53
1:A:68:TRP:N	1:A:69:PRO:CD	2.72	0.53
1:A:202:HIS:HE1	1:A:270:SER:OG	1.91	0.53
1:A:267:LEU:HD12	1:A:291:PHE:HE1	1.73	0.53
1:A:151:LEU:CD2	1:A:359:ALA:HB2	2.37	0.53
1:A:68:TRP:HE3	1:A:68:TRP:N	2.07	0.53
1:A:216:ALA:HB2	1:A:250:TYR:HE1	1.74	0.52
1:A:78:LEU:O	1:A:79:THR:HG23	2.09	0.52
1:A:504:GLN:OE1	1:A:606:ILE:HG12	2.09	0.52
1:A:632:ASP:OD2	1:A:645:CYS:HB2	2.09	0.52
1:A:4:GLY:HA3	1:A:24:LEU:O	2.10	0.52
1:A:42:ILE:CD1	1:A:94:ILE:HD12	2.39	0.52
1:A:272:LEU:HD13	1:A:281:GLU:CD	2.30	0.51
1:A:29:ILE:O	1:A:96:TYR:OH	2.27	0.51
1:A:40:PHE:HB3	1:A:70:LEU:HD23	1.93	0.51
1:A:358:GLN:HE21	1:A:658:TRP:HD1	1.57	0.51
1:A:497:CYS:HB3	1:A:570:LEU:HD13	1.92	0.51
1:A:510:GLY:HA2	1:A:526:ILE:HG23	1.91	0.51
1:A:600:LYS:HB2	1:A:630:ILE:O	2.11	0.51
1:A:333:LYS:HG3	1:A:334:LEU:H	1.73	0.51
1:A:52:ILE:HD11	1:A:67:THR:OG1	2.10	0.51
1:A:604:PRO:HB2	1:A:611:CYS:SG	2.51	0.51
1:A:433:SER:HB3	1:A:465:ASP:OD1	2.11	0.50
1:A:127:VAL:HG11	1:A:182:LEU:HD23	1.93	0.50
1:A:625:LEU:N	1:A:625:LEU:HD22	2.26	0.50
1:A:598:ILE:O	1:A:629:PHE:HA	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:657:LYS:HB3	1:A:659:TRP:CE2	2.46	0.50
1:A:299:THR:HG23	1:A:299:THR:O	2.12	0.50
1:A:123:ARG:HD2	1:A:147:GLY:O	2.12	0.50
1:A:467:LEU:CD1	1:A:474:GLU:HB2	2.42	0.50
1:A:493:SER:CB	1:A:566:ASP:HB3	2.42	0.50
1:A:156:ARG:HG3	1:A:156:ARG:HH11	1.76	0.49
1:A:28:ASP:OD2	1:A:31:SER:HB3	2.12	0.49
1:A:67:THR:C	1:A:68:TRP:CE3	2.84	0.49
1:A:124:THR:HG21	1:A:126:LYS:NZ	2.28	0.49
1:A:354:ILE:HD12	1:A:354:ILE:N	2.27	0.49
1:A:68:TRP:H	1:A:69:PRO:HD3	1.77	0.49
1:A:489:LEU:HD23	1:A:490:LEU:N	2.26	0.49
1:A:267:LEU:HD12	1:A:291:PHE:CE1	2.48	0.49
1:A:427:ARG:O	1:A:429:LEU:HD13	2.13	0.49
1:A:149:ILE:HD13	1:A:659:TRP:CE3	2.48	0.49
1:A:96:TYR:O	1:A:103:PRO:HA	2.12	0.49
1:A:323:VAL:HG13	1:A:324:THR:N	2.28	0.49
1:A:412:VAL:HG13	1:A:428:ILE:HD13	1.94	0.49
1:A:52:ILE:HA	1:A:75:GLU:O	2.12	0.48
1:A:113:VAL:HB	1:A:189:THR:HG22	1.95	0.48
1:A:362:LYS:HD2	1:A:363:THR:N	2.28	0.48
1:A:298:MET:SD	1:A:412:VAL:HG22	2.53	0.48
1:A:457:GLN:O	1:A:458:ALA:C	2.50	0.48
1:A:527:LYS:C	1:A:527:LYS:HD3	2.33	0.48
1:A:362:LYS:HE3	1:A:364:LEU:HD12	1.94	0.48
1:A:625:LEU:HD22	1:A:625:LEU:H	1.78	0.48
1:A:212:ARG:HG2	1:A:212:ARG:HH11	1.78	0.48
1:A:368:PHE:CD2	1:A:407:PHE:CE1	3.02	0.48
1:A:41:SER:HB2	1:A:95:SER:HB2	1.95	0.48
1:A:14:PRO:HB3	1:A:107:LEU:HB2	1.96	0.48
1:A:190:PRO:HG2	1:A:193:PHE:HB2	1.96	0.47
1:A:480:PRO:HG2	1:A:593:GLY:O	2.14	0.47
1:A:277:LEU:H	1:A:277:LEU:CD1	2.21	0.47
1:A:514:LEU:HD23	1:A:603:GLY:HA2	1.96	0.47
1:A:21:LEU:HD21	1:A:82:VAL:HA	1.95	0.47
1:A:487:PHE:C	1:A:487:PHE:CD1	2.88	0.47
1:A:526:ILE:O	1:A:530:LEU:HD22	2.14	0.47
1:A:489:LEU:HD22	1:A:491:LEU:HG	1.97	0.47
1:A:495:ARG:HB2	1:A:543:GLU:OE2	2.14	0.47
1:A:621:GLU:C	1:A:623:LEU:H	2.17	0.47
1:A:176:ASP:O	1:A:177:LEU:HD23	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:143:PRO:HA	1:A:660:ASN:ND2	2.30	0.47
1:A:156:ARG:NH1	1:A:156:ARG:HG3	2.31	0.46
1:A:212:ARG:HB3	1:A:252:GLU:HG3	1.96	0.46
1:A:594:LYS:HG3	1:A:594:LYS:O	2.15	0.46
1:A:307:GLU:OE2	1:A:333:LYS:HE2	2.15	0.46
1:A:441:ARG:NH1	1:A:441:ARG:HG3	2.30	0.46
1:A:80:MET:HG2	1:A:112:GLY:HA3	1.97	0.46
1:A:217:THR:HG21	1:A:224:LYS:NZ	2.31	0.46
1:A:13:GLN:HB2	1:A:14:PRO:CD	2.45	0.46
1:A:423:TYR:CD2	1:A:427:ARG:HD2	2.50	0.46
1:A:394:ARG:HB2	1:A:394:ARG:NH1	2.31	0.46
1:A:476:LEU:HA	1:A:490:LEU:O	2.16	0.46
1:A:661:MET:HG2	1:A:662:VAL:N	2.31	0.46
1:A:217:THR:HG21	1:A:224:LYS:HZ1	1.80	0.45
1:A:650:ARG:CG	1:A:650:ARG:NH1	2.70	0.45
1:A:80:MET:HE3	1:A:112:GLY:N	2.31	0.45
1:A:151:LEU:HD21	1:A:359:ALA:CB	2.43	0.45
1:A:203:VAL:HG23	1:A:229:LEU:HD13	1.98	0.45
1:A:82:VAL:HG12	1:A:83:ALA:N	2.31	0.45
1:A:200:VAL:CG1	1:A:270:SER:HB2	2.47	0.45
1:A:362:LYS:HD2	1:A:363:THR:C	2.37	0.45
1:A:80:MET:HE2	1:A:112:GLY:HA2	1.98	0.45
1:A:354:ILE:HG21	1:A:650:ARG:CG	2.28	0.45
1:A:586:MET:SD	1:A:601:PRO:HG3	2.56	0.45
1:A:68:TRP:N	1:A:69:PRO:HD3	2.32	0.45
1:A:216:ALA:HB2	1:A:250:TYR:CE1	2.52	0.45
1:A:300:PRO:HG3	1:A:654:PHE:HZ	1.82	0.45
1:A:409:ASN:OD1	1:A:472:VAL:HG13	2.17	0.45
1:A:98:GLY:HA3	1:A:99:PRO:HD2	1.75	0.44
1:A:368:PHE:HE1	1:A:394:ARG:H	1.65	0.44
1:A:185:LEU:O	1:A:246:ASN:HA	2.17	0.44
1:A:3:GLN:HG3	1:A:4:GLY:H	1.80	0.44
1:A:218:ARG:HA	1:A:218:ARG:NE	2.33	0.44
1:A:269:ILE:HG22	1:A:287:ASP:O	2.18	0.44
1:A:394:ARG:HB2	1:A:394:ARG:CZ	2.48	0.44
1:A:525:LYS:C	1:A:527:LYS:H	2.22	0.44
1:A:68:TRP:CE3	1:A:68:TRP:N	2.85	0.44
1:A:80:MET:HE3	1:A:111:THR:C	2.38	0.44
1:A:80:MET:HE1	1:A:110:LEU:HB3	2.00	0.43
1:A:613:GLU:HG3	1:A:629:PHE:CZ	2.53	0.43
1:A:425:LEU:HD12	1:A:456:VAL:HG22	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:484:ARG:HG2	1:A:563:ASP:OD1	2.18	0.43
1:A:660:ASN:HD22	1:A:660:ASN:HA	1.67	0.43
1:A:476:LEU:C	1:A:476:LEU:HD12	2.39	0.43
1:A:127:VAL:HG23	1:A:127:VAL:O	2.19	0.43
1:A:437:SER:HB2	1:A:440:SER:OG	2.19	0.43
1:A:245:HIS:CG	1:A:246:ASN:N	2.86	0.43
1:A:240:VAL:HG22	1:A:247:MET:CE	2.49	0.43
1:A:404:LEU:CD2	1:A:470:GLY:O	2.67	0.43
1:A:210:LYS:HD2	1:A:261:PHE:CE1	2.54	0.43
1:A:394:ARG:HA	1:A:394:ARG:HH11	1.84	0.43
1:A:538:HIS:CD2	1:A:573:LEU:HB2	2.54	0.43
1:A:81:LYS:HE3	1:A:81:LYS:HA	1.99	0.43
1:A:354:ILE:HG13	1:A:367:VAL:HG22	2.01	0.42
1:A:523:GLN:HG2	1:A:523:GLN:H	1.64	0.42
1:A:621:GLU:N	1:A:622:PRO:HD2	2.34	0.42
1:A:367:VAL:HG23	1:A:389:PHE:HD2	1.83	0.42
1:A:211:VAL:HG22	1:A:212:ARG:N	2.34	0.42
1:A:354:ILE:HD12	1:A:354:ILE:H	1.83	0.42
1:A:82:VAL:CG1	1:A:83:ALA:N	2.83	0.42
1:A:94:ILE:HB	1:A:106:ALA:HB3	2.01	0.42
1:A:427:ARG:NH1	1:A:458:ALA:O	2.52	0.42
1:A:574:LYS:HG3	1:A:580:GLU:CD	2.40	0.42
1:A:574:LYS:HG3	1:A:580:GLU:OE2	2.18	0.42
1:A:658:TRP:NE1	1:A:659:TRP:HE3	2.18	0.42
1:A:205:ARG:O	1:A:208:MET:HG2	2.20	0.42
1:A:430:PHE:CZ	1:A:461:LYS:HG2	2.55	0.42
1:A:590:LEU:CD2	1:A:592:LEU:HD22	2.49	0.42
1:A:127:VAL:CG1	1:A:182:LEU:HD23	2.50	0.41
1:A:9:VAL:HG21	1:A:94:ILE:HG13	2.02	0.41
1:A:177:LEU:HD22	1:A:180:MET:SD	2.60	0.41
1:A:483:ASP:OD1	1:A:488:ARG:NH2	2.53	0.41
1:A:224:LYS:N	1:A:224:LYS:HD3	2.34	0.41
1:A:391:TYR:CD1	1:A:391:TYR:N	2.88	0.41
1:A:427:ARG:HH11	1:A:427:ARG:CG	2.32	0.41
1:A:514:LEU:O	1:A:515:PHE:CB	2.68	0.41
1:A:416:VAL:HG22	1:A:417:THR:N	2.34	0.41
1:A:86:SER:HA	1:A:190:PRO:HB3	2.03	0.41
1:A:213:VAL:O	1:A:228:VAL:HG22	2.19	0.41
1:A:210:LYS:HD2	1:A:261:PHE:CD1	2.55	0.41
1:A:326:LEU:HD22	1:A:326:LEU:O	2.20	0.41
1:A:488:ARG:HG2	1:A:565:ILE:CG1	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:509:HIS:CD2	1:A:606:ILE:HG13	2.56	0.41
1:A:621:GLU:C	1:A:623:LEU:N	2.74	0.41
1:A:97:TYR:CB	1:A:103:PRO:HG3	2.51	0.41
1:A:126:LYS:HZ2	1:A:126:LYS:HB3	1.86	0.41
1:A:586:MET:SD	1:A:616:VAL:HG21	2.61	0.41
1:A:298:MET:HB2	1:A:298:MET:HE3	1.90	0.41
1:A:514:LEU:HD23	1:A:602:PHE:O	2.21	0.41
1:A:97:TYR:HB3	1:A:103:PRO:HG3	2.02	0.41
1:A:354:ILE:CD1	1:A:648:ASN:HB3	2.51	0.41
1:A:525:LYS:C	1:A:527:LYS:N	2.74	0.41
1:A:488:ARG:HG2	1:A:565:ILE:HG12	2.03	0.41
1:A:590:LEU:HD21	1:A:592:LEU:HD22	2.03	0.41
1:A:326:LEU:HD21	1:A:595:HIS:HB3	2.02	0.41
1:A:358:GLN:OE1	1:A:657:LYS:HD3	2.21	0.40
1:A:123:ARG:HG2	1:A:659:TRP:CD1	2.56	0.40
1:A:233:TRP:N	1:A:233:TRP:CD1	2.89	0.40
1:A:514:LEU:O	1:A:515:PHE:HB2	2.22	0.40
1:A:330:ALA:O	1:A:331:LYS:HB2	2.21	0.40
1:A:441:ARG:HH12	1:A:578:LYS:HE3	1.85	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	535/666 (80%)	488 (91%)	37 (7%)	10 (2%)	8 13

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	99	PRO
1	A	455	GLN

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Mol	Chain	Res	Type
1	A	484	ARG
1	A	12	GLU
1	A	458	ALA
1	A	602	PHE
1	A	191	LYS
1	A	362	LYS
1	A	584	PRO
1	A	526	ILE

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	497/590 (84%)	444 (89%)	53 (11%)	6 13

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	52	ILE
1	A	68	TRP
1	A	70	LEU
1	A	80	MET
1	A	81	LYS
1	A	90	GLN
1	A	100	LYS
1	A	101	THR
1	A	104	VAL
1	A	117	LEU
1	A	123	ARG
1	A	128	LYS
1	A	156	ARG
1	A	157	ASP
1	A	175	GLU
1	A	185	LEU
1	A	201	LEU
1	A	224	LYS

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Mol	Chain	Res	Type
1	A	226	SER
1	A	233	TRP
1	A	244	LYS
1	A	278	GLU
1	A	324	THR
1	A	326	LEU
1	A	329	LYS
1	A	332	CYS
1	A	333	LYS
1	A	350	ASP
1	A	352	MET
1	A	363	THR
1	A	391	TYR
1	A	394	ARG
1	A	427	ARG
1	A	439	ASP
1	A	483	ASP
1	A	489	LEU
1	A	500	LEU
1	A	504	GLN
1	A	507	GLU
1	A	514	LEU
1	A	522	LYS
1	A	527	LYS
1	A	530	LEU
1	A	535	LEU
1	A	544	ARG
1	A	557	LEU
1	A	570	LEU
1	A	585	ASN
1	A	592	LEU
1	A	607	ASN
1	A	609	ARG
1	A	628	THR
1	A	650	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	GLN
1	A	54	HIS
1	A	90	GLN

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Mol	Chain	Res	Type
1	A	197	HIS
1	A	202	HIS
1	A	215	GLN
1	A	358	GLN
1	A	444	HIS
1	A	445	GLN
1	A	448	GLN
1	A	455	GLN
1	A	471	HIS
1	A	505	GLN
1	A	506	ASN
1	A	524	GLN
1	A	538	HIS
1	A	585	ASN
1	A	595	HIS
1	A	607	ASN
1	A	660	ASN

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 carbohydrates 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 ⓘ

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	559/666 (83%)	0.38	49 (8%) 10 10	35, 63, 102, 113	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	156	ARG	5.5
1	A	67	THR	5.3
1	A	128	LYS	5.3
1	A	66	SER	5.2
1	A	350	ASP	4.9
1	A	157	ASP	4.9
1	A	311	CYS	4.5
1	A	102	PRO	4.4
1	A	395	GLY	4.3
1	A	217	THR	4.3
1	A	349	GLN	4.1
1	A	439	ASP	4.0
1	A	96	TYR	4.0
1	A	645	CYS	3.9
1	A	312	SER	3.9
1	A	224	LYS	3.8
1	A	81	LYS	3.2
1	A	50	VAL	3.1
1	A	54	HIS	3.1
1	A	99	PRO	3.0
1	A	515	PHE	2.9
1	A	74	VAL	2.8
1	A	337	CYS	2.8
1	A	370	SER	2.6
1	A	218	ARG	2.6
1	A	507	GLU	2.6
1	A	527	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	388	ASP	2.4
1	A	5	THR	2.4
1	A	391	TYR	2.4
1	A	75	GLU	2.4
1	A	393	THR	2.4
1	A	438	ASN	2.3
1	A	3	GLN	2.3
1	A	351	GLU	2.3
1	A	173	ASP	2.2
1	A	321	LYS	2.2
1	A	331	LYS	2.1
1	A	310	ALA	2.1
1	A	126	LYS	2.1
1	A	649	VAL	2.1
1	A	484	ARG	2.1
1	A	100	LYS	2.1
1	A	53	ALA	2.0
1	A	369	ASP	2.0
1	A	336	ILE	2.0
1	A	587	VAL	2.0
1	A	4	GLY	2.0
1	A	70	LEU	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 ⓘ

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.