



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 03:38 AM UTC

PDB ID : 9H9A / pdb_00009h9a
Title : native structure of the full-length pesticidal protein Cry8Ba2, from crystals formed in vivo (form 1)
Authors : Williamson, L.J.; Best, H.L.; Galchenkova, M.; Rizkallah, P.J.; Oberthur, D.; Berry, C.
Deposited on : 2024-10-30
Resolution : 2.27 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

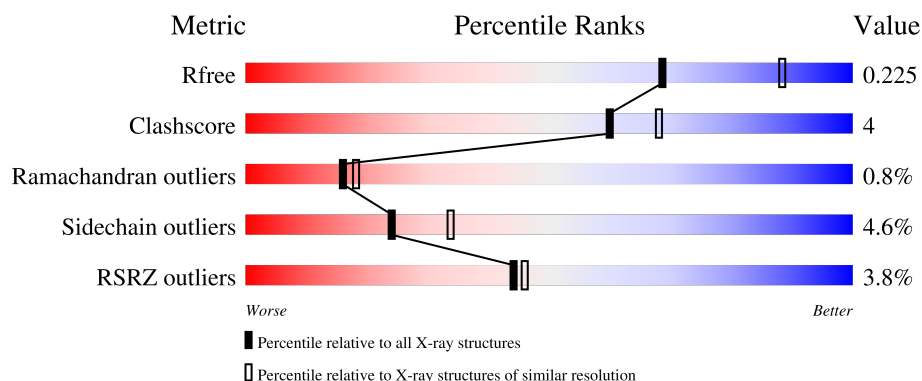
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.27 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	9078 (2.30-2.26)
Clashscore	190562	9802 (2.30-2.26)
Ramachandran outliers	187476	9690 (2.30-2.26)
Sidechain outliers	187428	9691 (2.30-2.26)
RSRZ outliers	180081	9085 (2.30-2.26)

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	1169	 4% 82% 13% . .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9353 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 Cry8Ba2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1135	Total	C	N	O	S	0	0	0
			9176	5795	1539	1820	22			

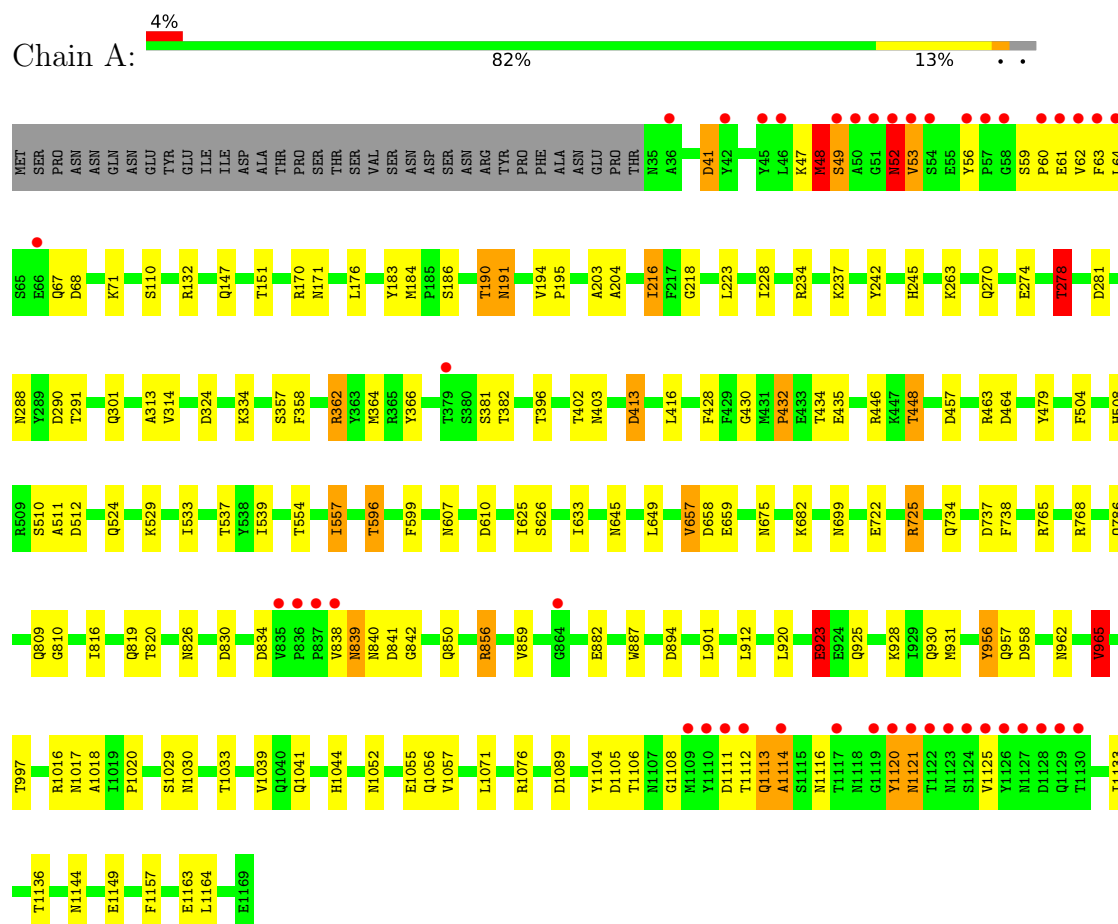
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	177	Total	O	0	0
			177	177		

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: Cry8Ba2



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	92.23Å 92.23Å 308.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.17 – 2.27 28.17 – 2.27	Depositor EDS
% Data completeness (in resolution range)	99.9 (28.17-2.27) 99.9 (28.17-2.27)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.33 (at 2.26Å)	Xtriage
Refinement program	REFMAC 5.8.0425	Depositor
R, R_{free}	0.180 , 0.224 0.185 , 0.225	Depositor DCC
R_{free} test set	3164 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	37.0	Xtriage
Anisotropy	0.072	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 35.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9353	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.09% 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	0.56	0/9380	1.14	40/12751 (0.3%)

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	7

There are no bond length outliers.

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	290	ASP	CA-CB-CG	9.82	122.42	112.60
1	A	923	GLU	N-CA-CB	9.02	123.09	110.01
1	A	1055	GLU	N-CA-CB	-7.77	97.31	110.83
1	A	1056	GLN	CB-CA-C	-7.61	94.09	110.45
1	A	432	PRO	N-CA-CB	-6.94	96.00	101.83
1	A	1105	ASP	CA-CB-CG	6.49	119.09	112.60
1	A	413	ASP	CA-CB-CG	6.32	118.92	112.60
1	A	965	VAL	N-CA-CB	6.23	117.32	110.53
1	A	41	ASP	CA-CB-CG	6.14	118.74	112.60
1	A	657	VAL	N-CA-CB	-6.08	100.69	111.93
1	A	923	GLU	CB-CA-C	-6.03	101.41	110.88
1	A	820	THR	CA-CB-OG1	-5.99	100.62	109.60
1	A	413	ASP	CB-CA-C	-5.92	101.04	110.81
1	A	362	ARG	N-CA-CB	-5.91	100.59	110.57
1	A	610	ASP	CA-CB-CG	5.87	118.47	112.60
1	A	1055	GLU	CB-CG-CD	5.71	122.32	112.60
1	A	1105	ASP	CB-CA-C	5.70	119.83	109.62
1	A	278	THR	N-CA-CB	-5.67	102.20	110.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	41	ASP	CB-CA-C	5.62	118.99	109.50
1	A	596	THR	N-CA-CB	-5.60	101.17	111.37
1	A	270	GLN	CB-CA-C	-5.54	102.19	110.88
1	A	1055	GLU	CB-CA-C	5.45	119.77	109.37
1	A	1157	PHE	CA-CB-CG	5.42	119.22	113.80
1	A	1149	GLU	CB-CA-C	5.39	119.08	109.65
1	A	882	GLU	CB-CA-C	5.39	119.73	110.79
1	A	894	ASP	CA-CB-CG	5.39	117.99	112.60
1	A	512	ASP	CA-CB-CG	5.38	117.98	112.60
1	A	1089	ASP	CA-CB-CG	5.38	117.98	112.60
1	A	997	THR	CA-CB-OG1	-5.37	101.54	109.60
1	A	599	PHE	CA-CB-CG	5.35	119.15	113.80
1	A	658	ASP	CA-CB-CG	5.33	117.93	112.60
1	A	901	LEU	N-CA-CB	-5.33	101.87	110.71
1	A	382	THR	CA-CB-OG1	-5.24	101.75	109.60
1	A	358	PHE	CB-CA-C	5.20	118.34	109.24
1	A	504	PHE	CA-CB-CG	5.16	118.96	113.80
1	A	464	ASP	CA-CB-CG	5.14	117.74	112.60
1	A	151	THR	CA-CB-OG1	-5.08	101.98	109.60
1	A	1149	GLU	N-CA-CB	-5.08	102.28	110.81
1	A	324	ASP	CA-CB-CG	5.04	117.64	112.60
1	A	281	ASP	CA-CB-CG	5.01	117.61	112.60

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1076	ARG	Sidechain
1	A	132	ARG	Sidechain
1	A	52	ASN	Peptide
1	A	725	ARG	Sidechain
1	A	768	ARG	Sidechain
1	A	856	ARG	Sidechain
1	A	859	VAL	Peptide

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	9176	0	8839	77	1
2	A	177	0	0	3	0
All	All	9353	0	8839	77	1

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 4.

All (77) 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:288:ASN:HD21	1:A:524:GLN:HE22	1.28	0.81
1:A:734:GLN:H	1:A:786:GLN:HE22	1.28	0.80
1:A:699:ASN:HD22	1:A:850:GLN:HE21	1.30	0.78
1:A:184:MET:HE1	1:A:203:ALA:HB1	1.67	0.75
1:A:61:GLU:O	1:A:68:ASP:OD2	2.06	0.74
1:A:288:ASN:ND2	1:A:524:GLN:HE22	1.87	0.72
1:A:364:MET:HE3	1:A:366:TYR:HB3	1.71	0.72
1:A:170:ARG:HD2	1:A:223:LEU:HD21	1.80	0.64
1:A:301:GLN:HE21	1:A:511:ALA:HA	1.62	0.64
1:A:184:MET:HE1	1:A:203:ALA:CB	2.29	0.62
1:A:675:ASN:OD1	1:A:682:LYS:NZ	2.34	0.60
1:A:508:HIS:HD2	1:A:510:SER:H	1.50	0.59
1:A:446:ARG:HD3	1:A:479:TYR:CD2	2.38	0.59
1:A:809:GLN:HA	1:A:826:ASN:HD22	1.69	0.58
1:A:1121:ASN:HD22	1:A:1121:ASN:N	2.00	0.58
1:A:362:ARG:HG2	1:A:416:LEU:HD11	1.87	0.57
1:A:218:GLY:HA3	1:A:228:ILE:CD1	2.34	0.57
1:A:56:TYR:HB2	1:A:59:SER:OG	2.04	0.57
1:A:734:GLN:N	1:A:786:GLN:HE22	2.00	0.56
1:A:1104:TYR:CE1	1:A:1133:ILE:HD11	2.44	0.53
1:A:816:ILE:HB	1:A:887:TRP:HB2	1.92	0.52
1:A:216:ILE:HG23	1:A:291:THR:HG21	1.92	0.52
1:A:1112:THR:HG21	1:A:1116:ASN:HD22	1.75	0.51
1:A:554:THR:HA	1:A:645:ASN:O	2.11	0.50
1:A:734:GLN:H	1:A:786:GLN:NE2	2.04	0.49
1:A:912:LEU:CD1	1:A:920:LEU:HD22	2.43	0.49
1:A:1120:TYR:C	1:A:1121:ASN:HD22	2.20	0.49
1:A:737:ASP:O	1:A:765:ARG:HD3	2.13	0.48
1:A:738:PHE:O	1:A:765:ARG:NH1	2.46	0.48
1:A:699:ASN:HD22	1:A:850:GLN:NE2	2.05	0.47
1:A:204:ALA:HB1	1:A:242:TYR:CD2	2.49	0.47
1:A:183:TYR:O	1:A:186:SER:HB2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1016:ARG:NH2	1:A:1163:GLU:OE2	2.38	0.47
1:A:463:ARG:HD3	2:A:1210:HOH:O	2.14	0.47
1:A:448:THR:HG22	2:A:1293:HOH:O	2.15	0.47
1:A:931:MET:HA	1:A:931:MET:HE2	1.96	0.47
1:A:245:HIS:HE1	2:A:1327:HOH:O	1.97	0.47
1:A:557:ILE:CG2	1:A:557:ILE:O	2.63	0.47
1:A:364:MET:CE	1:A:428:PHE:CE2	2.98	0.46
1:A:52:ASN:O	1:A:53:VAL:HG13	2.15	0.46
1:A:1113:GLN:O	1:A:1114:ALA:C	2.59	0.46
1:A:1017:ASN:ND2	1:A:1164:LEU:H	2.14	0.46
1:A:962:ASN:HB2	1:A:965:VAL:HG12	1.97	0.46
1:A:1121:ASN:N	1:A:1121:ASN:ND2	2.59	0.46
1:A:216:ILE:CG2	1:A:291:THR:HG21	2.46	0.46
1:A:60:PRO:O	1:A:71:LYS:HB2	2.16	0.45
1:A:274:GLU:O	1:A:278:THR:HB	2.17	0.45
1:A:810:GLY:H	1:A:826:ASN:ND2	2.15	0.45
1:A:819:GLN:HE22	1:A:923:GLU:HB3	1.80	0.45
1:A:60:PRO:HA	1:A:67:GLN:HB3	1.99	0.44
1:A:840:ASN:O	1:A:842:GLY:N	2.50	0.44
1:A:60:PRO:O	1:A:71:LYS:CB	2.66	0.44
1:A:190:THR:O	1:A:191:ASN:HB2	2.18	0.44
1:A:194:VAL:N	1:A:195:PRO:HD2	2.33	0.44
1:A:402:THR:O	1:A:403:ASN:HB2	2.18	0.44
1:A:1033:THR:HG22	1:A:1057:VAL:HG22	1.99	0.44
1:A:364:MET:CE	1:A:428:PHE:HE2	2.31	0.44
1:A:364:MET:HE1	1:A:430:GLY:HA3	2.00	0.43
1:A:1106:THR:HG22	1:A:1108:GLY:H	1.84	0.43
1:A:830:ASP:O	1:A:856:ARG:HD3	2.18	0.43
1:A:508:HIS:CD2	1:A:510:SER:H	2.32	0.43
1:A:957:GLN:O	1:A:958:ASP:HB2	2.19	0.43
1:A:47:LYS:O	1:A:48:MET:C	2.62	0.42
1:A:956:TYR:CD1	1:A:956:TYR:N	2.87	0.42
1:A:301:GLN:HE22	1:A:529:LYS:NZ	2.18	0.42
1:A:218:GLY:HA3	1:A:228:ILE:HD11	1.99	0.42
1:A:48:MET:O	1:A:49:SER:CB	2.67	0.42
1:A:1018:ALA:O	1:A:1020:PRO:HD3	2.20	0.41
1:A:1071:LEU:O	1:A:1136:THR:HA	2.19	0.41
1:A:176:LEU:HD23	1:A:176:LEU:HA	1.92	0.41
1:A:838:VAL:O	1:A:839:ASN:CB	2.68	0.41
1:A:722:GLU:OE1	1:A:725:ARG:NH1	2.54	0.41
1:A:649:LEU:C	1:A:649:LEU:HD23	2.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1029:SER:O	1:A:1030:ASN:HB2	2.21	0.41
1:A:434:THR:HG22	1:A:435:GLU:N	2.36	0.40
1:A:1044:HIS:CD2	1:A:1044:HIS:N	2.88	0.40
1:A:313:ALA:N	1:A:413:ASP:HB3	2.36	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:659:GLU:OE2	1:A:925:GLN:NE2[8_565]	2.18	0.02

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	1133/1169 (97%)	1084 (96%)	40 (4%)	9 (1%)	16 18

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	839	ASN
1	A	49	SER
1	A	841	ASP
1	A	1114	ALA
1	A	48	MET
1	A	62	VAL
1	A	1111	ASP
1	A	191	ASN
1	A	53	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	1009/1041 (97%)	963 (95%)	46 (5%)	24	34

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

Mol	Chain	Res	Type
1	A	41	ASP
1	A	48	MET
1	A	52	ASN
1	A	63	PHE
1	A	64	LEU
1	A	110	SER
1	A	147	GLN
1	A	171	ASN
1	A	190	THR
1	A	216	ILE
1	A	234	ARG
1	A	237	LYS
1	A	263	LYS
1	A	278	THR
1	A	314	VAL
1	A	334	LYS
1	A	357	SER
1	A	381	SER
1	A	396	THR
1	A	432	PRO
1	A	448	THR
1	A	457	ASP
1	A	533	ILE
1	A	537	THR
1	A	539	ILE
1	A	557	ILE
1	A	596	THR
1	A	607	ASN
1	A	625	ILE
1	A	626	SER

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Mol	Chain	Res	Type
1	A	633	ILE
1	A	657	VAL
1	A	834	ASP
1	A	923	GLU
1	A	928	LYS
1	A	930	GLN
1	A	956	TYR
1	A	965	VAL
1	A	1039	VAL
1	A	1041	GLN
1	A	1052	ASN
1	A	1113	GLN
1	A	1120	TYR
1	A	1121	ASN
1	A	1125	VAL
1	A	1144	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (40) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	52	ASN
1	A	124	ASN
1	A	133	ASN
1	A	144	ASN
1	A	191	ASN
1	A	205	ASN
1	A	230	ASN
1	A	235	GLN
1	A	245	HIS
1	A	288	ASN
1	A	301	GLN
1	A	403	ASN
1	A	441	GLN
1	A	508	HIS
1	A	524	GLN
1	A	536	ASN
1	A	563	GLN
1	A	600	ASN
1	A	607	ASN
1	A	680	ASN
1	A	711	ASN
1	A	786	GLN

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Mol	Chain	Res	Type
1	A	819	GLN
1	A	826	ASN
1	A	839	ASN
1	A	850	GLN
1	A	854	ASN
1	A	957	GLN
1	A	1017	ASN
1	A	1026	ASN
1	A	1038	ASN
1	A	1044	HIS
1	A	1052	ASN
1	A	1064	GLN
1	A	1082	ASN
1	A	1113	GLN
1	A	1118	ASN
1	A	1121	ASN
1	A	1129	GLN
1	A	1144	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 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 ⓘ

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	1135/1169 (97%)	-0.26	43 (3%)	44 46	24, 46, 126, 295	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	60	PRO	6.3
1	A	1125	VAL	5.2
1	A	53	VAL	4.6
1	A	62	VAL	4.4
1	A	51	GLY	4.3
1	A	64	LEU	4.0
1	A	1120	TYR	3.9
1	A	1117	THR	3.8
1	A	1122	THR	3.8
1	A	56	TYR	3.7
1	A	1123	ASN	3.7
1	A	1111	ASP	3.4
1	A	50	ALA	3.2
1	A	838	VAL	3.2
1	A	52	ASN	3.2
1	A	57	PRO	3.2
1	A	1110	TYR	3.2
1	A	1126	TYR	3.1
1	A	1130	THR	3.0
1	A	46	LEU	2.9
1	A	1121	ASN	2.8
1	A	61	GLU	2.8
1	A	42	TYR	2.8
1	A	63	PHE	2.7
1	A	1114	ALA	2.7
1	A	1124	SER	2.6
1	A	864	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	54	SER	2.6
1	A	1128	ASP	2.5
1	A	1109	MET	2.4
1	A	1112	THR	2.3
1	A	1127	ASN	2.3
1	A	58	GLY	2.2
1	A	836	PRO	2.2
1	A	49	SER	2.2
1	A	36	ALA	2.2
1	A	379	THR	2.2
1	A	66	GLU	2.1
1	A	45	TYR	2.1
1	A	835	VAL	2.1
1	A	837	PRO	2.1
1	A	1129	GLN	2.1
1	A	1119	GLY	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.