



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 05:18 AM UTC

PDB ID : 1RGP / pdb_00001rgp
Title : GTPASE-ACTIVATION DOMAIN FROM RHOGAP
Authors : Barrett, T.; Xiao, B.; Dodson, E.J.; Dodson, G.; Ludbrook, S.B.; Nurmahomed, K.; Gamblin, S.J.; Musacchio, A.; Smerdon, S.J.; Eccleston, J.F.
Deposited on : 1996-12-05
Resolution : 2.00 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

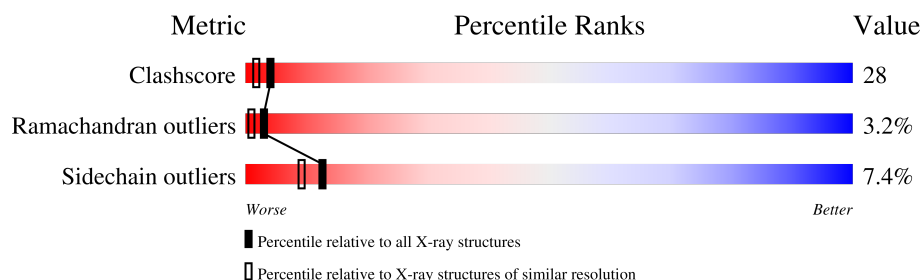
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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))
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	242	36% 25% 12% 5% 22%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1762 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 RHOGAP.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	189	Total	C	N	O	S	0	0	0
			1501	973	259	267	2			

- Molecule 2 is water.

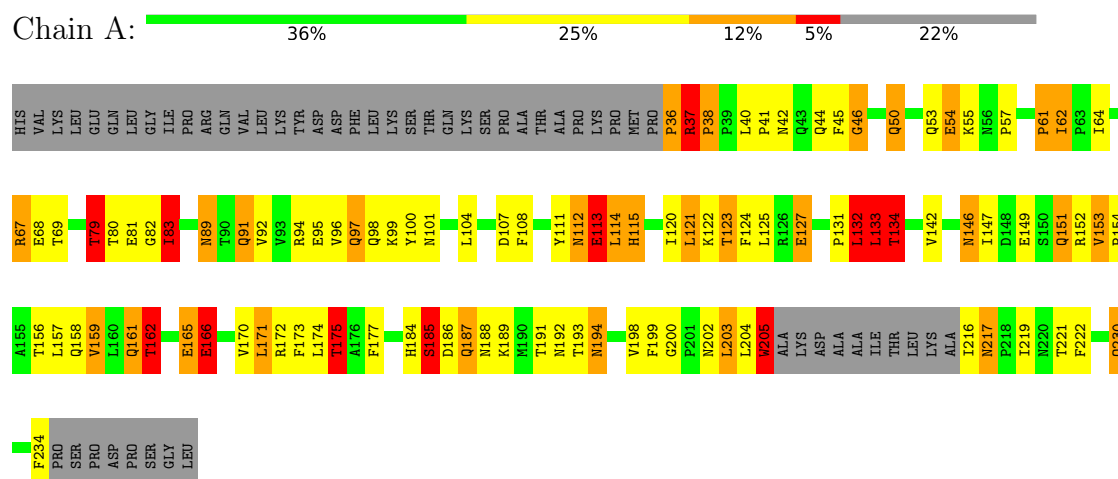
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	261	Total	O	6	0
			261	261		

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. 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. 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.

Note EDS was not executed.

• Molecule 1: RHOGAP



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	36.09Å 70.09Å 79.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00	Depositor
% Data completeness (in resolution range)	99.6 (20.00-2.00)	Depositor
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.220 , 0.283	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1762	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

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	1.53	17/1539 (1.1%)	2.59	126/2103 (6.0%)

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	6

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	36	PRO	CA-C	-12.17	1.27	1.52
1	A	62	ILE	N-CA	10.85	1.54	1.46
1	A	36	PRO	C-N	-8.07	1.16	1.33
1	A	37	ARG	C-O	-7.21	1.15	1.24
1	A	192	ASN	C-N	6.65	1.42	1.33
1	A	134	THR	CA-CB	6.45	1.64	1.53
1	A	69	THR	N-CA	6.21	1.53	1.46
1	A	46	GLY	CA-C	5.99	1.59	1.51
1	A	120	ILE	N-CA	5.87	1.53	1.46
1	A	185	SER	CA-CB	5.85	1.63	1.53
1	A	122	LYS	CA-CB	5.84	1.62	1.53
1	A	37	ARG	C-N	5.81	1.40	1.33
1	A	222	PHE	N-CA	5.66	1.53	1.46
1	A	175	THR	N-CA	5.65	1.53	1.46
1	A	132	LEU	C-N	-5.61	1.25	1.33
1	A	123	THR	CA-C	5.46	1.59	1.52
1	A	114	LEU	N-CA	-5.45	1.39	1.46

All (126) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	113	GLU	CA-C-N	19.93	159.62	121.54
1	A	113	GLU	C-N-CA	19.93	159.62	121.54
1	A	36	PRO	O-C-N	14.88	146.81	123.00
1	A	132	LEU	O-C-N	-14.59	105.47	122.68
1	A	67	ARG	CD-NE-CZ	12.29	141.60	124.40
1	A	133	LEU	CA-C-O	-11.96	103.41	120.51
1	A	113	GLU	CA-C-O	11.91	137.54	120.51
1	A	61	PRO	CA-C-N	-11.44	114.36	122.59
1	A	61	PRO	C-N-CA	-11.44	114.36	122.59
1	A	166	GLU	OE1-CD-OE2	-11.36	95.64	122.90
1	A	123	THR	O-C-N	11.25	134.97	122.15
1	A	67	ARG	NE-CZ-NH2	10.78	128.90	119.20
1	A	166	GLU	CB-CA-C	10.18	127.69	110.79
1	A	94	ARG	CD-NE-CZ	10.14	138.59	124.40
1	A	175	THR	N-CA-CB	-10.00	94.78	110.28
1	A	132	LEU	N-CA-C	-9.91	97.54	110.33
1	A	113	GLU	O-C-N	-9.80	109.55	122.59
1	A	98	GLN	OE1-CD-NE2	-9.79	112.81	122.60
1	A	151	GLN	OE1-CD-NE2	-9.75	112.85	122.60
1	A	162	THR	N-CA-CB	-9.49	95.58	110.28
1	A	79	THR	N-CA-CB	-8.49	97.19	111.20
1	A	166	GLU	CG-CD-OE1	8.43	137.79	118.40
1	A	194	ASN	CA-CB-CG	-8.40	104.20	112.60
1	A	185	SER	CA-CB-OG	-8.34	94.43	111.10
1	A	146	ASN	CA-C-N	8.31	134.20	122.23
1	A	146	ASN	C-N-CA	8.31	134.20	122.23
1	A	107	ASP	CA-C-O	-8.05	111.64	120.33
1	A	123	THR	CA-C-O	-8.03	111.91	120.42
1	A	81	GLU	O-C-N	-8.01	113.45	123.06
1	A	57	PRO	N-CA-CB	8.01	111.20	103.51
1	A	115	HIS	CA-CB-CG	-7.98	105.82	113.80
1	A	192	ASN	O-C-N	-7.94	113.70	122.12
1	A	64	ILE	CA-C-O	-7.92	112.71	120.95
1	A	165	GLU	CA-C-N	7.90	130.87	120.28
1	A	165	GLU	C-N-CA	7.90	130.87	120.28
1	A	97	GLN	OE1-CD-NE2	-7.80	114.80	122.60
1	A	50	GLN	CA-CB-CG	-7.69	98.72	114.10
1	A	221	THR	O-C-N	7.62	130.19	122.12
1	A	192	ASN	CA-C-O	7.47	128.47	120.55
1	A	153	VAL	N-CA-CB	7.45	116.26	110.45
1	A	112	ASN	N-CA-CB	7.35	122.29	110.16
1	A	50	GLN	OE1-CD-NE2	7.34	129.94	122.60
1	A	99	LYS	N-CA-CB	7.16	120.37	109.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	219	ILE	CA-C-O	7.14	128.42	120.85
1	A	83	ILE	N-CA-CB	7.09	121.19	110.13
1	A	36	PRO	CA-C-N	-7.07	104.55	121.80
1	A	36	PRO	C-N-CA	-7.07	104.55	121.80
1	A	166	GLU	N-CA-CB	-7.00	99.83	110.12
1	A	42	ASN	O-C-N	6.99	131.20	122.19
1	A	37	ARG	O-C-N	6.95	129.31	121.32
1	A	173	PHE	CA-CB-CG	6.94	120.74	113.80
1	A	101	ASN	CA-CB-CG	-6.87	105.73	112.60
1	A	124	PHE	CA-CB-CG	-6.80	107.00	113.80
1	A	198	VAL	CA-C-O	-6.80	112.78	119.92
1	A	91	GLN	OE1-CD-NE2	6.78	129.38	122.60
1	A	67	ARG	NH1-CZ-NH2	-6.74	110.54	119.30
1	A	98	GLN	CG-CD-NE2	6.71	126.46	116.40
1	A	184	HIS	CA-C-N	6.67	130.12	120.38
1	A	184	HIS	C-N-CA	6.67	130.12	120.38
1	A	151	GLN	CG-CD-NE2	6.61	126.32	116.40
1	A	159	VAL	N-CA-CB	6.59	123.40	110.95
1	A	112	ASN	CA-CB-CG	-6.52	106.08	112.60
1	A	171	LEU	O-C-N	-6.50	115.37	122.07
1	A	203	LEU	CD1-CG-CD2	-6.49	96.53	110.80
1	A	111	TYR	CA-C-N	-6.41	113.16	122.19
1	A	111	TYR	C-N-CA	-6.41	113.16	122.19
1	A	170	VAL	N-CA-C	-6.37	104.31	110.42
1	A	230	GLN	CA-C-O	-6.32	114.19	120.82
1	A	81	GLU	CG-CD-OE1	6.32	132.93	118.40
1	A	89	ASN	CA-C-N	6.29	129.02	120.54
1	A	89	ASN	C-N-CA	6.29	129.02	120.54
1	A	42	ASN	CA-C-O	-6.28	112.05	120.15
1	A	175	THR	CB-CA-C	6.21	122.59	110.67
1	A	127	GLU	CA-C-O	-6.20	111.78	119.28
1	A	68	GLU	CA-C-N	-6.15	112.45	120.44
1	A	68	GLU	C-N-CA	-6.15	112.45	120.44
1	A	166	GLU	CA-C-O	6.15	127.07	120.55
1	A	125	LEU	O-C-N	-6.12	115.72	122.09
1	A	101	ASN	N-CA-CB	6.07	119.68	110.28
1	A	177	PHE	CA-CB-CG	6.04	119.83	113.80
1	A	162	THR	CA-CB-CG2	6.00	120.70	110.50
1	A	166	GLU	O-C-N	-5.99	115.77	122.12
1	A	96	VAL	CA-C-O	-5.91	114.81	120.95
1	A	44	GLN	OE1-CD-NE2	5.89	128.49	122.60
1	A	53	GLN	O-C-N	5.87	129.49	122.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	174	LEU	CA-C-O	5.85	126.96	120.82
1	A	175	THR	OG1-CB-CG2	5.83	120.96	109.30
1	A	230	GLN	O-C-N	5.82	128.06	122.07
1	A	98	GLN	CA-C-O	-5.73	113.38	119.97
1	A	202	ASN	CA-CB-CG	-5.72	106.88	112.60
1	A	104	LEU	CA-C-N	5.62	125.80	119.90
1	A	104	LEU	C-N-CA	5.62	125.80	119.90
1	A	81	GLU	CA-C-O	5.59	127.05	120.96
1	A	151	GLN	CA-C-O	-5.58	112.79	119.15
1	A	175	THR	CA-CB-OG1	5.55	117.93	109.60
1	A	107	ASP	O-C-N	5.55	130.44	123.12
1	A	91	GLN	CA-CB-CG	-5.54	103.03	114.10
1	A	82	GLY	CA-C-N	-5.50	113.26	120.91
1	A	82	GLY	C-N-CA	-5.50	113.26	120.91
1	A	161	GLN	CA-C-N	5.49	128.65	120.31
1	A	161	GLN	C-N-CA	5.49	128.65	120.31
1	A	54	GLU	CA-C-O	5.47	126.35	120.55
1	A	100	TYR	CA-C-O	-5.47	114.72	120.63
1	A	81	GLU	CB-CG-CD	5.41	121.79	112.60
1	A	37	ARG	CA-C-O	-5.39	112.77	120.16
1	A	62	ILE	CA-C-N	5.38	125.30	119.76
1	A	62	ILE	C-N-CA	5.38	125.30	119.76
1	A	95	GLU	CB-CG-CD	-5.37	103.48	112.60
1	A	83	ILE	CB-CA-C	-5.32	103.17	111.26
1	A	121	LEU	CA-CB-CG	5.32	134.90	116.30
1	A	217	ASN	CA-C-O	-5.31	112.88	120.16
1	A	166	GLU	CA-CB-CG	5.31	124.72	114.10
1	A	166	GLU	N-CA-C	-5.28	105.53	111.28
1	A	234	PHE	CA-CB-CG	5.21	119.01	113.80
1	A	108	PHE	CA-CB-CG	-5.19	108.61	113.80
1	A	62	ILE	CA-CB-CG1	5.18	119.20	110.40
1	A	157	LEU	CA-C-O	5.15	126.01	120.55
1	A	156	THR	CA-CB-OG1	-5.12	101.93	109.60
1	A	205	TRP	CA-CB-CG	5.11	123.32	113.60
1	A	161	GLN	O-C-N	-5.11	115.98	122.27
1	A	222	PHE	CA-CB-CG	-5.11	108.69	113.80
1	A	146	ASN	O-C-N	-5.10	115.81	122.59
1	A	161	GLN	CA-C-O	5.05	125.78	119.97
1	A	91	GLN	CA-C-N	5.03	127.56	120.42
1	A	91	GLN	C-N-CA	5.03	127.56	120.42
1	A	68	GLU	O-C-N	5.03	128.76	122.23

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	113	GLU	Peptide
1	A	115	HIS	Mainchain
1	A	132	LEU	Peptide,Mainchain
1	A	134	THR	Mainchain
1	A	193	THR	Mainchain

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	1501	0	1473	82	29
2	A	261	0	0	32	22
All	All	1762	0	1473	82	29

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 28.

All (82) 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:36:PRO:O	1:A:38:PRO:CD	1.74	1.35
1:A:146:ASN:CG	2:A:416:HOH:O	1.88	1.11
1:A:37:ARG:CD	2:A:485:HOH:O	1.73	1.11
1:A:36:PRO:O	1:A:38:PRO:HD3	0.91	1.07
1:A:50:GLN:HE21	1:A:166:GLU:HG3	1.20	1.06
1:A:146:ASN:OD1	2:A:416:HOH:O	1.73	0.94
1:A:37:ARG:HD3	2:A:485:HOH:O	1.45	0.93
1:A:36:PRO:C	1:A:38:PRO:HD3	1.97	0.90
1:A:191:THR:HB	2:A:446:HOH:O	1.70	0.89
1:A:62:ILE:HB	1:A:67:ARG:HE	1.38	0.88
1:A:62:ILE:H	1:A:67:ARG:HH21	1.15	0.87
1:A:97:GLN:NE2	1:A:123:THR:HG21	1.92	0.84
1:A:50:GLN:HG2	1:A:166:GLU:OE2	1.80	0.81
1:A:36:PRO:C	1:A:38:PRO:CD	2.53	0.81
1:A:133:LEU:N	2:A:277:HOH:O	2.13	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:62:ILE:H	1:A:67:ARG:NH2	1.80	0.77
1:A:132:LEU:HA	2:A:277:HOH:O	1.85	0.75
1:A:154:PRO:O	1:A:158:GLN:HG3	1.86	0.74
1:A:37:ARG:O	1:A:37:ARG:HG3	1.86	0.74
1:A:205:TRP:O	2:A:440:HOH:O	2.06	0.73
1:A:191:THR:HG23	1:A:194:ASN:H	1.54	0.73
1:A:67:ARG:HD2	2:A:385:HOH:O	1.88	0.72
1:A:97:GLN:HE22	1:A:123:THR:HG21	1.56	0.70
1:A:175:THR:HG23	1:A:230:GLN:HG2	1.75	0.69
1:A:146:ASN:ND2	2:A:416:HOH:O	2.13	0.69
1:A:191:THR:CG2	1:A:194:ASN:H	2.06	0.68
1:A:199:PHE:O	1:A:203:LEU:HD23	1.94	0.66
1:A:89:ASN:ND2	1:A:92:VAL:HG23	2.11	0.65
1:A:175:THR:HG23	1:A:230:GLN:CG	2.27	0.65
1:A:89:ASN:HD22	1:A:92:VAL:HG23	1.62	0.65
1:A:37:ARG:O	1:A:37:ARG:CG	2.44	0.64
1:A:175:THR:CG2	1:A:230:GLN:HE21	2.12	0.63
1:A:62:ILE:N	1:A:67:ARG:HH21	1.93	0.63
1:A:40:LEU:HB3	1:A:41:PRO:HD2	1.81	0.63
1:A:50:GLN:HE21	1:A:166:GLU:CG	2.04	0.62
1:A:36:PRO:C	1:A:38:PRO:N	2.58	0.61
1:A:132:LEU:CA	2:A:277:HOH:O	2.46	0.61
1:A:50:GLN:NE2	1:A:166:GLU:HG3	2.05	0.60
1:A:159:VAL:O	1:A:162:THR:HB	2.02	0.59
1:A:134:THR:CB	2:A:344:HOH:O	2.51	0.58
1:A:62:ILE:HB	1:A:67:ARG:NE	2.15	0.57
1:A:50:GLN:O	1:A:54:GLU:HG3	2.06	0.56
1:A:89:ASN:HD22	1:A:92:VAL:H	1.54	0.56
1:A:146:ASN:ND2	2:A:327:HOH:O	2.38	0.56
1:A:131:PRO:C	1:A:132:LEU:O	2.48	0.56
1:A:79:THR:OG1	1:A:187:GLN:HG3	2.08	0.54
1:A:133:LEU:CB	2:A:278:HOH:O	2.56	0.54
1:A:171:LEU:O	1:A:175:THR:HB	2.08	0.53
1:A:132:LEU:C	2:A:277:HOH:O	2.50	0.53
1:A:112:ASN:HB2	2:A:431:HOH:O	2.09	0.53
1:A:172:ARG:NH2	2:A:412:HOH:O	2.41	0.52
1:A:45:PHE:HB3	2:A:499:HOH:O	2.08	0.52
1:A:50:GLN:CG	2:A:247:HOH:O	2.59	0.51
1:A:185:SER:HB3	2:A:427:HOH:O	2.10	0.51
1:A:134:THR:CA	2:A:344:HOH:O	2.60	0.50
1:A:123:THR:O	1:A:127:GLU:HG2	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:133:LEU:O	1:A:134:THR:CB	2.60	0.49
1:A:199:PHE:C	1:A:203:LEU:HD23	2.37	0.49
1:A:80:THR:O	1:A:83:ILE:HG13	2.12	0.48
1:A:67:ARG:HD2	2:A:338:HOH:O	2.14	0.48
1:A:46:GLY:HA2	1:A:127:GLU:O	2.14	0.47
1:A:151:GLN:HB3	2:A:316:HOH:O	2.13	0.47
1:A:175:THR:HG22	1:A:230:GLN:HE21	1.78	0.47
1:A:114:LEU:HA	1:A:114:LEU:HD23	1.73	0.47
1:A:216:ILE:N	2:A:481:HOH:O	2.47	0.46
1:A:191:THR:CB	2:A:446:HOH:O	2.46	0.46
1:A:188:ASN:O	1:A:189:LYS:HB2	2.17	0.45
1:A:50:GLN:CD	2:A:247:HOH:O	2.60	0.45
1:A:204:LEU:CB	2:A:251:HOH:O	2.65	0.44
1:A:133:LEU:CB	2:A:287:HOH:O	2.66	0.44
1:A:153:VAL:HB	1:A:154:PRO:HD3	1.99	0.43
1:A:89:ASN:HD21	1:A:91:GLN:HB2	1.85	0.42
1:A:165:GLU:HG3	2:A:340:HOH:O	2.19	0.42
1:A:37:ARG:HD2	2:A:485:HOH:O	1.74	0.41
1:A:61:PRO:HD2	1:A:67:ARG:HH22	1.85	0.41
1:A:204:LEU:CB	2:A:274:HOH:O	2.69	0.41
1:A:175:THR:HG23	1:A:230:GLN:HE21	1.84	0.41
1:A:149:GLU:HA	1:A:152:ARG:HD2	2.02	0.41
1:A:146:ASN:O	1:A:147:ILE:HG23	2.21	0.41
1:A:191:THR:HG23	1:A:194:ASN:N	2.30	0.40
1:A:55:LYS:HD3	2:A:497:HOH:O	2.19	0.40
1:A:199:PHE:O	1:A:200:GLY:C	2.64	0.40

All (29) 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:38:PRO:N	2:A:358:HOH:O[2_565]	0.44	1.76
1:A:38:PRO:CG	1:A:158:GLN:NE2[2_565]	0.54	1.66
1:A:37:ARG:CA	2:A:360:HOH:O[2_565]	0.56	1.64
1:A:36:PRO:CB	2:A:390:HOH:O[2_565]	0.62	1.58
1:A:37:ARG:C	2:A:358:HOH:O[2_565]	1.06	1.14
1:A:38:PRO:CB	1:A:158:GLN:NE2[2_565]	1.08	1.12
1:A:36:PRO:CA	2:A:371:HOH:O[2_565]	1.20	1.00
1:A:37:ARG:N	2:A:371:HOH:O[2_565]	1.22	0.98
1:A:37:ARG:N	2:A:360:HOH:O[2_565]	1.24	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:36:PRO:CG	2:A:390:HOH:O[2_565]	1.27	0.93
1:A:38:PRO:CG	1:A:158:GLN:CD[2_565]	1.29	0.91
1:A:36:PRO:C	2:A:371:HOH:O[2_565]	1.46	0.74
1:A:37:ARG:CB	2:A:360:HOH:O[2_565]	1.51	0.69
1:A:36:PRO:CA	2:A:390:HOH:O[2_565]	1.55	0.65
1:A:151:GLN:OE1	2:A:300:HOH:O[3_644]	1.58	0.62
1:A:151:GLN:CD	2:A:300:HOH:O[3_644]	1.67	0.53
1:A:38:PRO:CA	2:A:358:HOH:O[2_565]	1.75	0.45
1:A:38:PRO:CD	2:A:358:HOH:O[2_565]	1.77	0.43
1:A:38:PRO:CD	1:A:158:GLN:CD[2_565]	1.90	0.30
1:A:38:PRO:CD	1:A:158:GLN:NE2[2_565]	1.93	0.27
1:A:37:ARG:O	2:A:358:HOH:O[2_565]	1.99	0.21
1:A:36:PRO:C	2:A:360:HOH:O[2_565]	2.03	0.17
1:A:36:PRO:N	2:A:390:HOH:O[2_565]	2.05	0.15
1:A:37:ARG:C	2:A:360:HOH:O[2_565]	2.07	0.13
1:A:36:PRO:CD	2:A:390:HOH:O[2_565]	2.08	0.12
1:A:38:PRO:CB	1:A:158:GLN:CD[2_565]	2.09	0.11
1:A:151:GLN:NE2	2:A:300:HOH:O[3_644]	2.15	0.05
1:A:37:ARG:CA	2:A:358:HOH:O[2_565]	2.18	0.02
1:A:38:PRO:CG	1:A:158:GLN:CG[2_565]	2.18	0.02

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	185/242 (76%)	174 (94%)	5 (3%)	6 (3%)	3 1

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	37	ARG
1	A	217	ASN
1	A	133	LEU

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Mol	Chain	Res	Type
1	A	134	THR
1	A	113	GLU
1	A	38	PRO

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	162/219 (74%)	150 (93%)	12 (7%)	13 9

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	79	THR
1	A	83	ILE
1	A	121	LEU
1	A	142	VAL
1	A	161	GLN
1	A	162	THR
1	A	166	GLU
1	A	175	THR
1	A	185	SER
1	A	186	ASP
1	A	187	GLN
1	A	205	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	50	GLN
1	A	89	ASN
1	A	97	GLN
1	A	112	ASN
1	A	140	HIS
1	A	167	ASN

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Mol	Chain	Res	Type
1	A	180	GLN
1	A	187	GLN
1	A	230	GLN

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 [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	36:PRO	C	37:ARG	N	1.16

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.