



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:04 PM UTC

PDB ID : 1QNL / pdb_00001qnl
Title : AMIDE RECEPTOR/NEGATIVE REGULATOR OF THE AMIDASE
OPERON OF PSEUDOMONAS AERUGINOSA (AMIC) COMPLEXED
WITH BUTYRAMIDE
Authors : Pearl, L.H.; O'Hara, B.P.; Roe, S.M.
Deposited on : 1999-10-19
Resolution : 2.70 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
Mogul : 2022.3.0, CSD as543be (2022)
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

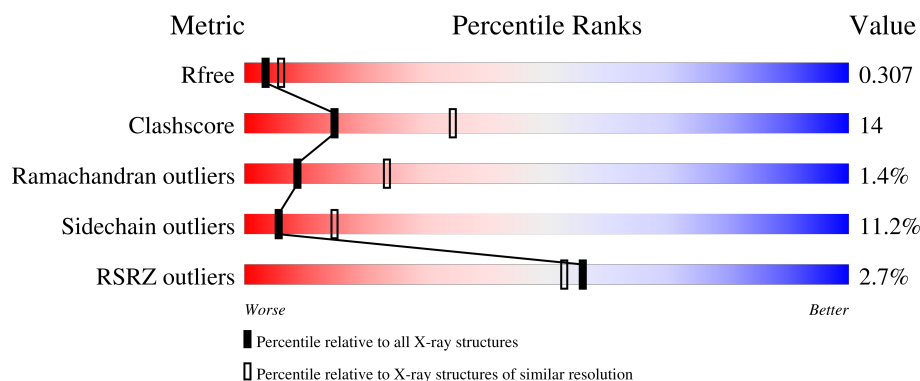
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	385	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	BMD	A	1001	-	X	X	-

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2963 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.

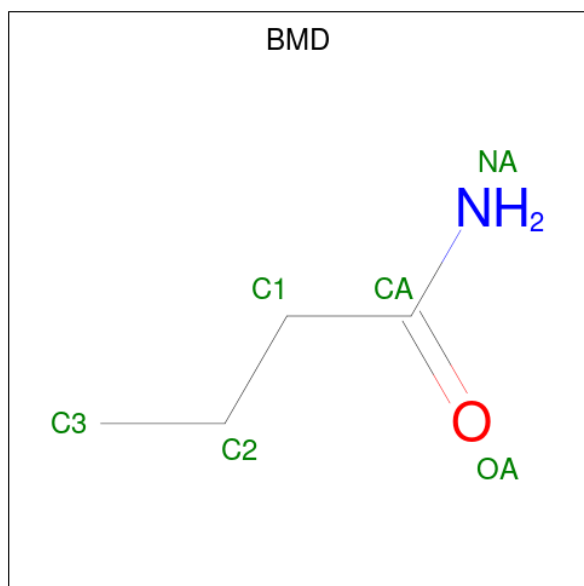
- Molecule 1 is a protein called ALIPHATIC AMIDASE EXPRESSION-REGULATING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	368	Total	C	N	O	S	259	0	0
			2914	1835	526	545	8			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	27	GLN	HIS	conflict	UNP P27017
A	28	ARG	ALA	conflict	UNP P27017

- Molecule 2 is BUTYRAMIDE (CCD ID: BMD) (formula: C₄H₉NO).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			6	4	1	1		

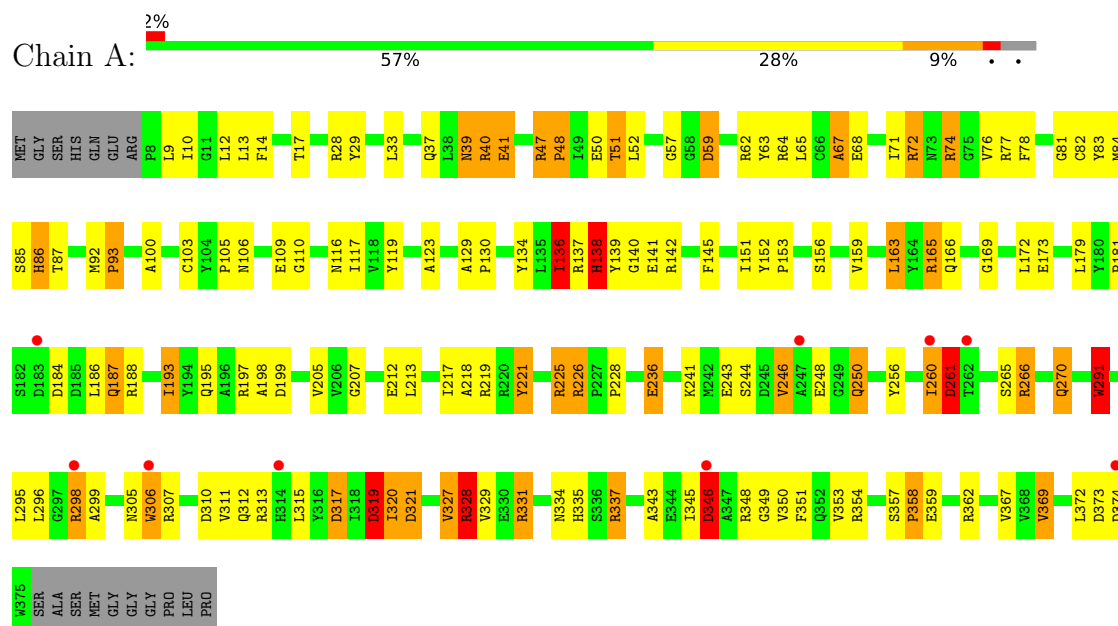
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	43	Total 43	O 43	5	0

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: ALIPHATIC AMIDASE EXPRESSION-REGULATING PROTEIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, α , β , γ	104.15Å 104.15Å 65.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.70 15.00 – 2.70	Depositor EDS
% Data completeness (in resolution range)	97.0 (15.00-2.70) 96.4 (15.00-2.70)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.08 (at 2.72Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.269 , 0.314 0.244 , 0.307	Depositor DCC
R_{free} test set	480 reflections (4.76%)	wwPDB-VP
Wilson B-factor (Å ²)	41.1	Xtriage
Anisotropy	0.170	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 55.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	2963	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.16% 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:
BMD

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	1.22	20/2989 (0.7%)	2.46	108/4074 (2.7%)

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	13

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	307	ARG	C-N	22.74	1.61	1.33
1	A	67	ALA	C-N	19.55	1.58	1.33
1	A	221	TYR	C-N	-17.01	1.08	1.33
1	A	317	ASP	C-N	-16.42	1.11	1.33
1	A	50	GLU	C-N	-15.87	1.12	1.33
1	A	72	ARG	C-N	14.53	1.55	1.33
1	A	328	ARG	C-N	-13.72	1.15	1.33
1	A	327	VAL	C-N	-13.17	1.17	1.33
1	A	68	GLU	C-N	-12.49	1.17	1.33
1	A	358	PRO	C-N	-11.16	1.20	1.33
1	A	136	ILE	C-N	-10.52	1.20	1.33
1	A	71	ILE	C-N	9.03	1.46	1.33
1	A	260	ILE	C-N	7.84	1.44	1.33
1	A	346	ASP	C-N	-7.50	1.24	1.33
1	A	359	GLU	C-N	6.93	1.42	1.33
1	A	195	GLN	C-N	-6.86	1.23	1.33
1	A	319	ASP	C-N	-6.86	1.22	1.33
1	A	261	ASP	C-N	-6.57	0.97	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	37	GLN	CB-CG	-6.53	1.32	1.52
1	A	226	ARG	C-N	-5.63	1.28	1.33

All (108) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	328	ARG	O-C-N	-38.21	80.16	123.33
1	A	221	TYR	O-C-N	-33.48	74.87	122.41
1	A	317	ASP	O-C-N	-29.54	87.10	122.25
1	A	328	ARG	CA-C-N	27.03	170.62	121.97
1	A	328	ARG	C-N-CA	27.03	170.62	121.97
1	A	39	ASN	O-C-N	-26.16	90.51	122.17
1	A	346	ASP	O-C-N	-24.31	94.31	122.75
1	A	260	ILE	O-C-N	-20.86	99.87	123.03
1	A	193	ILE	O-C-N	-19.68	102.62	121.91
1	A	50	GLU	CA-C-N	19.23	151.13	120.94
1	A	50	GLU	C-N-CA	19.23	151.13	120.94
1	A	50	GLU	O-C-N	-17.27	103.23	123.27
1	A	68	GLU	CA-C-N	17.20	143.83	120.44
1	A	68	GLU	C-N-CA	17.20	143.83	120.44
1	A	68	GLU	O-C-N	-15.94	105.65	122.07
1	A	327	VAL	O-C-N	-12.56	109.53	122.97
1	A	319	ASP	O-C-N	10.67	135.32	123.27
1	A	307	ARG	CA-C-N	-10.64	102.84	120.30
1	A	307	ARG	C-N-CA	-10.64	102.84	120.30
1	A	319	ASP	CA-C-N	-10.55	106.86	122.68
1	A	319	ASP	C-N-CA	-10.55	106.86	122.68
1	A	261	ASP	O-C-N	-10.27	108.93	122.59
1	A	319	ASP	CA-C-O	-10.16	109.36	120.43
1	A	47	ARG	N-CA-CB	10.06	126.81	110.10
1	A	348	ARG	NE-CZ-NH2	9.96	128.16	119.20
1	A	74	ARG	NE-CZ-NH1	-9.96	111.54	121.50
1	A	226	ARG	O-C-N	9.36	131.77	121.94
1	A	165	ARG	CD-NE-CZ	9.18	137.25	124.40
1	A	328	ARG	CD-NE-CZ	9.05	137.07	124.40
1	A	266	ARG	NE-CZ-NH2	-8.87	111.22	119.20
1	A	305	ASN	CA-CB-CG	8.17	120.77	112.60
1	A	47	ARG	CD-NE-CZ	8.14	135.79	124.40
1	A	72	ARG	CB-CG-CD	7.94	129.57	111.30
1	A	334	ASN	CA-CB-CG	7.92	120.52	112.60
1	A	310	ASP	CA-CB-CG	7.92	120.52	112.60
1	A	59	ASP	CA-C-O	7.82	125.10	119.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	195	GLN	OE1-CD-NE2	-7.77	114.83	122.60
1	A	137	ARG	CD-NE-CZ	7.74	135.24	124.40
1	A	261	ASP	CA-CB-CG	7.72	120.32	112.60
1	A	47	ARG	NE-CZ-NH1	7.50	129.00	121.50
1	A	67	ALA	CA-C-N	7.35	129.99	120.44
1	A	67	ALA	C-N-CA	7.35	129.99	120.44
1	A	29	TYR	CA-CB-CG	-7.33	100.71	113.90
1	A	41	GLU	CG-CD-OE2	7.16	134.88	118.40
1	A	145	PHE	CA-CB-CG	7.15	120.95	113.80
1	A	50	GLU	CB-CG-CD	7.05	124.59	112.60
1	A	307	ARG	CB-CA-C	6.88	121.76	109.38
1	A	266	ARG	CD-NE-CZ	6.86	134.00	124.40
1	A	59	ASP	CA-CB-CG	6.84	119.44	112.60
1	A	256	TYR	N-CA-C	6.82	119.80	109.23
1	A	331	ARG	CD-NE-CZ	6.74	133.83	124.40
1	A	106	ASN	N-CA-C	6.68	119.05	108.23
1	A	319	ASP	CA-CB-CG	-6.60	106.00	112.60
1	A	85	SER	N-CA-C	6.59	118.47	111.28
1	A	328	ARG	NE-CZ-NH2	6.52	125.07	119.20
1	A	348	ARG	CA-C-O	6.42	127.53	119.95
1	A	48	PRO	CA-C-O	-6.32	114.20	121.98
1	A	261	ASP	CA-C-N	6.31	156.60	121.41
1	A	261	ASP	C-N-CA	6.31	156.60	121.41
1	A	68	GLU	CA-C-O	6.27	127.40	120.82
1	A	40	ARG	CA-C-N	6.26	133.50	121.54
1	A	40	ARG	C-N-CA	6.26	133.50	121.54
1	A	226	ARG	CA-C-O	-6.22	113.31	120.03
1	A	123	ALA	N-CA-C	-6.15	103.06	110.13
1	A	328	ARG	NH1-CZ-NH2	-6.15	111.31	119.30
1	A	221	TYR	CA-C-O	6.12	126.46	119.18
1	A	236	GLU	CA-C-N	6.11	128.38	120.44
1	A	236	GLU	C-N-CA	6.11	128.38	120.44
1	A	349	GLY	N-CA-C	6.09	124.28	114.90
1	A	243	GLU	CA-C-N	6.03	128.64	120.38
1	A	243	GLU	C-N-CA	6.03	128.64	120.38
1	A	74	ARG	NH1-CZ-NH2	6.02	127.12	119.30
1	A	260	ILE	CA-C-N	5.91	132.82	121.54
1	A	260	ILE	C-N-CA	5.91	132.82	121.54
1	A	337	ARG	N-CA-CB	5.89	119.47	109.87
1	A	165	ARG	CB-CG-CD	5.81	124.66	111.30
1	A	48	PRO	O-C-N	5.80	130.90	122.78
1	A	195	GLN	O-C-N	-5.76	114.77	122.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	93	PRO	CA-C-N	5.74	127.79	120.56
1	A	93	PRO	C-N-CA	5.74	127.79	120.56
1	A	93	PRO	O-C-N	-5.61	115.78	122.24
1	A	138	HIS	CA-CB-CG	5.59	119.39	113.80
1	A	137	ARG	CB-CG-CD	5.57	124.12	111.30
1	A	136	ILE	CA-C-N	5.56	132.55	122.27
1	A	136	ILE	C-N-CA	5.56	132.55	122.27
1	A	195	GLN	CG-CD-OE1	5.54	131.87	120.80
1	A	243	GLU	CB-CG-CD	5.49	121.92	112.60
1	A	306	TRP	CA-CB-CG	-5.48	103.19	113.60
1	A	193	ILE	CA-C-N	5.41	128.31	120.79
1	A	193	ILE	C-N-CA	5.41	128.31	120.79
1	A	348	ARG	NE-CZ-NH1	-5.41	116.09	121.50
1	A	261	ASP	N-CA-C	5.37	122.24	110.80
1	A	207	GLY	CA-C-N	5.35	128.19	120.38
1	A	207	GLY	C-N-CA	5.35	128.19	120.38
1	A	291	TRP	CA-CB-CG	5.33	123.73	113.60
1	A	156	SER	O-C-N	5.26	127.70	122.12
1	A	327	VAL	CA-C-N	5.24	131.13	121.85
1	A	327	VAL	C-N-CA	5.24	131.13	121.85
1	A	261	ASP	CB-CG-OD1	5.22	130.40	118.40
1	A	106	ASN	CA-C-O	5.21	125.22	119.91
1	A	307	ARG	CD-NE-CZ	5.14	131.59	124.40
1	A	110	GLY	O-C-N	-5.11	118.64	122.88
1	A	109	GLU	N-CA-C	5.08	118.95	112.34
1	A	248	GLU	N-CA-C	5.07	117.38	110.24
1	A	51	THR	CA-C-N	5.06	130.93	122.73
1	A	51	THR	C-N-CA	5.06	130.93	122.73
1	A	47	ARG	NH1-CZ-NH2	-5.03	112.76	119.30
1	A	151	ILE	N-CA-C	5.01	117.31	111.05

There are no chirality outliers.

All (13) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	136	ILE	Mainchain
1	A	193	ILE	Mainchain
1	A	221	TYR	Mainchain
1	A	260	ILE	Mainchain
1	A	261	ASP	Peptide
1	A	306	TRP	Mainchain
1	A	317	ASP	Mainchain

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Mol	Chain	Res	Type	Group
1	A	319	ASP	Mainchain
1	A	327	VAL	Mainchain
1	A	328	ARG	Peptide,Mainchain
1	A	346	ASP	Mainchain
1	A	39	ASN	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	2914	0	2803	63	0
2	A	6	0	4	12	0
3	A	43	0	0	0	0
All	All	2963	0	2807	72	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 14.

All (72) 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)
2:A:1001:BMD:NA	2:A:1001:BMD:CA	1.69	1.51
2:A:1001:BMD:CA	2:A:1001:BMD:C1	1.89	1.50
2:A:1001:BMD:C1	2:A:1001:BMD:C3	2.15	1.24
2:A:1001:BMD:C3	2:A:1001:BMD:C2	0.90	0.90
1:A:9:LEU:HD11	1:A:52:LEU:HD13	1.54	0.87
1:A:141:GLU:HB2	1:A:169:GLY:HA2	1.60	0.82
2:A:1001:BMD:CA	2:A:1001:BMD:C3	2.62	0.77
2:A:1001:BMD:C1	2:A:1001:BMD:C2	2.66	0.74
1:A:346:ASP:HB2	1:A:350:VAL:H	1.54	0.72
1:A:92:MET:HG3	1:A:117:ILE:HD11	1.71	0.71
1:A:337:ARG:HH21	1:A:362:ARG:HH11	1.43	0.66
1:A:13:LEU:HD11	1:A:67:ALA:HB2	1.79	0.64
1:A:134:TYR:O	1:A:138:HIS:HB2	2.00	0.62
1:A:136:ILE:HA	1:A:140:GLY:O	2.00	0.61
2:A:1001:BMD:NA	2:A:1001:BMD:OA	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:236:GLU:HG3	1:A:351:PHE:CE1	2.39	0.58
1:A:81:GLY:O	1:A:82:CYS:HB2	2.03	0.58
1:A:337:ARG:HG2	1:A:362:ARG:HA	1.87	0.57
1:A:139:TYR:CE1	1:A:228:PRO:HG3	2.40	0.57
1:A:213:LEU:O	1:A:217:ILE:HG13	2.05	0.56
1:A:92:MET:HG3	1:A:117:ILE:CD1	2.34	0.56
1:A:346:ASP:HB2	1:A:350:VAL:N	2.21	0.56
1:A:84:MET:HA	2:A:1001:BMD:OA	2.06	0.55
1:A:312:GLN:O	1:A:313:ARG:C	2.49	0.54
1:A:172:LEU:HD12	1:A:198:ALA:HB2	1.90	0.53
1:A:103:CYS:O	1:A:105:PRO:HD3	2.08	0.53
1:A:298:ARG:HD2	1:A:298:ARG:H	1.74	0.52
1:A:134:TYR:OH	1:A:354:ARG:HG3	2.10	0.51
1:A:320:ILE:HG22	1:A:321:ASP:N	2.26	0.51
1:A:298:ARG:HD2	1:A:298:ARG:N	2.25	0.51
1:A:59:ASP:HB3	1:A:62:ARG:HD3	1.93	0.50
1:A:184:ASP:HB3	1:A:188:ARG:NH1	2.28	0.49
1:A:218:ALA:CB	1:A:246:VAL:HG22	2.41	0.49
1:A:369:VAL:O	1:A:372:LEU:HB2	2.13	0.49
1:A:78:PHE:HD2	1:A:296:LEU:HD11	1.78	0.48
1:A:83:TYR:CE2	2:A:1001:BMD:C3	2.97	0.48
1:A:343:ALA:HA	1:A:353:VAL:HA	1.95	0.48
1:A:100:ALA:O	1:A:116:ASN:HB3	2.14	0.47
1:A:159:VAL:HG11	1:A:367:VAL:HG11	1.96	0.47
1:A:291:TRP:HZ3	1:A:295:LEU:HD22	1.80	0.47
1:A:14:PHE:CE1	1:A:81:GLY:HA2	2.50	0.47
1:A:10:ILE:O	1:A:51:THR:HA	2.14	0.47
1:A:86:HIS:CD2	1:A:86:HIS:H	2.32	0.46
1:A:236:GLU:HG3	1:A:351:PHE:HE1	1.79	0.46
1:A:152:TYR:HB3	1:A:153:PRO:HD3	1.98	0.46
1:A:187:GLN:NE2	1:A:187:GLN:HA	2.31	0.46
1:A:205:VAL:HG21	1:A:213:LEU:HD22	1.98	0.45
1:A:17:THR:O	1:A:57:GLY:HA2	2.17	0.45
1:A:299:ALA:HB3	1:A:311:VAL:HG13	1.99	0.45
1:A:129:ALA:HB3	1:A:130:PRO:CD	2.46	0.45
1:A:63:TYR:CD1	1:A:87:THR:HB	2.52	0.45
1:A:142:ARG:NH1	1:A:197:ARG:O	2.50	0.44
1:A:179:LEU:O	1:A:181:PRO:HD3	2.17	0.44
1:A:77:ARG:HG2	1:A:77:ARG:HH11	1.83	0.43
1:A:129:ALA:HB3	1:A:130:PRO:HD3	2.00	0.43
1:A:357:SER:HA	1:A:358:PRO:HD3	1.86	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:152:TYR:CG	2:A:1001:BMD:CA	3.02	0.43
1:A:184:ASP:HB3	1:A:188:ARG:HH12	1.84	0.43
1:A:10:ILE:HD13	1:A:10:ILE:HG21	1.87	0.42
1:A:266:ARG:O	1:A:270:GLN:HG2	2.19	0.42
1:A:163:LEU:HD13	1:A:369:VAL:HG22	2.00	0.42
2:A:1001:BMD:NA	2:A:1001:BMD:C1	2.80	0.42
1:A:9:LEU:HG	1:A:76:VAL:HG22	2.02	0.42
1:A:331:ARG:HE	1:A:331:ARG:HB3	1.68	0.41
1:A:119:TYR:HB2	1:A:335:HIS:HA	2.02	0.41
1:A:12:LEU:HD13	1:A:28:ARG:HG3	2.01	0.41
1:A:92:MET:HB3	1:A:93:PRO:HD3	2.03	0.41
1:A:186:LEU:HD11	1:A:212:GLU:HB3	2.02	0.41
1:A:250:GLN:O	1:A:345:ILE:HG13	2.20	0.41
1:A:199:ASP:O	1:A:228:PRO:HD2	2.21	0.41
2:A:1001:BMD:CA	2:A:1001:BMD:C2	2.99	0.41
1:A:166:GLN:HA	1:A:166:GLN:OE1	2.21	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	366/385 (95%)	335 (92%)	26 (7%)	5 (1%)	9	23

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	138	HIS
1	A	261	ASP
1	A	329	VAL
1	A	225	ARG
1	A	41	GLU

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	303/315 (96%)	269 (89%)	34 (11%)	6 15

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	LEU
1	A	40	ARG
1	A	47	ARG
1	A	48	PRO
1	A	64	ARG
1	A	65	LEU
1	A	72	ARG
1	A	74	ARG
1	A	86	HIS
1	A	138	HIS
1	A	163	LEU
1	A	165	ARG
1	A	173	GLU
1	A	187	GLN
1	A	219	ARG
1	A	225	ARG
1	A	226	ARG
1	A	241	LYS
1	A	244	SER
1	A	246	VAL
1	A	250	GLN
1	A	261	ASP
1	A	265	SER
1	A	270	GLN
1	A	291	TRP
1	A	298	ARG
1	A	315	LEU
1	A	319	ASP
1	A	320	ILE
1	A	321	ASP

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Mol	Chain	Res	Type
1	A	328	ARG
1	A	369	VAL
1	A	373	ASP
1	A	374	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	GLN
1	A	158	HIS
1	A	162	HIS
1	A	187	GLN
1	A	270	GLN
1	A	312	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](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	BMD	A	1001	-	5,5,5	12.81	5 (100%)	5,5,5	14.07	5 (100%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	BMD	A	1001	-	-	1/3/3/3	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1001	BMD	C2-C1	22.03	2.66	1.51
2	A	1001	BMD	CA-NA	11.39	1.69	1.32
2	A	1001	BMD	C1-CA	9.58	1.89	1.51
2	A	1001	BMD	C3-C2	-8.38	0.90	1.50
2	A	1001	BMD	OA-CA	6.53	1.44	1.23

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1001	BMD	C2-C1-CA	-21.96	80.08	113.19
2	A	1001	BMD	C3-C2-C1	-15.59	46.71	112.69
2	A	1001	BMD	OA-CA-C1	11.92	157.03	121.04
2	A	1001	BMD	OA-CA-NA	-10.21	95.27	122.53
2	A	1001	BMD	C1-CA-NA	-4.29	102.76	116.49

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1001	BMD	CA-C1-C2-C3

There are no ring outliers.

1 monomer is involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1001	BMD	12	0

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	8

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	307:ARG	C	308:VAL	N	1.61
1	A	68:GLU	C	69:ASP	N	1.17
1	A	327:VAL	C	328:ARG	N	1.17
1	A	328:ARG	C	329:VAL	N	1.15
1	A	50:GLU	C	51:THR	N	1.12
1	A	317:ASP	C	318:ILE	N	1.11
1	A	221:TYR	C	222:GLY	N	1.08
1	A	261:ASP	C	262:THR	N	0.97

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	338/385 (87%)	0.08	9 (2%) 56 53	10, 28, 51, 64	3 (0%)

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	346	ASP	3.2
1	A	314	HIS	3.1
1	A	306	TRP	2.7
1	A	260	ILE	2.5
1	A	247	ALA	2.2
1	A	262	THR	2.2
1	A	298	ARG	2.1
1	A	374	ASP	2.1
1	A	183	ASP	2.0

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($\text{\AA}^2$)	Q<0.9
2	BMD	A	1001	6/6	0.95	0.08	3,4,12,16	0

6.5 Other polymers [i](#)

There are no such residues in this entry.