



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 12:13 PM UTC

PDB ID : 1MY2 / pdb_00001my2
Title : crystal titration experiment (AMPA complex control)
Authors : Jin, R.; Gouaux, E.
Deposited on : 2002-10-03
Resolution : 1.80 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)	:	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

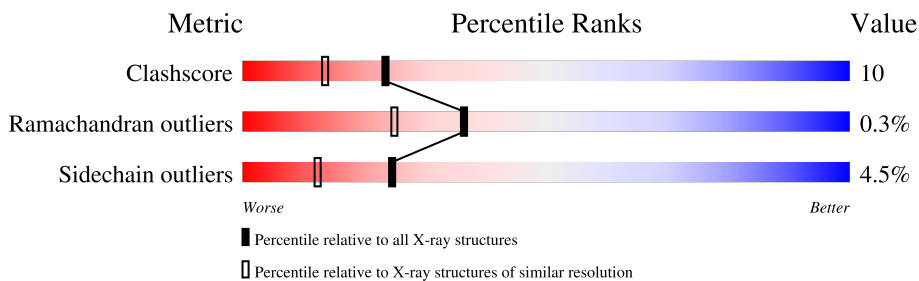
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)

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	263	
1	B	263	
1	C	263	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6513 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 GLUTAMATE RECEPTOR 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	258	Total	C	N	O	S	0	0	0
			2018	1286	336	382	14			
1	B	258	Total	C	N	O	S	0	0	0
			2018	1286	336	382	14			
1	C	258	Total	C	N	O	S	0	0	0
			2013	1282	335	382	14			

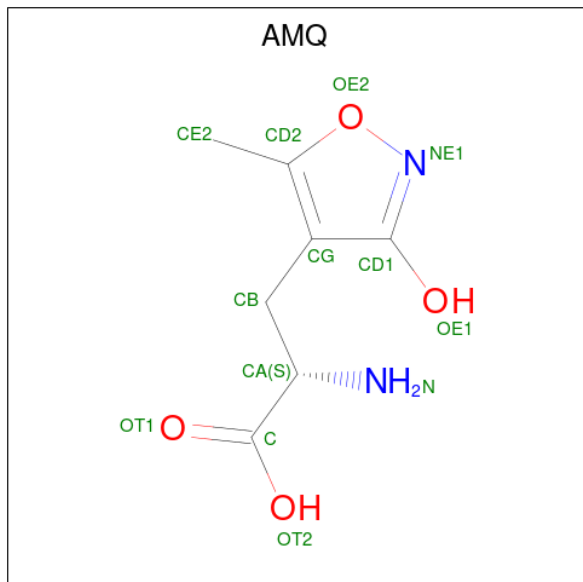
There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	cloning artifact	UNP P19491
A	2	ALA	-	cloning artifact	UNP P19491
A	118	GLY	-	linker	UNP P19491
A	119	THR	-	linker	UNP P19491
B	1	GLY	-	cloning artifact	UNP P19491
B	2	ALA	-	cloning artifact	UNP P19491
B	118	GLY	-	linker	UNP P19491
B	119	THR	-	linker	UNP P19491
C	1	GLY	-	cloning artifact	UNP P19491
C	2	ALA	-	cloning artifact	UNP P19491
C	118	GLY	-	linker	UNP P19491
C	119	THR	-	linker	UNP P19491

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 3 is (S)-ALPHA-AMINO-3-HYDROXY-5-METHYL-4-ISOXAZOLEPROPIONIC ACID (CCD ID: AMQ) (formula: C₇H₁₀N₂O₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			13	7	2	4		
3	B	1	Total	C	N	O	0	0
			13	7	2	4		
3	C	1	Total	C	N	O	0	0
			13	7	2	4		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	138	Total	O	0	0
			138	138		
4	B	164	Total	O	0	0
			164	164		
4	C	118	Total	O	0	0
			118	118		

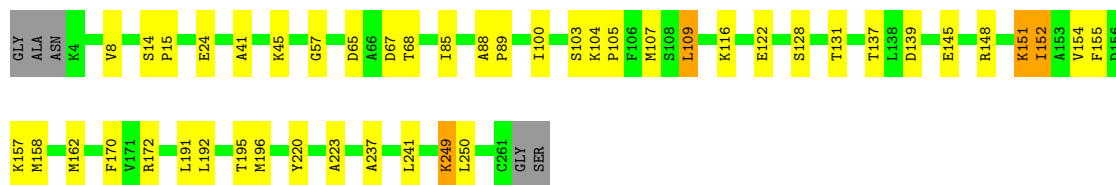
3 Residue-property plots [i](#)

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. 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.

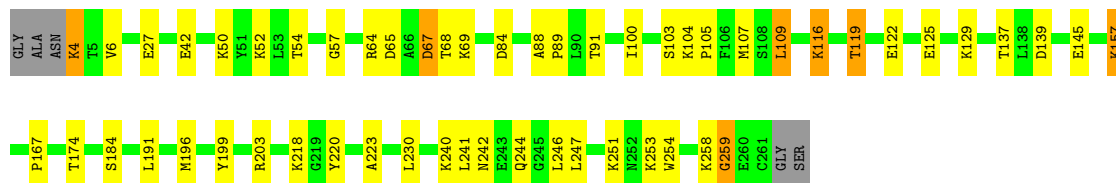
• Molecule 1: GLUTAMATE RECEPTOR 2

Chain A:  81% 16% ..



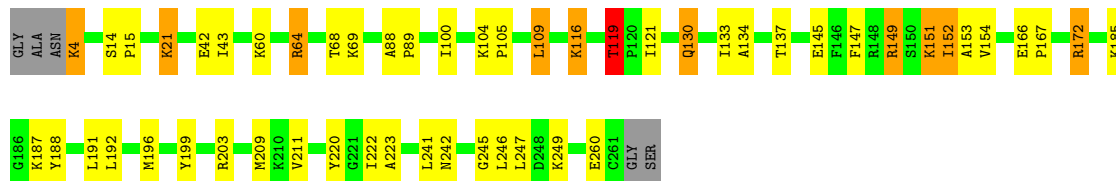
• Molecule 1: GLUTAMATE RECEPTOR 2

Chain B:  78% 18% ..



• Molecule 1: GLUTAMATE RECEPTOR 2

Chain C:  78% 16% ..



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 2	Depositor
Cell constants a, b, c, α , β , γ	114.54Å 164.10Å 47.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.73 – 1.80	Depositor
% Data completeness (in resolution range)	94.2 (29.73-1.80)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.225 , 0.244	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6513	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: AMQ, ZN

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	0.39	0/2054	0.81	4/2762 (0.1%)
1	B	0.38	0/2054	0.84	4/2762 (0.1%)
1	C	0.38	0/2049	0.86	4/2756 (0.1%)
All	All	0.38	0/6157	0.84	12/8280 (0.1%)

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	116	LYS	N-CA-C	-6.06	100.63	110.20
1	B	57	GLY	N-CA-C	5.87	119.75	112.64
1	B	104	LYS	N-CA-C	-5.76	101.83	109.84
1	A	104	LYS	N-CA-C	-5.74	101.86	109.84
1	A	116	LYS	N-CA-C	-5.74	101.13	110.20
1	C	104	LYS	N-CA-C	-5.67	101.95	109.84
1	B	103	SER	N-CA-C	-5.61	103.29	110.53
1	C	116	LYS	N-CA-C	-5.51	101.49	110.20
1	C	119	THR	CA-C-N	5.35	126.52	119.84
1	C	119	THR	C-N-CA	5.35	126.52	119.84
1	A	103	SER	N-CA-C	-5.12	103.93	110.53
1	A	57	GLY	N-CA-C	5.11	118.43	112.50

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	2018	0	2050	32	0
1	B	2018	0	2050	42	0
1	C	2013	0	2038	54	0
2	A	1	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
3	A	13	0	8	0	0
3	B	13	0	8	0	0
3	C	13	0	8	0	0
4	A	138	0	0	1	0
4	B	164	0	0	4	0
4	C	118	0	0	3	0
All	All	6513	0	6162	125	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 10.

All (125) 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:C:130:GLN:HE22	1:C:133:ILE:H	1.00	0.94
1:B:157:LYS:HA	1:B:157:LYS:HE3	1.55	0.88
1:C:116:LYS:O	1:C:119:THR:HG23	1.80	0.81
1:C:130:GLN:NE2	1:C:133:ILE:H	1.77	0.81
1:A:151:LYS:HA	1:A:151:LYS:HE2	1.65	0.76
1:C:130:GLN:HE22	1:C:133:ILE:N	1.80	0.74
1:A:145:GLU:CD	1:A:148:ARG:HH21	1.96	0.74
1:B:116:LYS:O	1:B:119:THR:HG23	1.88	0.74
1:B:4:LYS:HE3	1:B:4:LYS:HA	1.69	0.73
1:B:67:ASP:OD1	1:B:68:THR:HG23	1.87	0.72
1:C:21:LYS:HZ3	1:C:21:LYS:HA	1.55	0.71
1:C:21:LYS:HA	1:C:21:LYS:NZ	2.06	0.70
1:A:249:LYS:NZ	1:A:249:LYS:HB3	2.07	0.69
1:B:241:LEU:HD22	1:B:246:LEU:HD22	1.73	0.69
1:B:42:GLU:HG3	1:B:246:LEU:HD21	1.73	0.69
1:C:245:GLY:O	1:C:249:LYS:HG2	1.93	0.69
1:A:151:LYS:HA	1:A:151:LYS:CE	2.24	0.67
1:B:184:SER:HB2	4:B:865:HOH:O	1.95	0.66
1:C:199:TYR:CZ	1:C:203:ARG:HD2	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:88:ALA:HB1	1:C:89:PRO:HD2	1.77	0.65
1:A:152:ILE:HD11	1:A:154:VAL:HB	1.80	0.64
1:C:119:THR:HG21	4:C:773:HOH:O	1.98	0.64
1:A:88:ALA:HB1	1:A:89:PRO:HD2	1.80	0.63
1:C:14:SER:O	1:C:196:MET:HE1	1.99	0.63
1:A:137:THR:HG22	1:A:191:LEU:HB2	1.81	0.62
1:C:60:LYS:HG2	1:C:172:ARG:NH2	2.15	0.62
1:C:42:GLU:HG3	1:C:246:LEU:HD21	1.80	0.61
1:C:152:ILE:C	1:C:152:ILE:HD13	2.26	0.60
1:C:149:ARG:HH11	1:C:149:ARG:HG2	1.67	0.60
1:C:43:ILE:HD13	1:C:222:ILE:HD13	1.85	0.59
1:C:109:LEU:N	1:C:109:LEU:HD13	2.18	0.59
1:A:41:ALA:O	1:A:45:LYS:HG3	2.02	0.59
1:C:209:MET:HE2	1:C:211:VAL:HG12	1.86	0.57
1:C:64:ARG:HH11	1:C:64:ARG:HB3	1.69	0.57
1:C:137:THR:HG22	1:C:191:LEU:HB2	1.85	0.56
1:C:60:LYS:HZ3	1:C:172:ARG:NE	2.03	0.56
1:A:172:ARG:CZ	1:A:172:ARG:HB3	2.36	0.56
1:B:137:THR:HG22	1:B:191:LEU:HB2	1.86	0.55
1:B:119:THR:HG21	4:B:719:HOH:O	2.07	0.55
1:A:109:LEU:HD13	1:A:109:LEU:N	2.22	0.55
1:B:50:LYS:HE2	4:B:791:HOH:O	2.07	0.54
1:B:109:LEU:HD13	1:B:109:LEU:N	2.22	0.54
1:C:42:GLU:HG3	1:C:246:LEU:CD2	2.38	0.53
1:A:109:LEU:HB3	1:A:195:THR:HG23	1.91	0.53
1:C:149:ARG:HG2	1:C:149:ARG:NH1	2.21	0.53
1:B:88:ALA:HB1	1:B:89:PRO:HD2	1.89	0.52
1:C:43:ILE:HD13	1:C:222:ILE:CD1	2.39	0.52
1:C:242:ASN:HB2	1:C:247:LEU:HD12	1.92	0.52
1:B:42:GLU:HG3	1:B:246:LEU:CD2	2.39	0.52
1:C:100:ILE:HD12	1:C:223:ALA:HB1	1.91	0.52
1:A:8:VAL:HG22	1:A:85:ILE:CG2	2.39	0.51
1:B:105:PRO:HA	1:B:220:TYR:O	2.11	0.50
1:B:64:ARG:NH1	1:B:69:LYS:HD2	2.26	0.50
1:C:109:LEU:HD22	1:C:109:LEU:C	2.37	0.50
1:B:107:MET:HE2	1:B:251:LYS:HD3	1.93	0.50
1:B:254:TRP:CE3	1:B:258:LYS:HE3	2.46	0.50
1:C:105:PRO:HA	1:C:220:TYR:O	2.11	0.50
1:B:122:GLU:O	1:B:122:GLU:HG3	2.12	0.49
1:C:64:ARG:NH2	1:C:69:LYS:HD2	2.26	0.49
1:A:105:PRO:HA	1:A:220:TYR:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:64:ARG:HH21	1:C:69:LYS:HD2	1.77	0.49
1:C:199:TYR:CE2	1:C:203:ARG:HD2	2.48	0.49
1:C:154:VAL:HG23	4:C:795:HOH:O	2.11	0.49
1:A:14:SER:O	1:A:196:MET:HE1	2.13	0.49
1:B:145:GLU:HG3	4:B:815:HOH:O	2.11	0.49
1:B:199:TYR:O	1:B:203:ARG:HG2	2.13	0.48
1:B:100:ILE:HD12	1:B:223:ALA:HB1	1.95	0.48
1:A:192:LEU:HD23	1:A:192:LEU:H	1.78	0.48
1:A:249:LYS:HE3	1:B:167:PRO:CD	2.43	0.48
1:B:241:LEU:HD22	1:B:246:LEU:CD2	2.41	0.47
1:A:249:LYS:NZ	1:B:167:PRO:HD3	2.28	0.47
1:B:157:LYS:HA	1:B:157:LYS:CE	2.37	0.47
1:C:43:ILE:HD11	1:C:222:ILE:HD11	1.97	0.46
1:C:60:LYS:HG2	1:C:172:ARG:HH22	1.80	0.46
1:B:242:ASN:HB2	1:B:247:LEU:HD12	1.96	0.46
1:B:52:LYS:HZ2	1:B:54:THR:HG22	1.79	0.46
1:C:192:LEU:H	1:C:192:LEU:HD23	1.80	0.46
1:A:249:LYS:HE3	1:B:167:PRO:HD2	1.98	0.46
1:B:253:LYS:O	1:B:258:LYS:HE2	2.16	0.46
1:A:249:LYS:HB3	1:A:249:LYS:HZ2	1.80	0.46
1:B:67:ASP:CG	1:B:68:THR:N	2.74	0.45
1:B:91:THR:HG21	1:B:218:LYS:HD2	1.98	0.45
1:C:241:LEU:HD22	1:C:246:LEU:HD22	1.99	0.45
1:C:187:LYS:HG2	1:C:187:LYS:O	2.17	0.45
1:A:249:LYS:HB3	1:A:249:LYS:HZ3	1.78	0.45
1:A:107:MET:HE3	4:A:744:HOH:O	2.17	0.44
1:B:125:GLU:CD	1:B:129:LYS:HZ2	2.24	0.44
1:A:131:THR:O	1:A:131:THR:HG22	2.16	0.44
1:A:65:ASP:HB3	1:A:68:THR:OG1	2.17	0.44
1:C:43:ILE:CD1	1:C:222:ILE:CD1	2.96	0.44
1:C:134:ALA:O	1:C:188:TYR:HA	2.17	0.44
1:C:152:ILE:HD13	1:C:152:ILE:O	2.17	0.44
1:A:152:ILE:HG12	1:A:155:PHE:CD2	2.53	0.44
1:B:125:GLU:CD	1:B:129:LYS:NZ	2.76	0.44
1:B:109:LEU:C	1:B:109:LEU:HD22	2.43	0.44
1:C:151:LYS:HD3	1:C:151:LYS:C	2.43	0.44
1:A:128:SER:O	1:A:157:LYS:HE3	2.17	0.44
1:B:65:ASP:OD1	1:B:67:ASP:N	2.50	0.43
1:B:258:LYS:O	1:B:259:GLY:C	2.61	0.43
1:C:60:LYS:HZ3	1:C:172:ARG:CZ	2.32	0.43
1:C:4:LYS:HE3	1:C:4:LYS:N	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:240:LYS:O	1:B:244:GLN:HG3	2.18	0.43
1:C:203:ARG:HA	1:C:260:GLU:HG3	2.02	0.42
1:B:52:LYS:NZ	1:B:54:THR:CG2	2.82	0.42
1:C:121:ILE:HD11	1:C:133:ILE:HD12	2.02	0.42
1:C:147:PHE:CZ	1:C:191:LEU:HD13	2.54	0.42
1:A:139:ASP:OD2	1:A:170:PHE:HB3	2.19	0.42
1:A:192:LEU:HD23	1:A:192:LEU:N	2.34	0.42
1:B:174:THR:HG21	1:B:196:MET:HE2	2.01	0.42
1:B:6:VAL:HG13	1:B:84:ASP:HB2	2.01	0.42
1:C:109:LEU:N	1:C:109:LEU:CD1	2.82	0.42
1:B:65:ASP:O	1:B:69:LYS:HA	2.20	0.41
1:B:64:ARG:CZ	1:B:69:LYS:HD2	2.50	0.41
1:C:43:ILE:CD1	1:C:222:ILE:HD11	2.50	0.41
1:A:152:ILE:C	1:A:152:ILE:HD12	2.45	0.41
1:C:68:THR:O	1:C:69:LYS:HB2	2.19	0.41
1:A:237:ALA:O	1:A:241:LEU:HG	2.21	0.41
1:A:100:ILE:HD12	1:A:223:ALA:HB1	2.03	0.41
1:A:158:MET:O	1:A:162:MET:HG3	2.21	0.41
1:C:166:GLU:HA	1:C:167:PRO:C	2.44	0.41
1:C:192:LEU:HD23	1:C:192:LEU:N	2.35	0.41
1:C:60:LYS:HZ2	1:C:172:ARG:NH2	2.19	0.41
1:C:60:LYS:NZ	1:C:172:ARG:CZ	2.84	0.40
1:A:152:ILE:O	1:A:152:ILE:HG13	2.20	0.40
1:C:145:GLU:HG2	4:C:762:HOH:O	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	256/263 (97%)	254 (99%)	2 (1%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	256/263 (97%)	250 (98%)	5 (2%)	1 (0%)	30	19
1	C	256/263 (97%)	249 (97%)	6 (2%)	1 (0%)	30	19
All	All	768/789 (97%)	753 (98%)	13 (2%)	2 (0%)	36	25

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	259	GLY
1	C	153	ALA

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	217/219 (99%)	208 (96%)	9 (4%)	27	15
1	B	217/219 (99%)	209 (96%)	8 (4%)	30	18
1	C	216/219 (99%)	204 (94%)	12 (6%)	19	8
All	All	650/657 (99%)	621 (96%)	29 (4%)	24	12

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	PRO
1	A	24	GLU
1	A	67	ASP
1	A	109	LEU
1	A	122	GLU
1	A	151	LYS
1	A	152	ILE
1	A	249	LYS
1	A	250	LEU
1	B	4	LYS
1	B	27	GLU
1	B	67	ASP

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Mol	Chain	Res	Type
1	B	109	LEU
1	B	119	THR
1	B	139	ASP
1	B	157	LYS
1	B	230	LEU
1	C	4	LYS
1	C	15	PRO
1	C	21	LYS
1	C	64	ARG
1	C	109	LEU
1	C	119	THR
1	C	130	GLN
1	C	149	ARG
1	C	151	LYS
1	C	152	ILE
1	C	172	ARG
1	C	185	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	130	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](#)

Of 8 ligands modelled in this entry, 5 are monoatomic - leaving 3 for Mogul analysis.

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$
3	AMQ	C	601	-	12,13,13	1.06	2 (16%)	9,18,18	1.26	1 (11%)
3	AMQ	B	603	-	12,13,13	1.00	1 (8%)	9,18,18	1.20	1 (11%)
3	AMQ	A	602	-	12,13,13	1.00	1 (8%)	9,18,18	1.17	1 (11%)

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
3	AMQ	C	601	-	-	1/8/8/8	0/1/1/1
3	AMQ	B	603	-	-	0/8/8/8	0/1/1/1
3	AMQ	A	602	-	-	0/8/8/8	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	601	AMQ	OE2-CD2	2.07	1.38	1.34
3	A	602	AMQ	OE2-CD2	2.06	1.38	1.34
3	C	601	AMQ	OT1-C	2.04	1.28	1.22
3	B	603	AMQ	OE2-CD2	2.02	1.38	1.34

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	601	AMQ	OE1-CD1-CG	-3.05	116.48	124.43
3	A	602	AMQ	OE1-CD1-CG	-2.81	117.08	124.43
3	B	603	AMQ	OE1-CD1-CG	-2.81	117.10	124.43

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	601	AMQ	OT1-C-CA-N

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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.