



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:48 AM UTC

PDB ID : 3PVU / pdb_00003pvu
Title : Bovine GRK2 in complex with Gbetagamma subunits and a selective kinase inhibitor (CMPD101)
Authors : Thal, D.M.; Tesmer, J.J.
Deposited on : 2010-12-07
Resolution : 2.48 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
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

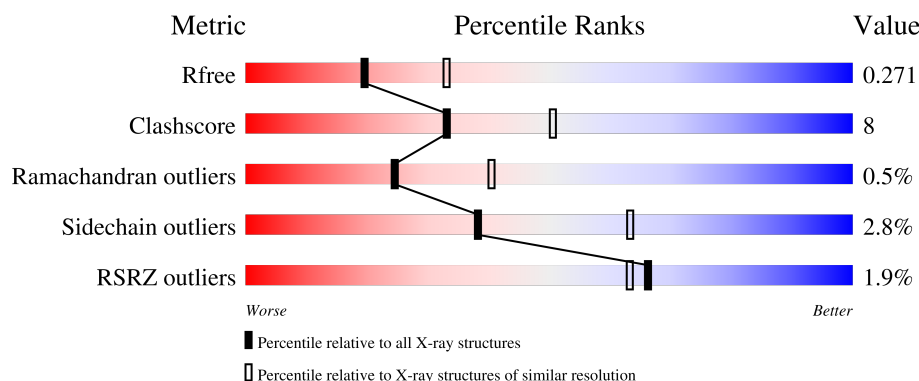
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.48 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	7589 (2.50-2.46)
Clashscore	190562	8295 (2.50-2.46)
Ramachandran outliers	187476	8164 (2.50-2.46)
Sidechain outliers	187428	8166 (2.50-2.46)
RSRZ outliers	180081	7593 (2.50-2.46)

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	695	 2% 72% 14% 12%
2	B	340	 82% 15%
3	G	74	 3% 69% 14% 18%

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
3	CMT	G	68	-	X	-	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 8132 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 Beta-adrenergic receptor kinase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	609	Total	C	N	O	S	0	0	0
			4998	3189	870	903	36			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	670	ALA	SER	engineered mutation	UNP P21146
A	690	HIS	-	expression tag	UNP P21146
A	691	HIS	-	expression tag	UNP P21146
A	692	HIS	-	expression tag	UNP P21146
A	693	HIS	-	expression tag	UNP P21146
A	694	HIS	-	expression tag	UNP P21146
A	695	HIS	-	expression tag	UNP P21146

- Molecule 2 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	339	Total	C	N	O	S	0	0	0
			2607	1607	468	511	21			

- Molecule 3 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	61	Total	C	N	O	S	0	0	0
			481	305	83	89	4			

There are 6 discrepancies between the modelled and reference sequences:

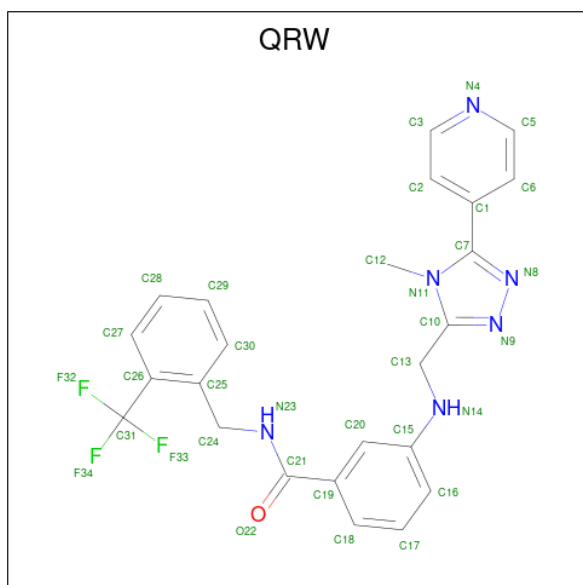
Chain	Residue	Modelled	Actual	Comment	Reference
G	-5	HIS	-	expression tag	UNP P63212

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-4	HIS	-	expression tag	UNP P63212
G	-3	HIS	-	expression tag	UNP P63212
G	-2	HIS	-	expression tag	UNP P63212
G	-1	HIS	-	expression tag	UNP P63212
G	0	HIS	-	expression tag	UNP P63212

- Molecule 4 is 3-([4-methyl-5-(pyridin-4-yl)-4H-1,2,4-triazol-3-yl]methyl)amino)-N-[2-(trifluoromethyl)benzyl]benzamide (CCD ID: QRW) (formula: C₂₄H₂₁F₃N₆O).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	F	N	O	0	0
			34	24	3	6	1		

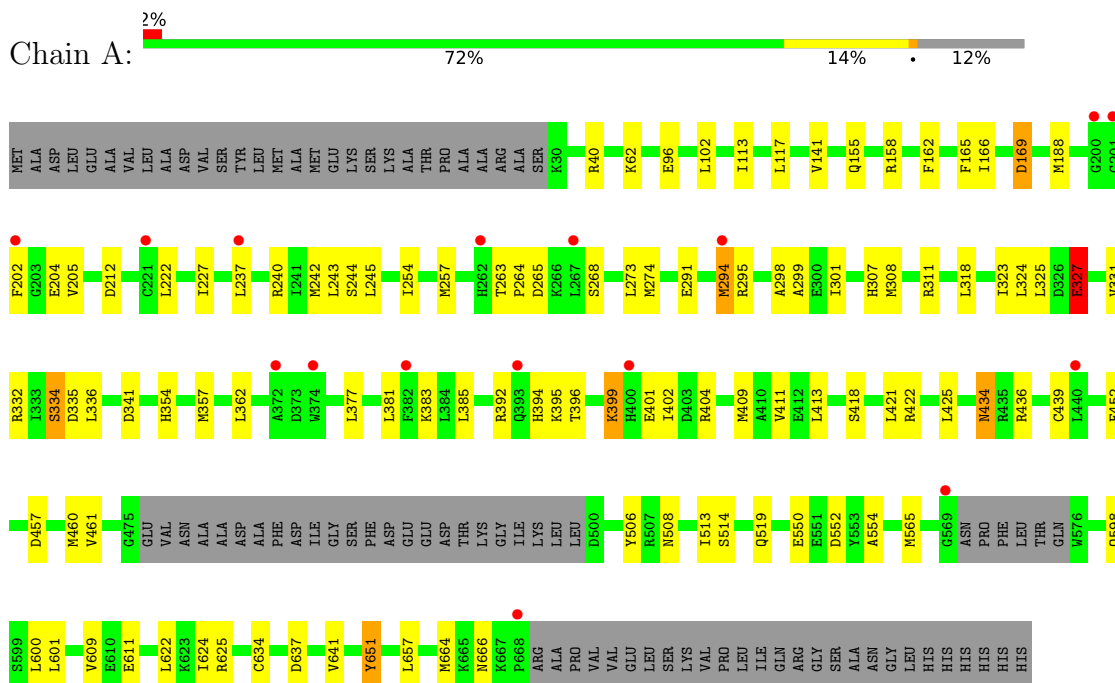
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	8	Total	O	0	0
			8	8		
5	B	4	Total	O	0	0
			4	4		

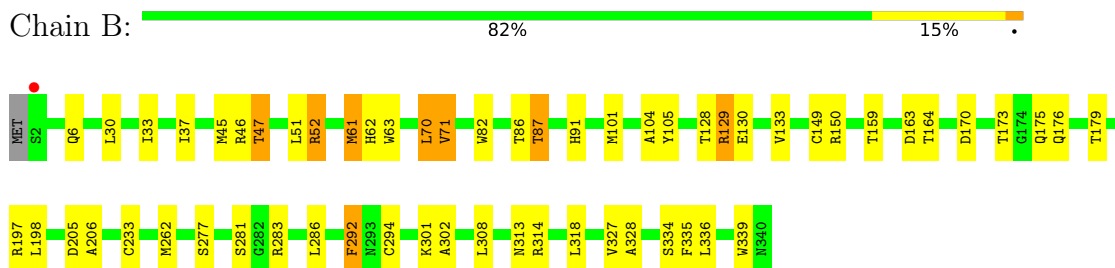
3 Residue-property plots

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 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.

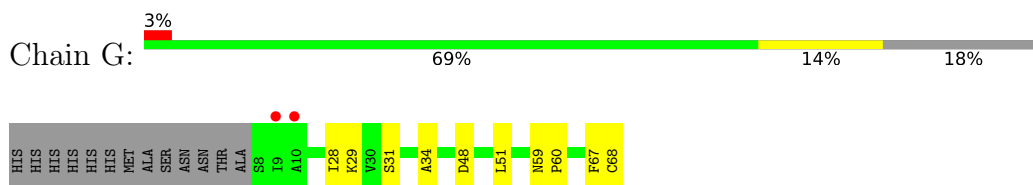
- Molecule 1: Beta-adrenergic receptor kinase 1



- Molecule 2: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1



- Molecule 3: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	186.50Å 73.50Å 121.99Å 90.00° 115.10° 90.00°	Depositor
Resolution (Å)	30.00 – 2.48 30.00 – 2.48	Depositor EDS
% Data completeness (in resolution range)	96.9 (30.00-2.48) 97.0 (30.00-2.48)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.23 (at 2.48Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.226 , 0.274 0.229 , 0.271	Depositor DCC
R_{free} test set	2636 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	73.4	Xtriage
Anisotropy	0.066	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 43.0	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	0.95	EDS
Total number of atoms	8132	wwPDB-VP
Average B, all atoms (Å ²)	89.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.86% 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: QRW, CMT

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	0.53	1/5111 (0.0%)	0.77	1/6866 (0.0%)
2	B	0.60	0/2654	0.75	0/3597
3	G	0.55	0/481	0.78	0/646
All	All	0.55	1/8246 (0.0%)	0.76	1/11109 (0.0%)

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
3	G	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	334	SER	CA-C	5.34	1.56	1.53

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	334	SER	N-CA-C	7.49	115.94	108.75

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	G	67	PHE	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	4998	0	4991	72	1
2	B	2607	0	2510	52	1
3	G	481	0	493	8	0
4	A	34	0	21	2	0
5	A	8	0	0	1	0
5	B	4	0	0	0	0
All	All	8132	0	8015	125	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 8.

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)
2:B:30:LEU:HD23	2:B:262:MET:HE2	1.50	0.90
2:B:86:THR:O	2:B:87:THR:HB	1.68	0.90
2:B:61:MET:HE2	2:B:62:HIS:N	1.89	0.86
1:A:609:VAL:HG22	1:A:622:LEU:HD22	1.65	0.77
2:B:128:THR:HG22	2:B:130:GLU:H	1.51	0.75
2:B:45:MET:HE3	2:B:308:LEU:HD21	1.68	0.75
2:B:176:GLN:NE2	2:B:179:THR:HG22	2.03	0.74
1:A:354:HIS:HA	1:A:357:MET:HE2	1.69	0.72
2:B:176:GLN:HE21	2:B:179:THR:HG22	1.54	0.71
1:A:202:PHE:CD2	4:A:800:QRW:H24	2.24	0.71
1:A:294:MET:HE2	1:A:295:ARG:HA	1.77	0.67
1:A:274:MET:HE2	1:A:332:ARG:HB2	1.75	0.67
1:A:609:VAL:HG22	1:A:622:LEU:CD2	2.24	0.66
2:B:33:ILE:HD11	3:G:31:SER:HA	1.76	0.65
1:A:409:MET:HE3	1:A:411:VAL:HA	1.79	0.64
1:A:399:LYS:HA	1:A:402:ILE:HD12	1.80	0.63
2:B:63:TRP:CZ2	2:B:328:ALA:HB2	2.35	0.62
1:A:565:MET:HE3	1:A:634:CYS:SG	2.40	0.62
2:B:47:THR:HG22	2:B:339:TRP:CZ3	2.35	0.62
2:B:286:LEU:HD12	2:B:286:LEU:N	2.15	0.61
2:B:61:MET:HE3	2:B:70:LEU:HD13	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:149:CYS:O	2:B:150:ARG:NH1	2.35	0.60
2:B:61:MET:HE3	2:B:70:LEU:CD1	2.31	0.60
1:A:155:GLN:OE1	1:A:158:ARG:NH1	2.35	0.59
2:B:52:ARG:HD2	2:B:335:PHE:HE1	1.67	0.59
2:B:173:THR:HG22	2:B:175:GLN:HG2	1.84	0.59
1:A:62:LYS:NZ	1:A:519:GLN:OE1	2.35	0.59
1:A:202:PHE:HB2	1:A:222:LEU:HD22	1.87	0.57
1:A:357:MET:HB2	1:A:362:LEU:HD21	1.86	0.57
2:B:71:VAL:HG23	2:B:105:TYR:CD2	2.40	0.57
1:A:245:LEU:O	1:A:311:ARG:HD3	2.05	0.56
1:A:237:LEU:C	1:A:237:LEU:HD23	2.30	0.56
1:A:308:MET:HE2	1:A:336:LEU:HD21	1.89	0.54
1:A:308:MET:CE	1:A:336:LEU:HD21	2.39	0.52
2:B:30:LEU:CD2	2:B:262:MET:HE2	2.32	0.52
1:A:169:ASP:N	1:A:169:ASP:OD1	2.41	0.52
1:A:385:LEU:HD13	1:A:421:LEU:HD21	1.91	0.52
1:A:457:ASP:OD2	1:A:457:ASP:C	2.52	0.52
1:A:294:MET:HE2	1:A:295:ARG:CA	2.40	0.51
2:B:86:THR:O	2:B:87:THR:CB	2.49	0.51
1:A:294:MET:HE3	1:A:298:ALA:CB	2.41	0.51
2:B:318:LEU:HA	2:B:328:ALA:O	2.10	0.51
2:B:33:ILE:HD12	3:G:34:ALA:HB3	1.91	0.51
1:A:434:ASN:HD22	1:A:434:ASN:H	1.59	0.51
2:B:318:LEU:C	2:B:318:LEU:HD12	2.37	0.50
1:A:383:LYS:NZ	5:A:702:HOH:O	2.43	0.50
2:B:37:ILE:O	2:B:301:LYS:NZ	2.44	0.50
1:A:298:ALA:HB2	1:A:381:LEU:CD2	2.42	0.50
1:A:357:MET:CB	1:A:362:LEU:HD21	2.42	0.50
2:B:233:CYS:SG	2:B:277:SER:HA	2.52	0.50
2:B:313:ASN:O	2:B:314:ARG:C	2.55	0.50
1:A:385:LEU:CD1	1:A:421:LEU:HD21	2.42	0.50
3:G:28:ILE:HG22	3:G:29:LYS:O	2.12	0.50
2:B:70:LEU:HD11	2:B:336:LEU:HD22	1.92	0.49
2:B:281:SER:HB3	3:G:48:ASP:HB2	1.93	0.49
1:A:294:MET:HE1	1:A:452:PHE:CE2	2.48	0.49
1:A:301:ILE:HD11	1:A:323:ILE:HD13	1.95	0.49
1:A:318:LEU:HD21	1:A:377:LEU:HD13	1.94	0.49
2:B:283:ARG:HB3	3:G:51:LEU:HD11	1.94	0.49
2:B:173:THR:HG22	2:B:175:GLN:CG	2.43	0.49
1:A:227:ILE:HG21	1:A:506:TYR:OH	2.13	0.48
2:B:51:LEU:HD13	2:B:82:TRP:CD2	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:651:TYR:C	1:A:651:TYR:CD1	2.92	0.48
2:B:301:LYS:O	2:B:302:ALA:HB3	2.14	0.47
1:A:141:VAL:O	1:A:141:VAL:HG23	2.13	0.47
2:B:163:ASP:C	2:B:164:THR:HG23	2.39	0.47
1:A:40:ARG:NH2	1:A:166:ILE:O	2.45	0.47
2:B:33:ILE:CD1	3:G:34:ALA:HB3	2.44	0.47
2:B:286:LEU:CD2	2:B:327:VAL:HG21	2.44	0.47
1:A:113:ILE:O	1:A:117:LEU:HB2	2.15	0.46
1:A:299:ALA:HB1	1:A:461:VAL:HG11	1.97	0.46
2:B:292:PHE:CD1	2:B:292:PHE:N	2.83	0.46
1:A:334:SER:O	1:A:335:ASP:C	2.59	0.46
1:A:294:MET:HE2	1:A:295:ARG:N	2.31	0.46
1:A:291:GLU:HG2	1:A:421:LEU:HD22	1.98	0.45
1:A:294:MET:HE2	1:A:294:MET:C	2.42	0.45
1:A:294:MET:HE3	1:A:298:ALA:HB2	1.98	0.45
2:B:33:ILE:CD1	3:G:31:SER:HA	2.46	0.45
1:A:401:GLU:HA	1:A:404:ARG:HG2	1.99	0.45
1:A:513:ILE:O	1:A:514:SER:C	2.59	0.45
1:A:325:LEU:HD12	1:A:331:VAL:HG12	1.99	0.45
2:B:128:THR:O	2:B:130:GLU:N	2.50	0.44
2:B:63:TRP:HZ2	2:B:328:ALA:HB2	1.80	0.44
2:B:128:THR:O	2:B:129:ARG:C	2.60	0.44
1:A:273:LEU:HD12	1:A:274:MET:H	1.82	0.44
2:B:205:ASP:O	2:B:206:ALA:HB3	2.18	0.44
1:A:357:MET:HE3	1:A:362:LEU:CD2	2.48	0.44
1:A:409:MET:CE	1:A:411:VAL:HG22	2.48	0.44
2:B:149:CYS:HB3	2:B:159:THR:HG22	2.00	0.43
1:A:637:ASP:O	1:A:641:VAL:HG23	2.18	0.43
2:B:128:THR:C	2:B:130:GLU:N	2.77	0.43
2:B:61:MET:HE3	2:B:70:LEU:HD12	2.01	0.43
2:B:197:ARG:O	2:B:198:LEU:HD23	2.18	0.43
1:A:298:ALA:HB2	1:A:381:LEU:HD21	2.01	0.43
2:B:71:VAL:CG2	2:B:105:TYR:CD2	3.02	0.43
1:A:436:ARG:HG2	1:A:439:CYS:SG	2.59	0.43
1:A:327:GLU:H	1:A:327:GLU:CD	2.27	0.43
1:A:664:MET:HE3	2:B:101:MET:HG3	2.00	0.43
1:A:243:LEU:HD22	1:A:257:MET:HB2	2.00	0.42
1:A:421:LEU:HD11	1:A:425:LEU:HD11	1.99	0.42
1:A:565:MET:CE	1:A:634:CYS:SG	3.06	0.42
1:A:102:LEU:HA	1:A:141:VAL:HG11	2.01	0.42
1:A:254:ILE:HD11	1:A:307:HIS:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:286:LEU:N	2:B:286:LEU:CD1	2.82	0.42
2:B:170:ASP:HB3	2:B:173:THR:HB	2.02	0.42
2:B:61:MET:HE2	2:B:62:HIS:CA	2.48	0.42
1:A:96:GLU:HG2	1:A:460:MET:HE1	2.02	0.42
1:A:188:MET:HE1	1:A:268:SER:OG	2.19	0.42
2:B:91:HIS:CD2	2:B:133:VAL:HG21	2.54	0.42
1:A:418:SER:O	1:A:422:ARG:HG3	2.20	0.42
1:A:552:ASP:OD2	1:A:554:ALA:HB3	2.20	0.41
1:A:600:LEU:C	1:A:600:LEU:HD12	2.45	0.41
1:A:263:THR:HB	1:A:264:PRO:HD2	2.01	0.41
2:B:104:ALA:HB2	2:B:149:CYS:O	2.20	0.41
3:G:59:ASN:HA	3:G:60:PRO:HD2	1.88	0.41
1:A:411:VAL:HG12	1:A:413:LEU:HD23	2.03	0.41
1:A:96:GLU:HG2	1:A:460:MET:CE	2.50	0.41
1:A:205:VAL:HG11	4:A:800:QRW:C2	2.51	0.41
1:A:666:ASN:N	1:A:666:ASN:HD22	2.18	0.41
1:A:242:MET:HE1	1:A:341:ASP:HB2	2.02	0.41
1:A:624:ILE:HG22	1:A:625:ARG:N	2.36	0.41
1:A:324:LEU:O	1:A:331:VAL:HA	2.21	0.40
1:A:392:ARG:NH2	1:A:395:LYS:O	2.54	0.40
1:A:162:PHE:O	1:A:165:PHE:HB3	2.22	0.40
2:B:163:ASP:C	2:B:163:ASP:OD1	2.65	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:598:GLN:OE1	2:B:46:ARG:NH2[2_657]	2.19	0.01

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	603/695 (87%)	562 (93%)	38 (6%)	3 (0%)	24	40
2	B	337/340 (99%)	316 (94%)	19 (6%)	2 (1%)	21	35
3	G	59/74 (80%)	56 (95%)	3 (5%)	0	100	100
All	All	999/1109 (90%)	934 (94%)	60 (6%)	5 (0%)	24	40

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	129	ARG
1	A	212	ASP
1	A	327	GLU
1	A	394	HIS
2	B	334	SER

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	548/617 (89%)	532 (97%)	16 (3%)	37	62
2	B	282/283 (100%)	273 (97%)	9 (3%)	34	58
3	G	50/61 (82%)	50 (100%)	0	100	100
All	All	880/961 (92%)	855 (97%)	25 (3%)	38	63

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	169	ASP
1	A	204	GLU
1	A	240	ARG
1	A	244	SER
1	A	265	ASP
1	A	294	MET
1	A	327	GLU
1	A	396	THR

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Mol	Chain	Res	Type
1	A	399	LYS
1	A	434	ASN
1	A	508	ASN
1	A	550	GLU
1	A	601	LEU
1	A	611	GLU
1	A	651	TYR
1	A	657	LEU
2	B	6	GLN
2	B	47	THR
2	B	52	ARG
2	B	61	MET
2	B	70	LEU
2	B	71	VAL
2	B	87	THR
2	B	292	PHE
2	B	294	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	140	GLN
1	A	194	HIS
1	A	310	ASN
1	A	434	ASN
1	A	607	GLN
1	A	666	ASN
2	B	91	HIS
2	B	176	GLN
2	B	239	ASN
2	B	259	GLN
2	B	293	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue 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	$\# Z > 2$
3	CMT	G	68	3	7,7,7	2.23	1 (14%)	6,8,8	2.15	3 (50%)

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	CMT	G	68	3	-	6/8/8/8	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	68	CMT	OXT-C	5.79	1.47	1.33

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	68	CMT	OXT-C-CA	3.59	120.62	111.50
3	G	68	CMT	C1-OXT-C	2.43	121.44	115.92
3	G	68	CMT	CA-CB-SG	-2.43	109.21	114.40

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	G	68	CMT	O-C-OXT-C1
3	G	68	CMT	CA-C-OXT-C1
3	G	68	CMT	O-C-CA-N
3	G	68	CMT	OXT-C-CA-N
3	G	68	CMT	N-CA-CB-SG
3	G	68	CMT	C-CA-CB-SG

There are no ring outliers.

No monomer is involved in short contacts.

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
4	QRW	A	800	-	37,37,37	2.03	6 (16%)	50,52,52	2.01	10 (20%)

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
4	QRW	A	800	-	-	3/24/24/24	0/4/4/4

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	800	QRW	N9-N8	-7.33	1.24	1.39
4	A	800	QRW	C13-C10	5.50	1.53	1.49
4	A	800	QRW	C1-C7	-5.08	1.39	1.47
4	A	800	QRW	C7-N11	-2.64	1.33	1.37
4	A	800	QRW	C31-C26	2.63	1.56	1.50
4	A	800	QRW	C10-N11	-2.36	1.32	1.36

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	800	QRW	N11-C7-N8	-9.72	105.77	110.28
4	A	800	QRW	N11-C10-N9	-3.31	105.99	110.42
4	A	800	QRW	C1-C7-N11	3.31	129.46	125.01
4	A	800	QRW	C25-C24-N23	-3.29	106.52	113.15
4	A	800	QRW	C13-C10-N11	3.03	127.00	123.12
4	A	800	QRW	C24-C25-C30	-2.81	114.78	120.98
4	A	800	QRW	F34-C31-C26	-2.78	107.71	112.65
4	A	800	QRW	C31-C26-C25	2.62	123.57	121.06
4	A	800	QRW	C10-N9-N8	2.09	109.88	107.59
4	A	800	QRW	C12-N11-C10	-2.05	124.62	126.96

There are no chirality outliers.

All (3) torsion outliers are listed below:

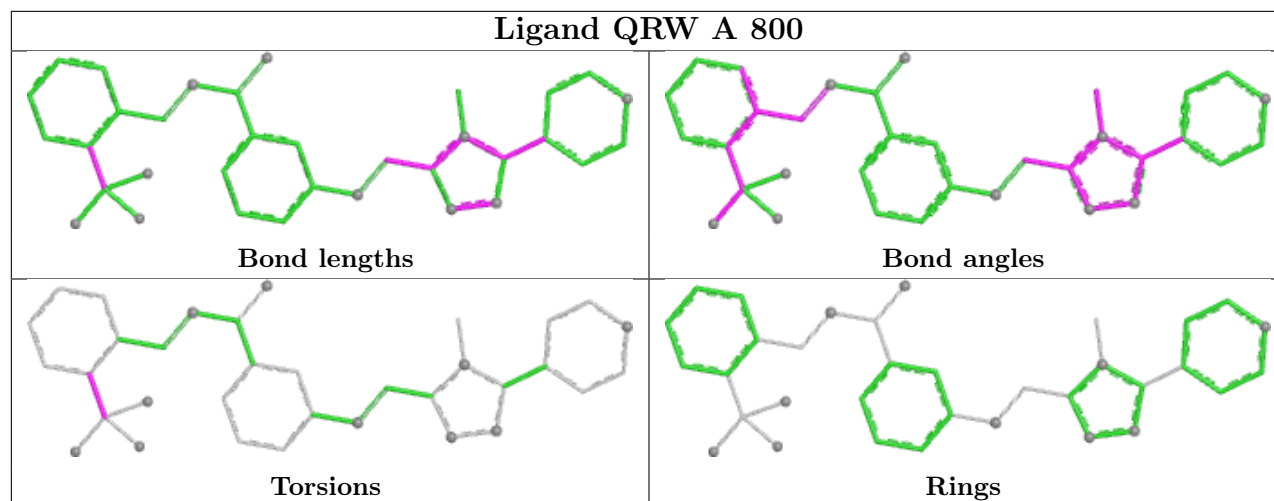
Mol	Chain	Res	Type	Atoms
4	A	800	QRW	C25-C26-C31-F34
4	A	800	QRW	C25-C26-C31-F33
4	A	800	QRW	C25-C26-C31-F32

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	800	QRW	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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

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	609/695 (87%)	0.34	16 (2%) 57 53	63, 90, 132, 182	0
2	B	339/340 (99%)	0.04	1 (0%) 90 88	54, 74, 120, 208	0
3	G	60/74 (81%)	0.28	2 (3%) 49 45	63, 82, 161, 176	0
All	All	1008/1109 (90%)	0.24	19 (1%) 66 63	54, 84, 132, 208	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	G	9	ILE	4.6
1	A	440	LEU	4.1
1	A	202	PHE	3.6
1	A	668	PRO	3.5
1	A	200	GLY	3.1
1	A	382	PHE	3.0
2	B	2	SER	2.8
1	A	569	GLY	2.7
1	A	374	TRP	2.5
1	A	267	LEU	2.5
1	A	372	ALA	2.4
3	G	10	ALA	2.4
1	A	393	GLN	2.3
1	A	221	CYS	2.3
1	A	400	HIS	2.2
1	A	201	GLY	2.1
1	A	237	LEU	2.1
1	A	294	MET	2.0
1	A	262	HIS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
3	CMT	G	68	8/8	0.66	0.14	85,88,93,95	0

6.3 Carbohydrates [i](#)

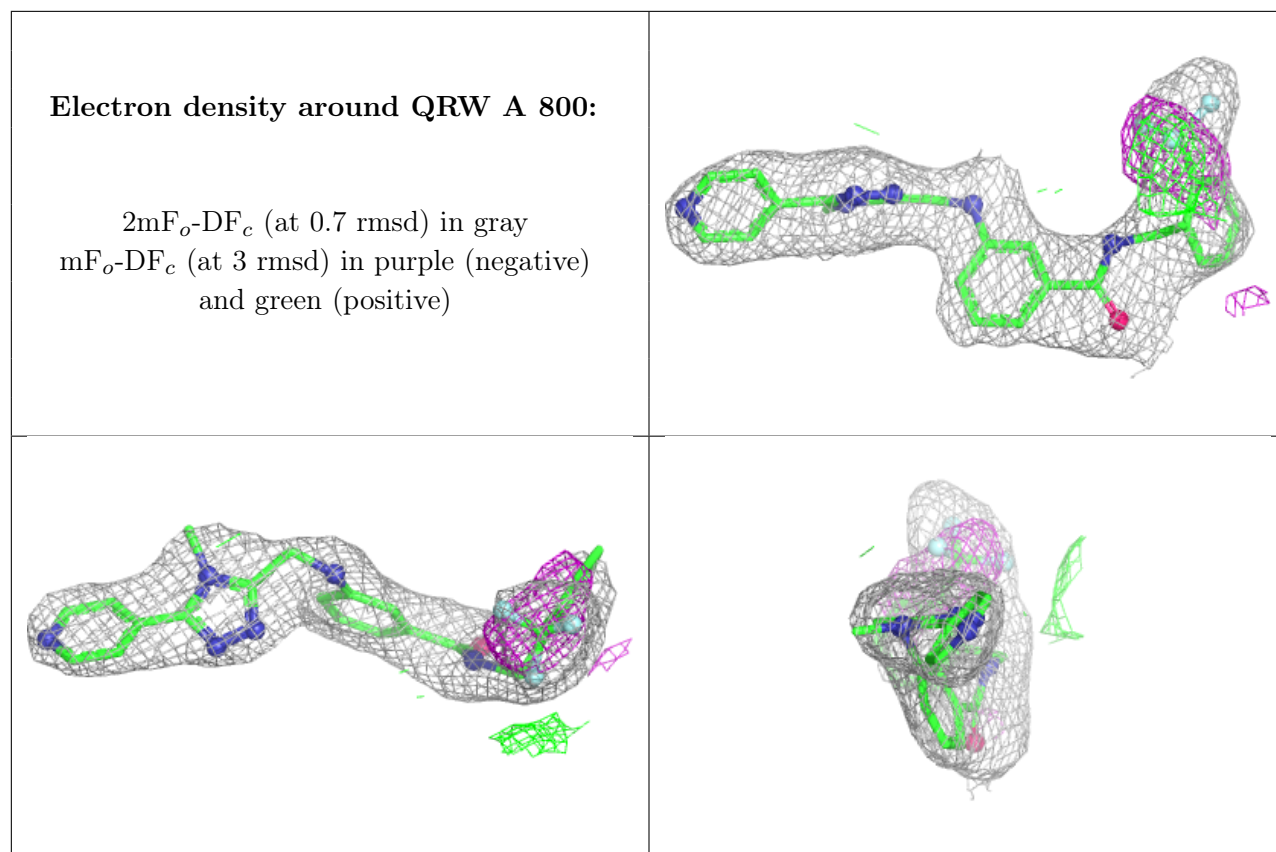
There are no oligosaccharides in this entry.

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(Å ²)	Q<0.9
4	QRW	A	800	34/34	0.86	0.13	78,84,99,100	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers [i](#)

There are no such residues in this entry.