



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 9, 2026 – 04:10 pm BST

PDB ID : 9RHH / pdb_00009rhh
Title : Crystal structure of Kinase domain of HRI kinase
Authors : Rajasekaran, M.B.; Roe, S.M.; Spencer, J.
Deposited on : 2025-06-09
Resolution : 2.08 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 : 1.8.4, CSD as541be (2020)
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 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

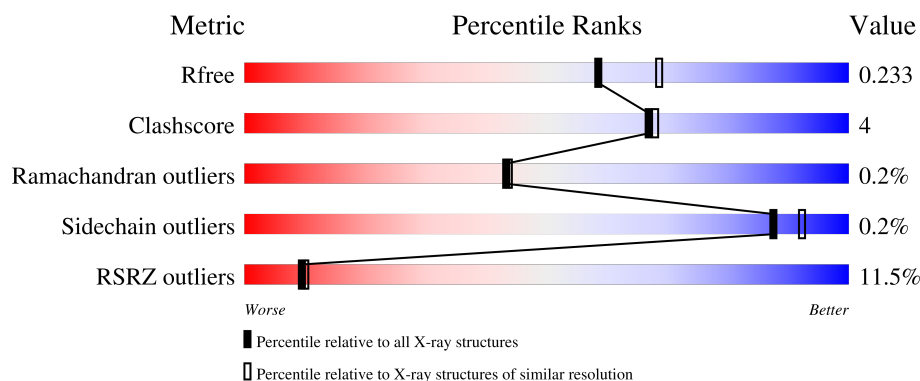
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.08 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	8172 (2.10-2.06)
Clashscore	190562	8714 (2.10-2.06)
Ramachandran outliers	187476	8641 (2.10-2.06)
Sidechain outliers	187428	8642 (2.10-2.06)
RSRZ outliers	180081	8177 (2.10-2.06)

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	310	9% 80% 8% 12%
1	B	310	11% 77% 8% 15%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4373 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.

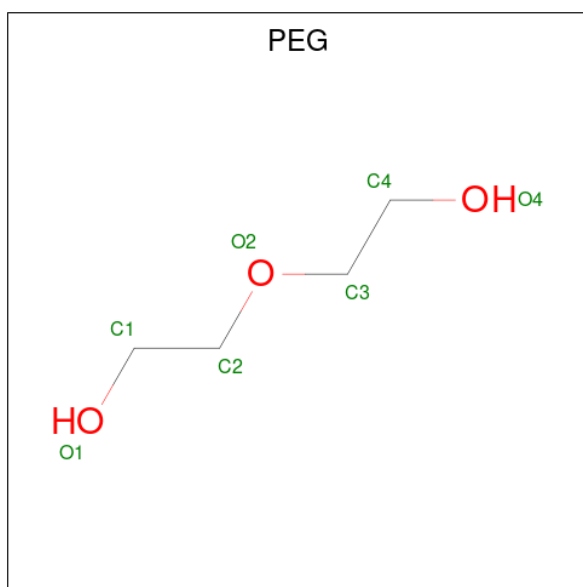
- Molecule 1 is a protein called Eukaryotic translation initiation factor 2-alpha kinase 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	274	Total	C	N	O	P	S	0	0	0
			2125	1361	367	385	1	11			
1	B	264	Total	C	N	O	S		0	0	0
			2004	1294	344	356	10				

There are 16 discrepancies between the modelled and reference sequences:

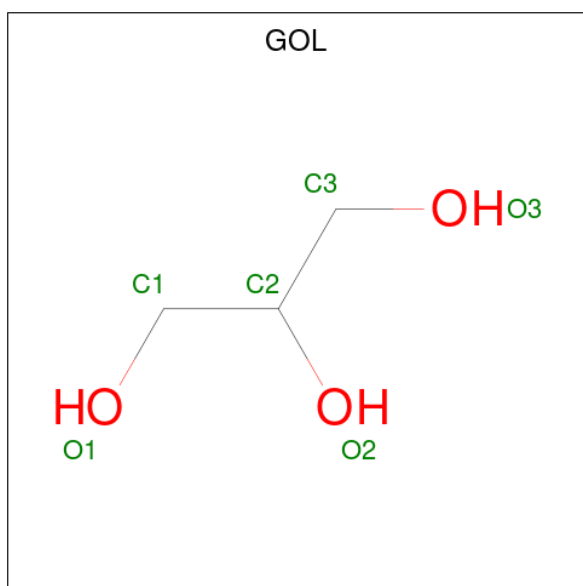
Chain	Residue	Modelled	Actual	Comment	Reference
A	149	GLY	-	expression tag	UNP Q9BQI3
A	150	PRO	-	expression tag	UNP Q9BQI3
A	151	LEU	-	expression tag	UNP Q9BQI3
A	152	GLY	-	expression tag	UNP Q9BQI3
A	153	SER	-	expression tag	UNP Q9BQI3
A	154	MET	-	expression tag	UNP Q9BQI3
A	372	GLY	-	linker	UNP Q9BQI3
A	373	SER	-	linker	UNP Q9BQI3
B	149	GLY	-	expression tag	UNP Q9BQI3
B	150	PRO	-	expression tag	UNP Q9BQI3
B	151	LEU	-	expression tag	UNP Q9BQI3
B	152	GLY	-	expression tag	UNP Q9BQI3
B	153	SER	-	expression tag	UNP Q9BQI3
B	154	MET	-	expression tag	UNP Q9BQI3
B	372	GLY	-	linker	UNP Q9BQI3
B	373	SER	-	linker	UNP Q9BQI3

- Molecule 2 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



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

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		

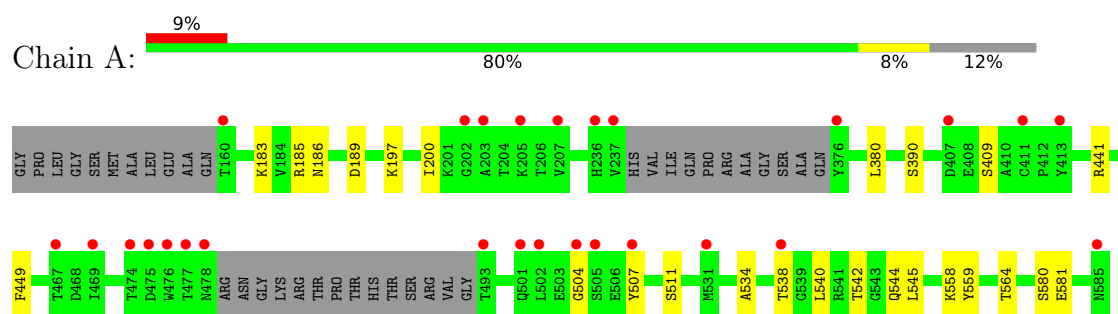
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	130	Total	O	0	0
			130	130		
4	B	87	Total	O	0	0
			87	87		

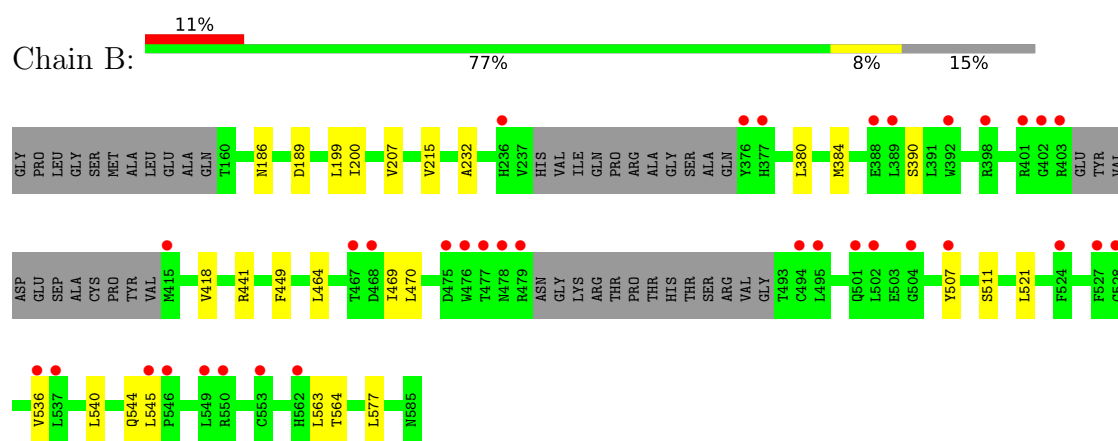
3 Residue-property plots [i](#)

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: Eukaryotic translation initiation factor 2-alpha kinase 1



- Molecule 1: Eukaryotic translation initiation factor 2-alpha kinase 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	56.37Å 78.14Å 90.17Å 90.00° 99.22° 90.00°	Depositor
Resolution (Å)	44.11 – 2.08 44.11 – 2.08	Depositor EDS
% Data completeness (in resolution range)	69.1 (44.11-2.08) 69.2 (44.11-2.08)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.89 (at 2.08Å)	Xtriage
Refinement program	PHENIX 1.21.1_5286	Depositor
R, R_{free}	0.206 , 0.232 0.207 , 0.233	Depositor DCC
R_{free} test set	1611 reflections (3.46%)	wwPDB-VP
Wilson B-factor (Å ²)	39.9	Xtriage
Anisotropy	0.013	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 54.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4373	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.85% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SEP, GOL, PEG

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	0.08	0/2157	0.25	0/2923
1	B	0.08	0/2044	0.23	0/2771
All	All	0.08	0/4201	0.24	0/5694

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	2125	0	2054	16	0
1	B	2004	0	1931	14	0
2	A	7	0	10	2	0
2	B	14	0	20	2	0
3	A	6	0	8	0	0
4	A	130	0	0	1	0
4	B	87	0	0	0	0
All	All	4373	0	4023	30	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 4.

All (30) 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:B:540:LEU:HD13	1:B:564:THR:HG21	1.75	0.69
1:A:540:LEU:HD13	1:A:564:THR:HG21	1.80	0.64
1:B:441:ARG:HA	1:B:507:TYR:CZ	2.33	0.62
1:B:200:ILE:HD11	1:B:380:LEU:HB2	1.87	0.55
1:A:441:ARG:HA	1:A:507:TYR:CZ	2.42	0.54
1:A:183:LYS:HZ3	2:A:601:PEG:H12	1.75	0.52
1:B:215:VAL:HG11	1:B:232:ALA:HB2	1.94	0.50
1:A:185:ARG:NH2	2:B:602:PEG:H11	2.28	0.49
1:A:534:ALA:O	1:A:538:THR:OG1	2.20	0.48
1:B:507:TYR:CE1	1:B:511:SER:HB2	2.48	0.48
1:A:200:ILE:HD11	1:A:380:LEU:HB2	1.95	0.47
1:A:185:ARG:HH22	2:B:602:PEG:H11	1.80	0.46
1:A:507:TYR:CE1	1:A:511:SER:HB2	2.51	0.45
1:B:207:VAL:HG13	1:B:469:ILE:HD13	1.98	0.45
1:A:197:LYS:NZ	4:A:703:HOH:O	2.49	0.45
1:A:186:ASN:HB3	1:A:189:ASP:OD1	2.17	0.45
1:B:563:LEU:HD21	1:B:577:LEU:HD11	1.99	0.45
1:A:542:THR:OG1	1:A:544:GLN:OE1	2.33	0.44
1:A:183:LYS:NZ	2:A:601:PEG:H12	2.34	0.43
1:B:544:GLN:C	1:B:545:LEU:HD12	2.43	0.43
1:B:384:MET:HE3	1:B:384:MET:HB2	1.81	0.42
1:A:544:GLN:C	1:A:545:LEU:HD12	2.44	0.42
1:B:199:LEU:HD12	1:B:199:LEU:HA	1.88	0.42
1:A:559:TYR:CZ	1:A:580:SER:HB2	2.55	0.42
1:B:390:SER:HA	1:B:449:PHE:HA	2.02	0.41
1:B:464:LEU:HD12	1:B:470:LEU:HD11	2.01	0.41
1:B:521:LEU:HD21	1:B:536:VAL:HG12	2.03	0.41
1:A:390:SER:HA	1:A:449:PHE:HA	2.03	0.40
1:A:558:LYS:NZ	1:A:581:GLU:OE2	2.41	0.40
1:B:186:ASN:HB3	1:B:189:ASP:OD1	2.22	0.40

There are no symmetry-related clashes.

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	267/310 (86%)	258 (97%)	8 (3%)	1 (0%)	30	28
1	B	256/310 (83%)	249 (97%)	7 (3%)	0	100	100
All	All	523/620 (84%)	507 (97%)	15 (3%)	1 (0%)	43	44

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	504	GLY

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	213/267 (80%)	213 (100%)	0	100	100
1	B	197/267 (74%)	196 (100%)	1 (0%)	81	87
All	All	410/534 (77%)	409 (100%)	1 (0%)	87	92

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	418	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	544	GLN
1	B	236	HIS

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	$\# Z > 2$
1	SEP	A	409	1	8,9,10	1.53	1 (12%)	8,12,14	1.13	1 (12%)

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
1	SEP	A	409	1	-	2/5/8/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	409	SEP	P-O1P	3.33	1.61	1.50

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	409	SEP	P-OG-CB	-2.13	112.42	118.30

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	409	SEP	CB-OG-P-O2P
1	A	409	SEP	N-CA-CB-OG

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](#)

4 ligands are 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	PEG	B	601	-	6,6,6	0.24	0	5,5,5	0.27	0
2	PEG	B	602	-	6,6,6	0.24	0	5,5,5	0.31	0
2	PEG	A	601	-	6,6,6	0.24	0	5,5,5	0.27	0
3	GOL	A	602	-	5,5,5	0.28	0	5,5,5	0.27	0

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	PEG	B	601	-	-	2/4/4/4	-
2	PEG	B	602	-	-	1/4/4/4	-
2	PEG	A	601	-	-	1/4/4/4	-
3	GOL	A	602	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	602	PEG	O1-C1-C2-O2
2	B	601	PEG	C1-C2-O2-C3
2	B	601	PEG	C4-C3-O2-C2

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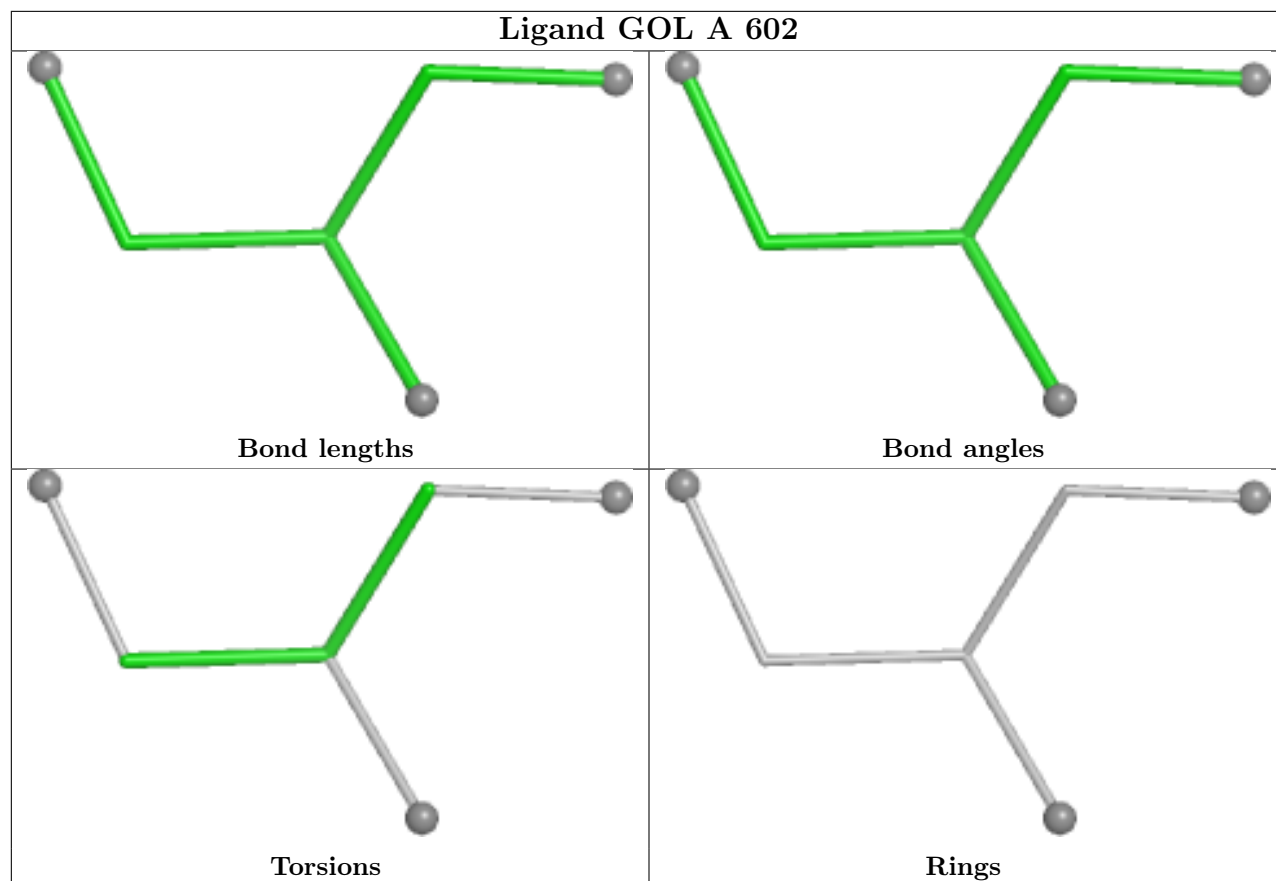
Mol	Chain	Res	Type	Atoms
2	A	601	PEG	C4-C3-O2-C2

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	602	PEG	2	0
2	A	601	PEG	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	273/310 (88%)	0.46	27 (9%) 13 13	25, 42, 78, 102	0
1	B	264/310 (85%)	0.72	35 (13%) 7 7	27, 49, 83, 114	0
All	All	537/620 (86%)	0.59	62 (11%) 9 10	25, 45, 82, 114	0

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	376	TYR	4.6
1	B	545	LEU	4.6
1	A	203	ALA	4.6
1	B	392	TRP	4.5
1	A	478	ASN	4.2
1	B	388	GLU	4.1
1	A	493	THR	3.9
1	B	415	MET	3.6
1	B	502	LEU	3.6
1	A	202	GLY	3.6
1	B	476	TRP	3.4
1	A	413	TYR	3.4
1	B	467	THR	3.4
1	B	477	THR	3.3
1	A	376	TYR	3.3
1	B	507	TYR	3.1
1	B	495	LEU	3.1
1	B	527	PHE	3.1
1	A	502	LEU	3.0
1	A	411	CYS	3.0
1	B	478	ASN	3.0
1	A	467	THR	3.0
1	A	476	TRP	3.0
1	A	507	TYR	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	377	HIS	2.8
1	B	479	ARG	2.7
1	A	477	THR	2.6
1	B	468	ASP	2.6
1	A	237	VAL	2.6
1	B	501	GLN	2.6
1	B	536	VAL	2.6
1	A	538	THR	2.6
1	A	475	ASP	2.6
1	B	403	ARG	2.6
1	B	524	PHE	2.5
1	B	475	ASP	2.5
1	B	389	LEU	2.5
1	B	549	LEU	2.5
1	B	550	ARG	2.4
1	B	528	GLY	2.4
1	B	494	CYS	2.4
1	B	553	CYS	2.4
1	A	504	GLY	2.4
1	A	469	ILE	2.3
1	A	207	VAL	2.3
1	A	236	HIS	2.3
1	B	562	HIS	2.3
1	B	401	ARG	2.3
1	A	531	MET	2.3
1	A	501	GLN	2.3
1	B	504	GLY	2.3
1	A	585	ASN	2.2
1	B	236	HIS	2.2
1	B	546	PRO	2.2
1	B	402	GLY	2.2
1	B	537	LEU	2.1
1	A	505	SER	2.1
1	B	398	ARG	2.0
1	A	160	THR	2.0
1	A	474	THR	2.0
1	A	407	ASP	2.0
1	A	205	LYS	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
1	SEP	A	409	10/11	0.79	0.13	47,72,85,87	4

6.3 Carbohydrates [i](#)

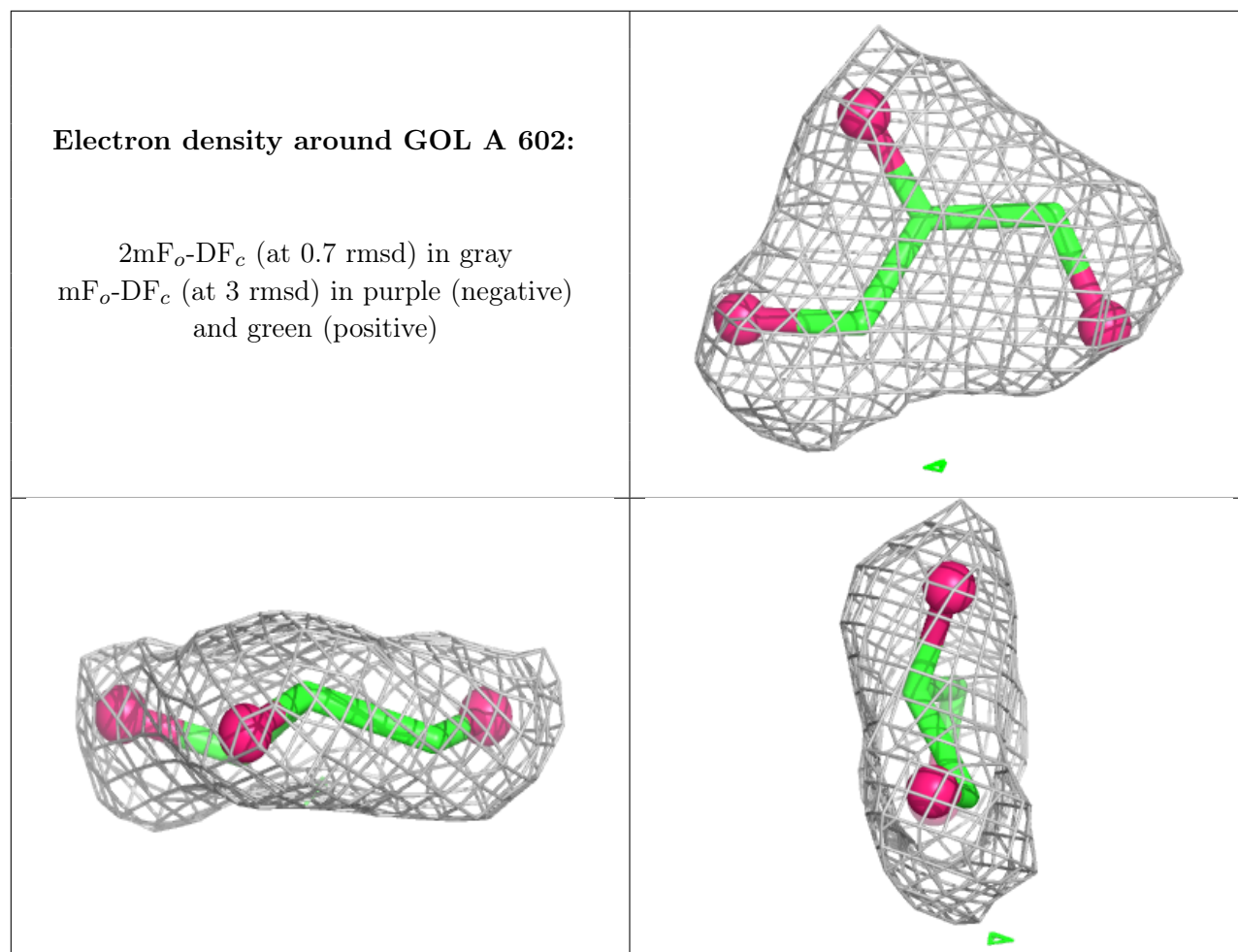
There are no oligosaccharides in this entry.

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
2	PEG	B	601	7/7	0.80	0.14	53,58,67,68	0
3	GOL	A	602	6/6	0.83	0.14	59,61,68,77	0
2	PEG	B	602	7/7	0.87	0.13	47,48,66,72	0
2	PEG	A	601	7/7	0.89	0.13	41,47,68,68	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.