



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 5, 2026 – 10:32 AM EDT

PDB ID : 1WQ1 / pdb_00001wq1
Title : RAS-RASGAP COMPLEX
Authors : Scheffzek, K.; Ahmadian, M.R.; Kabsch, W.; Wiesmueller, L.; Lautwein, A.; Schmitz, F.; Wittinghofer, A.
Deposited on : 1997-07-03
Resolution : 2.50 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
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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)	:	2.50

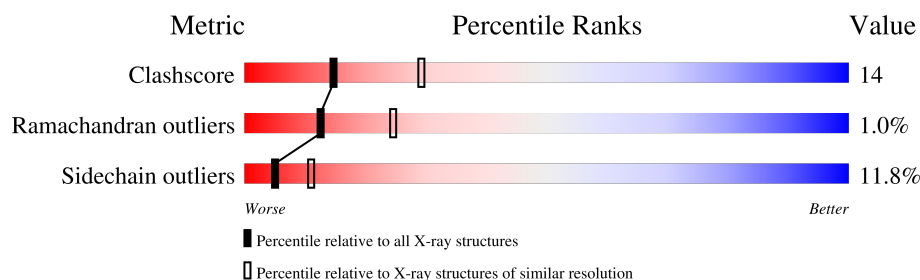
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)

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	R	166	
2	G	334	

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 3922 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 H-RAS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	R	166	Total	C	N	O	S	0	0	0
			1322	823	228	264	7			

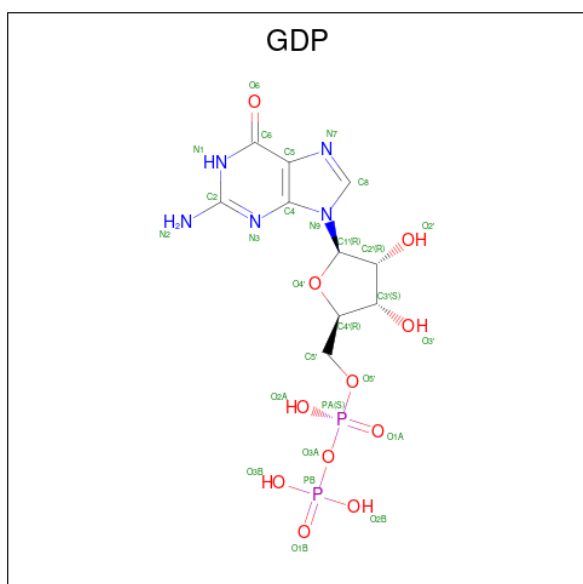
- Molecule 2 is a protein called P120GAP.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	320	Total	C	N	O	S	0	0	0
			2532	1611	431	473	17			

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

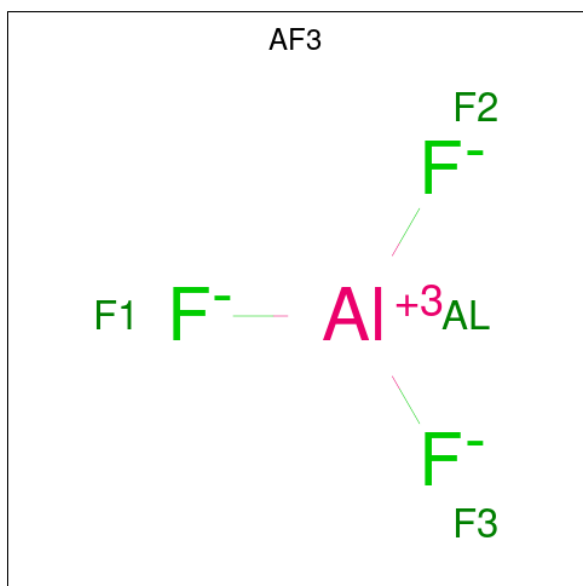
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	R	1	Total	Mg	0	0
			1	1		

- Molecule 4 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	R	1	Total	C	N	O	P	0	0
			28	10	5	11	2		

- Molecule 5 is ALUMINUM FLUORIDE (CCD ID: AF3) (formula: AlF_3).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	R	1	Total	Al	F	0	0
			4	1	3		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	R	11	Total	O	0	0
			11	11		
6	G	24	Total	O	0	0
			24	24		

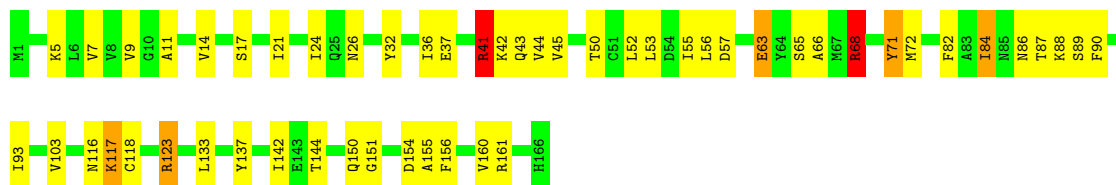
3 Residue-property plots [i](#)

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.

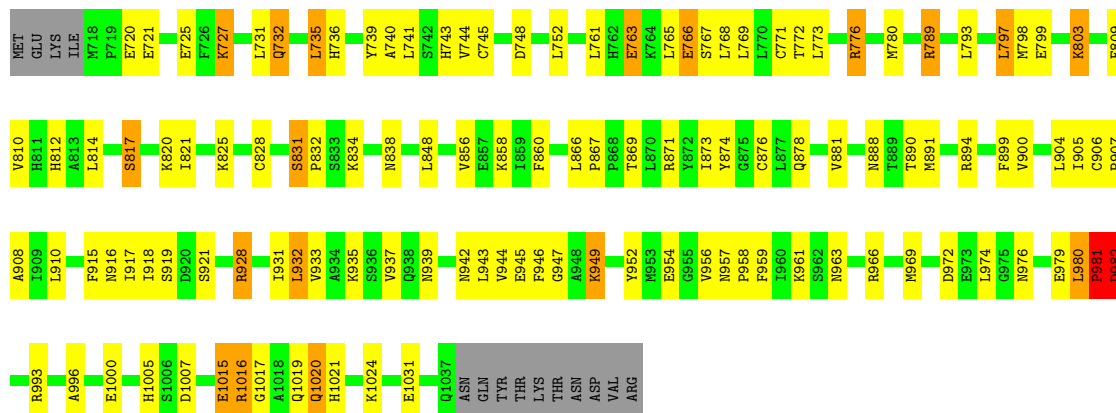
• Molecule 1: H-RAS

Chain R:  68% 28% ..



• Molecule 2: P120GAP

Chain G:  59% 31% 5% ..



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	71.90Å 41.10Å 89.00Å 90.00° 108.40° 90.00°	Depositor
Resolution (Å)	30.00 – 2.50	Depositor
% Data completeness (in resolution range)	77.3 (30.00-2.50)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
Refinement program	X-PLOR 3.8	Depositor
R, R_{free}	0.233 , 0.319	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3922	wwPDB-VP
Average B, all atoms (Å ²)	38.0	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: AF3, GDP, MG

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	R	0.51	0/1341	0.78	0/1808
2	G	0.56	1/2574 (0.0%)	0.88	7/3483 (0.2%)
All	All	0.55	1/3915 (0.0%)	0.85	7/5291 (0.1%)

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	R	0	4
2	G	0	2
All	All	0	6

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	981	PRO	C-O	12.59	1.39	1.24

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	981	PRO	N-CA-C	10.79	129.17	114.18
2	G	982	ASP	N-CA-C	9.17	130.33	110.80
2	G	980	LEU	CA-C-N	6.43	126.14	119.64
2	G	980	LEU	C-N-CA	6.43	126.14	119.64
2	G	956	VAL	N-CA-C	-5.67	107.46	112.90
2	G	921	SER	CA-C-N	5.39	125.31	119.76
2	G	921	SER	C-N-CA	5.39	125.31	119.76

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	G	981	PRO	Peptide
2	G	982	ASP	Mainchain
1	R	123	ARG	Sidechain
1	R	41	ARG	Sidechain
1	R	68	ARG	Sidechain
1	R	71	TYR	Sidechain

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	R	1322	0	1290	32	0
2	G	2532	0	2587	80	0
3	R	1	0	0	0	0
4	R	28	0	12	1	0
5	R	4	0	0	0	0
6	G	24	0	0	1	0
6	R	11	0	0	0	0
All	All	3922	0	3889	107	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 (107) 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:G:761:LEU:HD23	2:G:766:GLU:HG2	1.59	0.84
2:G:739:TYR:CE1	2:G:773:LEU:HD12	2.15	0.81
2:G:832:PRO:HD3	2:G:952:TYR:HB3	1.68	0.76
1:R:41:ARG:HE	1:R:52:LEU:HD21	1.51	0.74
2:G:803:LYS:HZ2	2:G:915:PHE:HZ	1.38	0.72
2:G:736:HIS:CD2	2:G:1019:GLN:HG2	2.28	0.69
1:R:84:ILE:HD12	1:R:123:ARG:HB2	1.78	0.65
2:G:957:ASN:HB3	2:G:961:LYS:NZ	2.14	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:866:LEU:HD21	2:G:874:TYR:HE2	1.66	0.60
2:G:727:LYS:HD3	2:G:731:LEU:HD11	1.83	0.60
2:G:957:ASN:N	2:G:958:PRO:HD2	2.17	0.60
1:R:142:ILE:HD13	1:R:155:ALA:HA	1.83	0.60
2:G:799:GLU:O	2:G:803:LYS:HD3	2.01	0.59
2:G:946:PHE:H	2:G:957:ASN:HD21	1.49	0.59
2:G:810:VAL:HG13	2:G:814:LEU:HD22	1.84	0.59
2:G:776:ARG:NH1	2:G:780:MET:SD	2.75	0.59
2:G:810:VAL:O	2:G:814:LEU:HB2	2.03	0.58
1:R:42:LYS:HE2	1:R:44:VAL:CG1	2.33	0.58
1:R:21:ILE:HD11	2:G:949:LYS:HG2	1.86	0.57
1:R:82:PHE:HB3	1:R:93:ILE:HD11	1.86	0.57
2:G:888:ASN:OD1	2:G:890:THR:HG22	2.04	0.57
1:R:68:ARG:HG2	1:R:72:MET:HE3	1.86	0.56
1:R:32:TYR:HB2	2:G:894:ARG:NH1	2.21	0.56
2:G:980:LEU:HD12	2:G:981:PRO:HD2	1.86	0.56
2:G:739:TYR:CE1	2:G:776:ARG:HG3	2.40	0.56
2:G:928:ARG:HD2	2:G:932:LEU:HD22	1.89	0.55
2:G:957:ASN:HB3	2:G:961:LYS:HZ3	1.72	0.55
2:G:908:ALA:HB2	2:G:915:PHE:CE1	2.42	0.54
2:G:741:LEU:HA	2:G:744:VAL:HG22	1.89	0.54
2:G:798:MET:HG3	2:G:899:PHE:CE1	2.44	0.52
2:G:740:ALA:HA	2:G:743:HIS:HD2	1.74	0.52
2:G:996:ALA:O	2:G:1000:GLU:HG3	2.10	0.51
1:R:68:ARG:HA	1:R:71:TYR:CE2	2.47	0.50
2:G:767:SER:O	2:G:771:CYS:HB2	2.12	0.49
1:R:68:ARG:HG3	1:R:71:TYR:OH	2.13	0.49
2:G:1017:GLY:O	2:G:1020:GLN:HB2	2.12	0.49
2:G:732:GLN:HA	2:G:732:GLN:HE21	1.77	0.48
2:G:942:ASN:O	2:G:943:LEU:HB2	2.14	0.48
2:G:963:ASN:HD22	2:G:966:ARG:HD3	1.79	0.48
2:G:1016:ARG:HA	2:G:1020:GLN:HG3	1.94	0.48
4:R:167:GDP:H5"	2:G:789:ARG:NH2	2.28	0.48
2:G:735:LEU:HD12	2:G:772:THR:HB	1.95	0.48
2:G:856:VAL:HG12	2:G:860:PHE:CE2	2.49	0.48
2:G:918:ILE:HG13	2:G:919:SER:H	1.78	0.48
1:R:84:ILE:HD12	1:R:123:ARG:CB	2.43	0.47
1:R:116:ASN:O	1:R:117:LYS:HB2	2.13	0.47
2:G:761:LEU:HD23	2:G:766:GLU:CG	2.39	0.47
2:G:856:VAL:HG21	2:G:959:PHE:HZ	1.79	0.47
2:G:933:VAL:O	2:G:937:VAL:HG23	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:1015:GLU:O	2:G:1020:GLN:HG3	2.15	0.47
2:G:740:ALA:HA	2:G:743:HIS:CD2	2.50	0.47
2:G:789:ARG:NH2	6:G:220:HOH:O	2.46	0.47
2:G:873:ILE:O	2:G:876:CYS:HB2	2.15	0.47
1:R:144:THR:HG22	1:R:151:GLY:C	2.40	0.46
2:G:900:VAL:O	2:G:905:ILE:HG12	2.15	0.46
1:R:65:SER:O	1:R:66:ALA:HB3	2.16	0.46
2:G:904:LEU:HD12	2:G:915:PHE:HZ	1.80	0.46
2:G:931:ILE:O	2:G:935:LYS:HG3	2.16	0.46
2:G:745:CYS:SG	2:G:752:LEU:HD22	2.55	0.46
2:G:763:GLU:O	2:G:765:LEU:HG	2.16	0.46
2:G:731:LEU:HD22	2:G:765:LEU:HD12	1.98	0.46
2:G:878:GLN:HA	2:G:881:VAL:HG22	1.97	0.46
2:G:969:MET:HE3	2:G:969:MET:HB3	1.83	0.45
2:G:803:LYS:NZ	2:G:915:PHE:HZ	2.10	0.45
1:R:36:ILE:HG23	2:G:910:LEU:HD11	1.97	0.45
2:G:735:LEU:HD11	2:G:769:LEU:HA	1.99	0.45
2:G:748:ASP:OD2	2:G:1005:HIS:HE1	1.99	0.45
1:R:156:PHE:O	1:R:160:VAL:HG23	2.17	0.45
2:G:810:VAL:HG12	2:G:917:ILE:HD11	1.99	0.45
1:R:21:ILE:HD11	2:G:949:LYS:CG	2.46	0.45
1:R:24:ILE:HD11	1:R:55:ILE:HD12	1.99	0.45
2:G:773:LEU:CD2	2:G:797:LEU:HD23	2.47	0.45
2:G:831:SER:HB2	2:G:834:LYS:HB2	1.98	0.45
1:R:144:THR:HA	1:R:150:GLN:O	2.17	0.45
2:G:809:PHE:HE2	2:G:905:ILE:HD11	1.81	0.45
1:R:87:THR:O	1:R:90:PHE:HB3	2.17	0.44
2:G:817:SER:O	2:G:821:ILE:HG13	2.18	0.44
2:G:793:LEU:HG	2:G:797:LEU:HD22	2.00	0.44
2:G:797:LEU:HD12	2:G:797:LEU:HA	1.79	0.43
2:G:828:CYS:HB3	2:G:848:LEU:HD13	2.00	0.43
1:R:133:LEU:HG	1:R:137:TYR:CE2	2.53	0.43
2:G:766:GLU:H	2:G:766:GLU:HG3	1.45	0.43
2:G:831:SER:HA	2:G:832:PRO:HD3	1.77	0.43
1:R:88:LYS:HB3	1:R:88:LYS:HE2	1.69	0.43
1:R:63:GLU:H	1:R:63:GLU:HG2	1.43	0.43
2:G:908:ALA:HB2	2:G:915:PHE:HE1	1.82	0.43
2:G:963:ASN:ND2	2:G:966:ARG:HH11	2.16	0.43
2:G:974:LEU:HD12	2:G:974:LEU:HA	1.80	0.42
2:G:809:PHE:CE2	2:G:905:ILE:HD11	2.54	0.42
1:R:72:MET:HB3	1:R:103:VAL:HG21	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:918:ILE:HG23	2:G:919:SER:N	2.35	0.42
1:R:7:VAL:HG12	1:R:9:VAL:HG13	2.02	0.42
1:R:144:THR:HG22	1:R:151:GLY:O	2.19	0.42
1:R:11:ALA:O	1:R:14:VAL:HG22	2.20	0.42
2:G:980:LEU:HD12	2:G:981:PRO:CD	2.50	0.41
2:G:735:LEU:HB3	2:G:739:TYR:CE2	2.56	0.41
1:R:17:SER:HA	1:R:57:ASP:OD2	2.19	0.41
2:G:888:ASN:ND2	2:G:891:MET:HG2	2.34	0.41
2:G:980:LEU:HA	2:G:981:PRO:HD3	1.67	0.41
1:R:32:TYR:CD2	2:G:894:ARG:HD3	2.55	0.41
2:G:1021:HIS:HA	2:G:1024:LYS:HD2	2.03	0.41
2:G:906:CYS:HB2	2:G:907:PRO:HD3	2.03	0.41
1:R:86:ASN:OD1	1:R:89:SER:HB3	2.21	0.40
2:G:867:PRO:O	2:G:871:ARG:HG3	2.21	0.40
2:G:904:LEU:HD12	2:G:915:PHE:CZ	2.57	0.40
1:R:42:LYS:HG2	1:R:44:VAL:HG13	2.02	0.40
1:R:118:CYS:SG	1:R:144:THR:O	2.78	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	R	164/166 (99%)	154 (94%)	8 (5%)	2 (1%)	10	20
2	G	318/334 (95%)	294 (92%)	21 (7%)	3 (1%)	14	27
All	All	482/500 (96%)	448 (93%)	29 (6%)	5 (1%)	12	24

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	G	947	GLY

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Mol	Chain	Res	Type
2	G	949	LYS
2	G	982	ASP
1	R	37	GLU
1	R	117	LYS

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	R	144/144 (100%)	131 (91%)	13 (9%)	9	19
2	G	287/307 (94%)	249 (87%)	38 (13%)	4	8
All	All	431/451 (96%)	380 (88%)	51 (12%)	5	11

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	R	5	LYS
1	R	26	ASN
1	R	41	ARG
1	R	43	GLN
1	R	45	VAL
1	R	50	THR
1	R	53	LEU
1	R	56	LEU
1	R	63	GLU
1	R	68	ARG
1	R	84	ILE
1	R	154	ASP
1	R	161	ARG
2	G	720	GLU
2	G	721	GLU
2	G	725	GLU
2	G	727	LYS
2	G	732	GLN
2	G	735	LEU

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Mol	Chain	Res	Type
2	G	763	GLU
2	G	766	GLU
2	G	768	LEU
2	G	776	ARG
2	G	789	ARG
2	G	797	LEU
2	G	803	LYS
2	G	812	HIS
2	G	817	SER
2	G	820	LYS
2	G	825	LYS
2	G	831	SER
2	G	838	ASN
2	G	858	LYS
2	G	869	THR
2	G	916	ASN
2	G	928	ARG
2	G	932	LEU
2	G	939	ASN
2	G	944	VAL
2	G	945	GLU
2	G	954	GLU
2	G	972	ASP
2	G	976	ASN
2	G	979	GLU
2	G	981	PRO
2	G	993	ARG
2	G	1007	ASP
2	G	1015	GLU
2	G	1016	ARG
2	G	1020	GLN
2	G	1031	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	R	22	GLN
1	R	94	HIS
1	R	129	GLN
1	R	150	GLN
2	G	732	GLN
2	G	736	HIS

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Mol	Chain	Res	Type
2	G	743	HIS
2	G	747	GLN
2	G	811	HIS
2	G	826	GLN
2	G	844	ASN
2	G	847	HIS
2	G	850	ASN
2	G	882	GLN
2	G	938	GLN
2	G	942	ASN
2	G	957	ASN
2	G	963	ASN
2	G	999	HIS
2	G	1005	HIS
2	G	1014	ASN
2	G	1037	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 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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
5	AF3	R	169	4,6	0,3,3	-	-	-		
4	GDP	R	167	3,5	29,30,30	1.08	2 (6%)	45,47,47	0.85	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
4	GDP	R	167	3,5	-	2/16/32/32	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	R	167	GDP	PB-O2B	-2.68	1.44	1.54
4	R	167	GDP	PA-O2A	-2.08	1.45	1.55

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	R	167	GDP	PA-O3A-PB-O3B
4	R	167	GDP	PA-O3A-PB-O1B

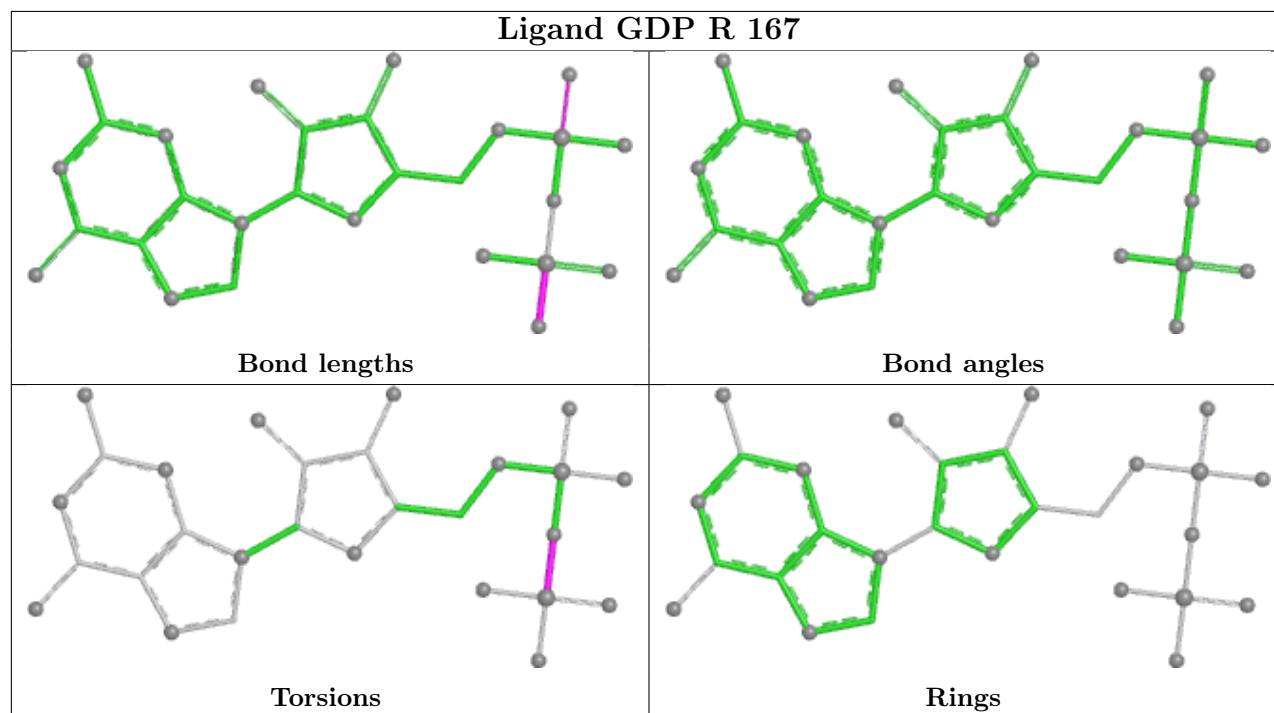
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	R	167	GDP	1	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

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.