



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 12:01 PM UTC

PDB ID : 1WER / pdb_00001wer
Title : RAS-GTPASE-ACTIVATING DOMAIN OF HUMAN P120GAP
Authors : Scheffzek, K.; Lautwein, A.; Kabsch, W.; Ahmadian, M.R.; Wittinghofer, A.
Deposited on : 1996-11-20
Resolution : 1.60 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
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

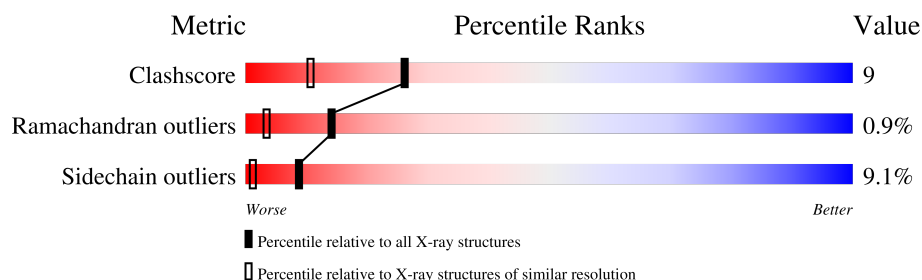
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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	4931 (1.60-1.60)
Ramachandran outliers	187476	4831 (1.60-1.60)
Sidechain outliers	187428	4830 (1.60-1.60)

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	334	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2770 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 P120GAP.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	324	Total	C	N	O	S	0	0	0
			2589	1643	442	487	17			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	181	Total	O	0	0
			181	181		

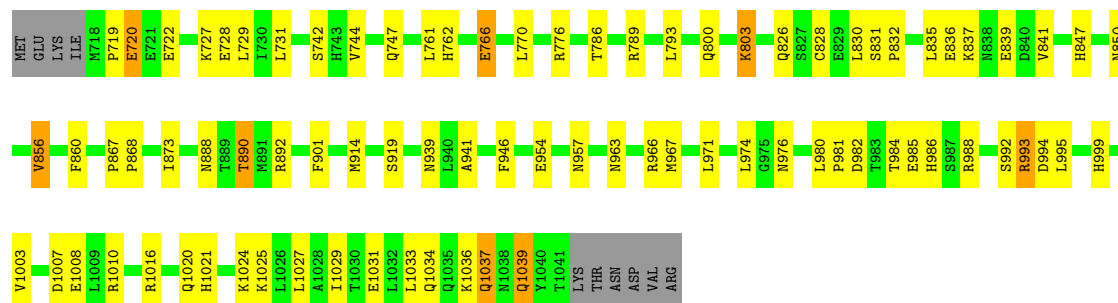
3 Residue-property plots

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. 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: P120GAP

Chain A: 



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 21	Depositor
Cell constants a, b, c, α , β , γ	42.20 Å 55.60 Å 142.20 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	5.00 – 1.60	Depositor
% Data completeness (in resolution range)	97.9 (5.00-1.60)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.221 , 0.271	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2770	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.46	0/2633	0.75	0/3563

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	2589	0	2651	49	0
2	A	181	0	0	5	0
All	All	2770	0	2651	49	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 9.

All (49) 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:A:941:ALA:HA	1:A:967:MET:HE2	1.34	1.10
1:A:967:MET:HE3	1:A:971:LEU:HD11	1.47	0.96
1:A:720:GLU:HA	1:A:992:SER:HB3	1.68	0.75
1:A:901:PHE:CE2	1:A:967:MET:HE1	2.22	0.74

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:888:ASN:OD1	1:A:890:THR:HG22	1.92	0.69
1:A:761:LEU:HD23	1:A:766:GLU:HG2	1.75	0.68
1:A:835:LEU:HD11	1:A:841:VAL:HG13	1.76	0.68
1:A:963:ASN:ND2	1:A:966:ARG:HH11	1.92	0.67
1:A:800:GLN:HA	1:A:803:LYS:HD3	1.75	0.67
1:A:729:LEU:HD22	1:A:1029:ILE:HD12	1.76	0.66
1:A:946:PHE:H	1:A:957:ASN:HD21	1.43	0.66
1:A:727:LYS:HG3	1:A:995:LEU:HD21	1.80	0.62
1:A:941:ALA:CA	1:A:967:MET:HE2	2.23	0.62
1:A:727:LYS:HE3	1:A:731:LEU:HD11	1.82	0.61
1:A:976:ASN:HB3	2:A:146:HOH:O	2.03	0.58
1:A:761:LEU:CD2	1:A:766:GLU:HG2	2.34	0.58
1:A:1010:ARG:HA	1:A:1027:LEU:HD11	1.86	0.58
1:A:856:VAL:HG13	1:A:860:PHE:CE2	2.40	0.56
1:A:901:PHE:CD2	1:A:967:MET:HE1	2.41	0.56
1:A:986:HIS:CE1	1:A:988:ARG:HB2	2.42	0.54
1:A:963:ASN:ND2	1:A:966:ARG:NH1	2.56	0.53
1:A:830:LEU:O	1:A:832:PRO:HD3	2.10	0.52
1:A:770:LEU:HD12	1:A:873:ILE:HD13	1.92	0.51
1:A:967:MET:HE3	1:A:971:LEU:CD1	2.30	0.51
1:A:980:LEU:HG	1:A:982:ASP:HB2	1.93	0.50
1:A:946:PHE:N	1:A:957:ASN:HD21	2.10	0.49
1:A:835:LEU:HD22	1:A:839:GLU:HG3	1.93	0.49
1:A:832:PRO:HA	1:A:835:LEU:HG	1.95	0.49
1:A:761:LEU:HA	1:A:766:GLU:HG3	1.94	0.48
1:A:828:CYS:SG	1:A:847:HIS:HD2	2.36	0.48
1:A:744:VAL:HG12	1:A:1008:GLU:HB3	1.97	0.47
1:A:786:THR:HB	2:A:76:HOH:O	2.14	0.47
1:A:762:HIS:CE1	1:A:988:ARG:HA	2.50	0.46
1:A:999:HIS:O	1:A:1003:VAL:HG23	2.17	0.45
1:A:826:GLN:HG2	1:A:847:HIS:CG	2.52	0.45
1:A:828:CYS:SG	1:A:847:HIS:CD2	3.10	0.45
1:A:868:PRO:HD2	2:A:16:HOH:O	2.17	0.44
1:A:850:ASN:ND2	2:A:180:HOH:O	2.49	0.44
1:A:963:ASN:HD22	1:A:966:ARG:HH11	1.64	0.44
1:A:1036:LYS:HA	1:A:1039:GLN:HE21	1.82	0.44
1:A:1037:GLN:HE21	1:A:1037:GLN:HB2	1.60	0.43
1:A:999:HIS:CE1	1:A:1033:LEU:HB2	2.55	0.42
1:A:742:SER:HB3	1:A:793:LEU:HD22	2.02	0.42
1:A:719:PRO:HD2	1:A:722:GLU:HG3	2.03	0.41
1:A:974:LEU:HD12	1:A:974:LEU:HA	1.95	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1020:GLN:HG2	1:A:1024:LYS:NZ	2.36	0.40
1:A:867:PRO:HA	1:A:868:PRO:HD3	1.88	0.40
1:A:993:ARG:HB3	2:A:102:HOH:O	2.21	0.40
1:A:946:PHE:H	1:A:957:ASN:ND2	2.12	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	322/334 (96%)	309 (96%)	10 (3%)	3 (1%)	14 3

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	836	GLU
1	A	981	PRO
1	A	985	GLU

5.3.2 Protein sidechains [i](#)

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	297/307 (97%)	270 (91%)	27 (9%)	9 1

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	720	GLU
1	A	728	GLU
1	A	747	GLN
1	A	766	GLU
1	A	776	ARG
1	A	789	ARG
1	A	803	LYS
1	A	831	SER
1	A	837	LYS
1	A	856	VAL
1	A	890	THR
1	A	892	ARG
1	A	914	MET
1	A	919	SER
1	A	939	ASN
1	A	954	GLU
1	A	984	THR
1	A	993	ARG
1	A	994	ASP
1	A	1007	ASP
1	A	1016	ARG
1	A	1021	HIS
1	A	1025	LYS
1	A	1031	GLU
1	A	1034	GLN
1	A	1037	GLN
1	A	1039	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	743	HIS
1	A	811	HIS
1	A	826	GLN
1	A	842	ASN
1	A	844	ASN
1	A	847	HIS
1	A	850	ASN
1	A	883	HIS
1	A	957	ASN
1	A	963	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	976	ASN
1	A	986	HIS
1	A	999	HIS
1	A	1014	ASN
1	A	1037	GLN
1	A	1039	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](#)

There are no ligands in this entry.

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.