



# Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 06:11 pm BST

PDB ID : 4ET7  
Title : Crystal structure of Eph receptor 5  
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Deposited on : 2012-04-24  
Resolution : 2.60 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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Xtrriage (Phenix) : 1.13  
EDS : 2.11  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

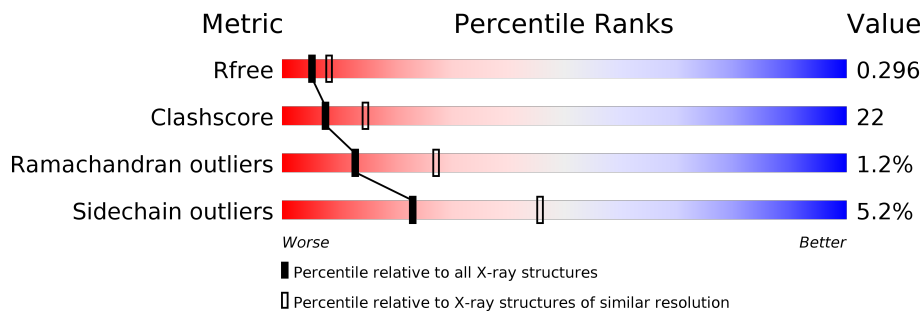
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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))
$R_{free}$	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	179	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1435 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 Ephrin type-A receptor 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	174	1399	886	231	274	8	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	57	GLY	-	EXPRESSION TAG	UNP P54756
A	58	SER	-	EXPRESSION TAG	UNP P54756
A	232	GLU	LYS	SEE REMARK 999	UNP P54756
A	233	ALA	CYS	ENGINEERED MUTATION	UNP P54756

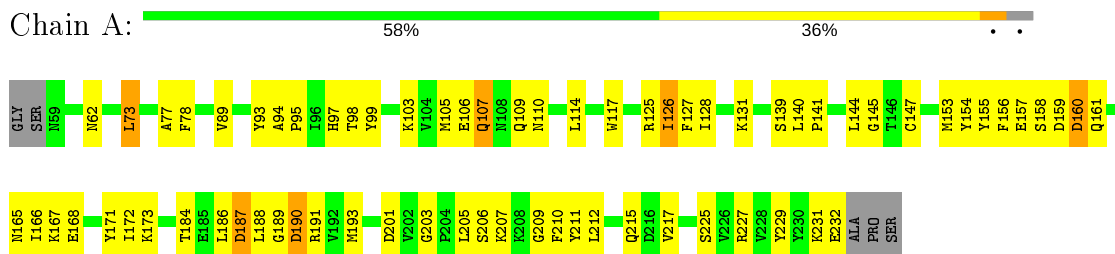
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	36	36	36	0	0

### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

- Molecule 1: Ephrin type-A receptor 5



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	55.04Å 82.72Å 81.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.68 – 2.60 41.36 – 2.08	Depositor EDS
% Data completeness (in resolution range)	90.6 (20.68-2.60) 90.4 (41.36-2.08)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.13	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.44 (at 2.08Å)	Xtrriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, $R_{free}$	0.205 , 0.282 0.213 , 0.296	Depositor DCC
$R_{free}$ test set	1039 reflections (10.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	23.1	Xtrriage
Anisotropy	0.634	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 49.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	1435	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.30% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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](#)

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	0.38	0/1427	0.57	0/1931

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	1399	0	1342	60	0
2	A	36	0	0	3	0
All	All	1435	0	1342	60	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 22.

All (60) 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:158:SER:HA	1:A:207:LYS:HD2	1.38	1.02
1:A:188:LEU:HD23	1:A:189:GLY:H	1.32	0.90
1:A:73:LEU:H	1:A:73:LEU:HD12	1.39	0.88
1:A:110:ASN:HD22	1:A:215:GLN:HE21	1.26	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:188:LEU:CD2	1:A:189:GLY:H	1.92	0.82
1:A:62:ASN:HD21	1:A:227:ARG:HE	1.30	0.77
1:A:156:PHE:HZ	1:A:165:ASN:HD21	1.36	0.73
1:A:107:GLN:HE21	1:A:145:GLY:HA2	1.55	0.70
1:A:89:VAL:CG1	1:A:93:TYR:HA	2.24	0.67
1:A:117:TRP:HB2	1:A:161:GLN:O	1.93	0.67
1:A:110:ASN:ND2	1:A:215:GLN:HE21	1.93	0.66
1:A:158:SER:CA	1:A:207:LYS:HD2	2.20	0.66
1:A:62:ASN:HD22	1:A:229:TYR:HB3	1.60	0.65
1:A:62:ASN:HD21	1:A:227:ARG:NE	1.93	0.65
1:A:62:ASN:ND2	1:A:227:ARG:HE	1.98	0.61
1:A:128:ILE:HD12	1:A:212:LEU:HD11	1.84	0.60
1:A:73:LEU:HD13	1:A:99:TYR:OH	2.03	0.58
1:A:107:GLN:NE2	1:A:145:GLY:HA2	2.19	0.57
1:A:139:SER:HB3	1:A:184:THR:HG22	1.87	0.57
1:A:159:ASP:OD1	1:A:207:LYS:HB3	2.06	0.56
1:A:73:LEU:HD11	1:A:97:HIS:HB2	1.88	0.55
1:A:73:LEU:H	1:A:73:LEU:CD1	2.17	0.55
1:A:89:VAL:HG13	1:A:93:TYR:HA	1.89	0.54
1:A:154:TYR:HB3	1:A:171:TYR:HB3	1.90	0.53
1:A:106:GLU:HG2	1:A:107:GLN:N	2.24	0.53
1:A:103:LYS:HA	1:A:105:MET:SD	2.49	0.53
1:A:168:GLU:HA	1:A:168:GLU:OE2	2.09	0.53
1:A:186:LEU:O	1:A:186:LEU:HD12	2.09	0.53
1:A:190:ASP:O	1:A:193:MET:HB2	2.09	0.52
1:A:126:ILE:HD12	1:A:210:PHE:CZ	2.45	0.52
1:A:131:LYS:HB2	1:A:225:SER:HB3	1.93	0.50
1:A:157:GLU:OE2	1:A:206:SER:N	2.41	0.48
1:A:127:PHE:CD1	1:A:201:ASP:HB3	2.48	0.48
1:A:98:THR:C	1:A:99:TYR:CD2	2.88	0.48
1:A:117:TRP:CE2	1:A:209:GLY:HA3	2.50	0.47
1:A:125:ARG:NH1	1:A:203:GLY:HA2	2.30	0.47
1:A:231:LYS:O	1:A:232:GLU:C	2.54	0.46
1:A:140:LEU:HD12	1:A:147:CYS:SG	2.56	0.46
1:A:106:GLU:C	1:A:107:GLN:HG2	2.36	0.46
1:A:73:LEU:HD12	1:A:73:LEU:N	2.18	0.46
1:A:125:ARG:CZ	1:A:203:GLY:HA2	2.47	0.45
1:A:154:TYR:CB	1:A:171:TYR:HB3	2.47	0.44
1:A:188:LEU:CD2	1:A:189:GLY:N	2.71	0.44
1:A:78:PHE:HE2	1:A:114:LEU:HD12	1.82	0.44
1:A:109:GLN:O	1:A:217:VAL:HA	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:62:ASN:ND2	1:A:229:TYR:HB3	2.32	0.43
1:A:186:LEU:O	1:A:187:ASP:O	2.36	0.43
1:A:127:PHE:CE2	1:A:231:LYS:HD2	2.52	0.43
1:A:94:ALA:HA	1:A:95:PRO:HD3	1.77	0.43
1:A:141:PRO:HB2	1:A:144:LEU:HG	2.00	0.43
1:A:155:TYR:CE2	1:A:172:ILE:HB	2.54	0.42
1:A:77:ALA:HB1	2:A:333:HOH:O	2.18	0.42
1:A:205:LEU:HD23	2:A:305:HOH:O	2.19	0.42
1:A:110:ASN:ND2	1:A:215:GLN:NE2	2.65	0.42
1:A:103:LYS:HE2	2:A:318:HOH:O	2.20	0.42
1:A:127:PHE:CZ	1:A:231:LYS:HD2	2.54	0.42
1:A:232:GLU:HG3	1:A:232:GLU:O	2.20	0.42
1:A:128:ILE:HG21	1:A:153:MET:SD	2.61	0.41
1:A:160:ASP:N	1:A:160:ASP:OD1	2.53	0.41
1:A:117:TRP:HD1	1:A:211:TYR:CE2	2.37	0.41

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	172/179 (96%)	148 (86%)	22 (13%)	2 (1%)	<b>13</b> <b>27</b>

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	187	ASP
1	A	166	ILE



### 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	153/156 (98%)	145 (95%)	8 (5%)	23 46

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	73	LEU
1	A	107	GLN
1	A	126	ILE
1	A	160	ASP
1	A	167	LYS
1	A	173	LYS
1	A	190	ASP
1	A	191	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	62	ASN
1	A	107	GLN
1	A	109	GLN
1	A	110	ASN
1	A	111	ASN
1	A	138	ASN
1	A	152	ASN
1	A	165	ASN
1	A	196	ASN

### 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 carbohydrates 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

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

### 6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.