



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 11:52 AM UTC

PDB ID : 7EED / pdb_00007eed
Title : Crystal structure of EphA7 mutant D751H
Authors : Chakraborty, S.; Varma, A.K.
Deposited on : 2021-03-18
Resolution : 3.05 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
Xtrriage (Phenix) : 2.0
EDS : 3.0
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

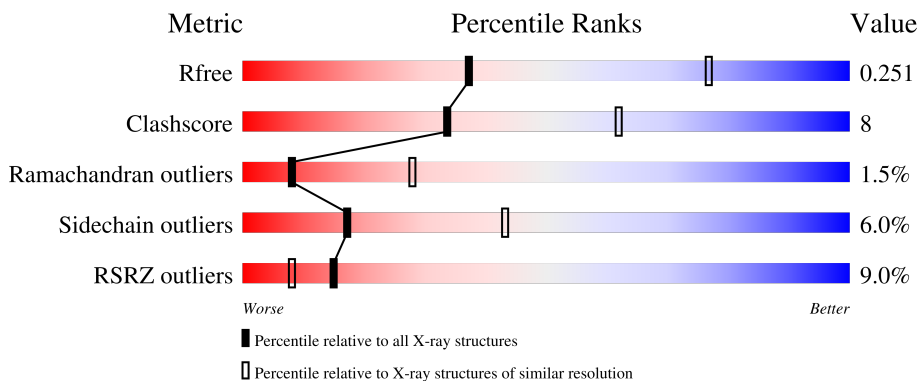
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.05 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	2469 (3.10-3.02)
Clashscore	190562	2569 (3.10-3.02)
Ramachandran outliers	187476	2424 (3.10-3.02)
Sidechain outliers	187428	2423 (3.10-3.02)
RSRZ outliers	180081	2469 (3.10-3.02)

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	304	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 2218 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 7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	278	2212	1405	392	397	18	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	751	HIS	ASP	engineered mutation	UNP Q15375
A	900	ALA	-	expression tag	UNP Q15375
A	901	HIS	-	expression tag	UNP Q15375
A	902	HIS	-	expression tag	UNP Q15375

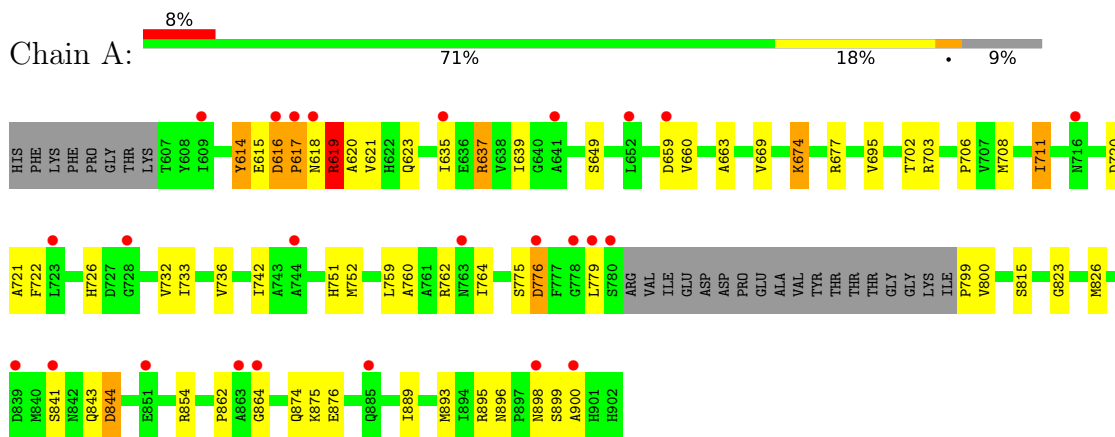
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	6	Total	O	0	0
			6	6		

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: Ephrin type-A receptor 7



4 Data and refinement statistics i

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	51.24Å 51.24Å 215.27Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	44.38 – 3.05 44.38 – 3.05	Depositor EDS
% Data completeness (in resolution range)	92.5 (44.38-3.05) 92.5 (44.38-3.05)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.15 (at 3.06Å)	Xtrriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.199 , 0.247 0.210 , 0.251	Depositor DCC
R_{free} test set	255 reflections (4.19%)	wwPDB-VP
Wilson B-factor (Å ²)	35.8	Xtrriage
Anisotropy	0.054	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 44.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtrriage
Estimated twinning fraction	0.139 for h,-h-k,-l	Xtrriage
F_o, F_c correlation	0.84	EDS
Total number of atoms	2218	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.49% 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

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	1.15	1/2262 (0.0%)	1.57	9/3054 (0.3%)

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	A	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	669	VAL	C-O	5.54	1.30	1.24

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	702	THR	CA-CB-OG1	-6.06	100.51	109.60
1	A	706	PRO	CA-C-N	6.01	129.15	120.98
1	A	706	PRO	C-N-CA	6.01	129.15	120.98
1	A	876	GLU	CA-C-N	5.48	127.63	120.28
1	A	876	GLU	C-N-CA	5.48	127.63	120.28
1	A	659	ASP	CA-CB-CG	5.48	118.08	112.60
1	A	711	ILE	CA-C-O	-5.33	116.60	121.72
1	A	762	ARG	CG-CD-NE	-5.23	100.49	112.00
1	A	844	ASP	CA-CB-CG	5.10	117.70	112.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	617	PRO	Peptide

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	2212	0	2198	34	0
2	A	6	0	0	0	0
All	All	2218	0	2198	34	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 8.

All (34) 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:616:ASP:O	1:A:618:ASN:O	2.05	0.75
1:A:616:ASP:O	1:A:619:ARG:HB2	1.87	0.73
1:A:722:PHE:O	1:A:726:HIS:HD2	1.72	0.72
1:A:751:HIS:CG	1:A:751:HIS:O	2.44	0.69
1:A:616:ASP:O	1:A:618:ASN:C	2.36	0.69
1:A:674:LYS:O	1:A:677:ARG:HG2	2.02	0.60
1:A:751:HIS:O	1:A:751:HIS:ND1	2.35	0.60
1:A:635:ILE:HD11	1:A:708:MET:HE1	1.83	0.60
1:A:617:PRO:HG3	1:A:620:ALA:HB3	1.85	0.58
1:A:775:SER:OG	1:A:776:ASP:N	2.37	0.57
1:A:889:ILE:O	1:A:893:MET:HG3	2.06	0.55
1:A:617:PRO:HB3	1:A:621:VAL:CG2	2.36	0.55
1:A:799:PRO:O	1:A:800:VAL:C	2.49	0.53
1:A:854:ARG:HH22	1:A:875:LYS:HE3	1.73	0.53
1:A:760:ALA:O	1:A:764:ILE:HG12	2.10	0.51
1:A:663:ALA:HB3	1:A:711:ILE:CG1	2.41	0.49
1:A:759:LEU:HD11	1:A:764:ILE:HD11	1.95	0.48
1:A:732:VAL:O	1:A:736:VAL:HG23	2.15	0.47
1:A:854:ARG:HH22	1:A:875:LYS:CE	2.27	0.47
1:A:862:PRO:CB	1:A:900:ALA:HB1	2.45	0.46
1:A:864:GLY:N	1:A:900:ALA:O	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:614:TYR:OH	1:A:623:GLN:NE2	2.42	0.45
1:A:615:GLU:O	1:A:616:ASP:HB2	2.17	0.45
1:A:720:ASP:OD1	1:A:721:ALA:N	2.50	0.44
1:A:618:ASN:HD21	1:A:703:ARG:HE	1.64	0.43
1:A:841:SER:O	1:A:844:ASP:N	2.51	0.43
1:A:617:PRO:HB3	1:A:621:VAL:HG23	2.01	0.42
1:A:637:ARG:O	1:A:649:SER:N	2.48	0.42
1:A:823:GLY:O	1:A:826:MET:HB2	2.20	0.41
1:A:674:LYS:HG2	1:A:677:ARG:HH21	1.86	0.41
1:A:722:PHE:O	1:A:726:HIS:CD2	2.62	0.41
1:A:742:ILE:HG12	1:A:764:ILE:HG21	2.03	0.41
1:A:896:ASN:OD1	1:A:898:ASN:ND2	2.52	0.41
1:A:663:ALA:HB3	1:A:711:ILE:HG12	2.03	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	274/304 (90%)	239 (87%)	31 (11%)	4 (2%)	8 28

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	619	ARG
1	A	776	ASP
1	A	752	MET
1	A	616	ASP

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	235/257 (91%)	221 (94%)	14 (6%)	17 43

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	614	TYR
1	A	619	ARG
1	A	637	ARG
1	A	639	ILE
1	A	660	VAL
1	A	674	LYS
1	A	695	VAL
1	A	733	ILE
1	A	779	LEU
1	A	815	SER
1	A	843	GLN
1	A	874	GLN
1	A	895	ARG
1	A	899	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	623	GLN
1	A	726	HIS
1	A	729	GLN
1	A	867	GLN
1	A	874	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

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	278/304 (91%)	0.63	25 (8%) 15 8	18, 26, 46, 60	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	763	ASN	5.2
1	A	851	GLU	4.8
1	A	618	ASN	4.5
1	A	744	ALA	4.0
1	A	779	LEU	3.9
1	A	728	GLY	3.8
1	A	839	ASP	2.9
1	A	898	ASN	2.9
1	A	841	SER	2.8
1	A	617	PRO	2.7
1	A	864	GLY	2.7
1	A	616	ASP	2.6
1	A	776	ASP	2.5
1	A	778	GLY	2.5
1	A	635	ILE	2.4
1	A	652	LEU	2.4
1	A	659	ASP	2.3
1	A	900	ALA	2.3
1	A	863	ALA	2.2
1	A	609	ILE	2.2
1	A	780	SER	2.2
1	A	641	ALA	2.1
1	A	885	GLN	2.1
1	A	716	ASN	2.0
1	A	723	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.