



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 04:12 PM UTC

PDB ID : 4NUU / pdb_00004nuu
Title : Heterotrimer structure of Region II from Plasmodium vivax Duffy Binding Protein (PvDBP) bound to the ectodomain of the Duffy Antigen Receptor for Chemokines (DARC)
Authors : Tolia, N.H.
Deposited on : 2013-12-04
Resolution : 1.95 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)	:	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

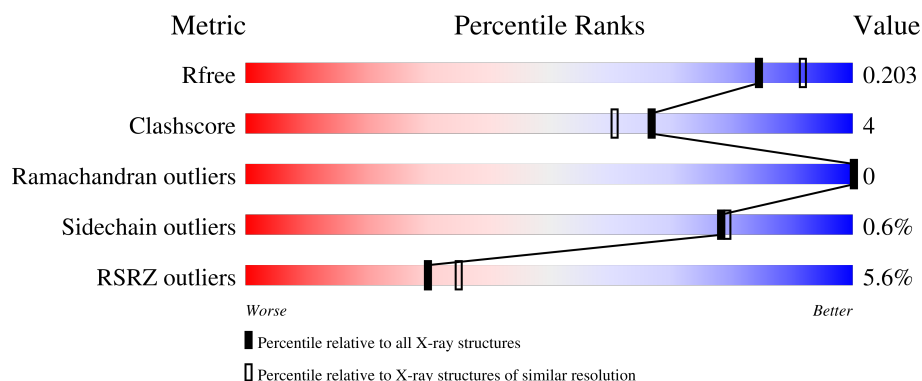
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	317	5% 82% 6% 11%
1	B	317	5% 83% 9% 8%
2	C	32	3% 25% 12% 62%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10257 atoms, of which 4866 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 Duffy receptor.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	282	Total	C	H	N	O	S	0	5	0
			4724	1497	2355	417	437	18			
1	B	292	Total	C	H	N	O	S	0	3	0
			4880	1555	2426	435	446	18			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	209	ALA	-	expression tag	UNP P22290
A	210	SER	-	expression tag	UNP P22290
B	209	ALA	-	expression tag	UNP P22290
B	210	SER	-	expression tag	UNP P22290

- Molecule 2 is a protein called Duffy antigen/chemokine receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	12	Total	C	H	N	O	0	0	0
			191	68	85	15	23			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	12	GLY	-	expression tag	UNP Q16570
C	13	PRO	-	expression tag	UNP Q16570
C	15	GLY	GLU	cloning artifact	UNP Q16570

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	202	Total	O	0	0
			202	202		

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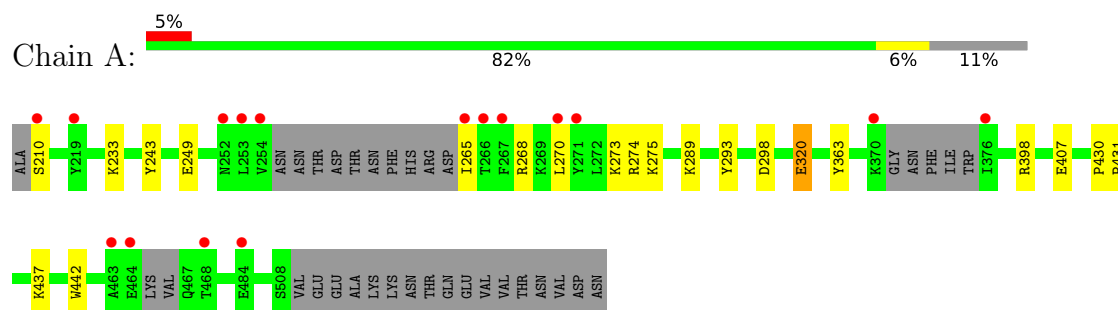
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	257	Total 257	O 257	0	0
3	C	3	Total 3	O 3	0	0

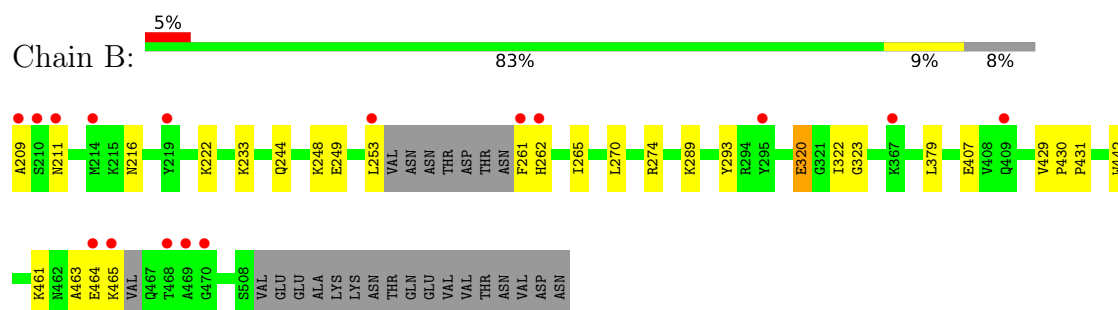
3 Residue-property plots [i](#)

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.

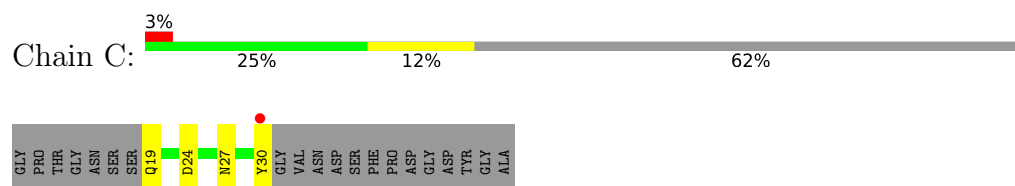
- Molecule 1: Duffy receptor



- Molecule 1: Duffy receptor



- Molecule 2: Duffy antigen/chemokine receptor



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	59.59Å 66.99Å 97.92Å 90.00° 102.11° 90.00°	Depositor
Resolution (Å)	19.86 – 1.95 19.86 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.9 (19.86-1.95) 99.8 (19.86-1.95)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.29 (at 1.94Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.165 , 0.202 0.168 , 0.203	Depositor DCC
R_{free} test set	1870 reflections (3.40%)	wwPDB-VP
Wilson B-factor (Å ²)	27.0	Xtriage
Anisotropy	0.183	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 54.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10257	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 32.97 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 8.6162e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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	0.32	0/2416	0.62	0/3245
1	B	0.33	0/2504	0.61	1/3363 (0.0%)
2	C	0.23	0/109	0.45	0/148
All	All	0.32	0/5029	0.61	1/6756 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	429	VAL	N-CA-C	5.30	112.38	107.56

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	2369	2355	2357	14	0
1	B	2454	2426	2435	23	0
2	C	106	85	85	3	0
3	A	202	0	0	2	0
3	B	257	0	0	1	0
3	C	3	0	0	0	0
All	All	5391	4866	4877	36	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 (36) 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:209:ALA:N	1:B:323:GLY:N	2.32	0.77
1:B:209:ALA:N	1:B:323:GLY:CA	2.58	0.66
1:B:216:ASN:HB2	1:B:244:GLN:O	1.97	0.64
1:B:464:GLU:O	1:B:465:LYS:HB2	1.98	0.63
1:B:248:LYS:NZ	1:B:249:GLU:OE2	2.33	0.62
1:A:274:ARG:NH1	1:B:262:HIS:NE2	2.50	0.60
1:A:265:ILE:N	3:A:786:HOH:O	2.37	0.57
1:B:253:LEU:HD12	1:B:253:LEU:C	2.32	0.55
1:A:265:ILE:HG13	1:A:268:ARG:H	1.73	0.53
1:A:298:ASP:OD1	1:A:398:ARG:NH2	2.43	0.52
1:B:253:LEU:HD13	1:B:261:PHE:N	2.27	0.50
1:B:289:LYS:HG2	1:B:293:TYR:CZ	2.46	0.50
1:B:209:ALA:N	1:B:322:ILE:HG23	2.27	0.49
1:B:222:LYS:HA	1:B:222:LYS:HE2	1.95	0.48
1:A:363:TYR:OH	2:C:24:ASP:OD2	2.26	0.48
1:A:289:LYS:HG2	1:A:293:TYR:CZ	2.49	0.48
1:B:430:PRO:HB2	1:B:431:PRO:HD3	1.97	0.47
1:A:437:LYS:NZ	3:A:769:HOH:O	2.47	0.47
1:A:233:LYS:HD2	1:A:320:GLU:O	2.15	0.47
1:B:233:LYS:HD2	1:B:320:GLU:O	2.15	0.47
1:B:407:GLU:HG3	1:B:442:TRP:CD2	2.50	0.46
1:B:211:ASN:ND2	1:B:322:ILE:O	2.50	0.45
1:B:461:LYS:O	1:B:464:GLU:O	2.34	0.45
1:A:249:GLU:HB3	1:A:275:LYS:HD2	1.98	0.44
1:B:270:LEU:O	1:B:274:ARG:HG2	2.18	0.43
1:B:464:GLU:O	1:B:465:LYS:CB	2.65	0.43
1:A:407:GLU:HG3	1:A:442:TRP:CD2	2.53	0.43
1:B:209:ALA:N	1:B:323:GLY:H	2.16	0.43
1:B:209:ALA:N	1:B:322:ILE:CG2	2.82	0.43
1:B:463:ALA:C	1:B:464:GLU:HG3	2.45	0.42
1:A:273:LYS:NZ	2:C:30:TYR:OH	2.48	0.42
1:B:265:ILE:HD11	2:C:27:ASN:O	2.19	0.42
1:A:430:PRO:HB2	1:A:431:PRO:HD3	2.02	0.41
1:B:379:LEU:C	1:B:379:LEU:HD23	2.46	0.41
1:A:270:LEU:CD1	3:B:851:HOH:O	2.69	0.41
1:A:210:SER:HB3	1:A:243:TYR:O	2.21	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	278/317 (88%)	273 (98%)	5 (2%)	0	100	100
1	B	288/317 (91%)	284 (99%)	4 (1%)	0	100	100
2	C	10/32 (31%)	10 (100%)	0	0	100	100
All	All	576/666 (86%)	567 (98%)	9 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	263/292 (90%)	262 (100%)	1 (0%)	84	85
1	B	270/292 (92%)	269 (100%)	1 (0%)	84	85
2	C	12/26 (46%)	11 (92%)	1 (8%)	10	3
All	All	545/610 (89%)	542 (99%)	3 (1%)	78	79

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	320	GLU
1	B	320	GLU
2	C	19	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	343	GLN
1	A	344	GLN
1	A	448	ASN
1	B	356	GLN
1	B	380	ASN
1	B	448	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 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	282/317 (88%)	-0.02	16 (5%)	29 34	13, 37, 80, 123	4 (1%)
1	B	292/317 (92%)	-0.05	16 (5%)	30 36	17, 34, 77, 132	2 (0%)
2	C	12/32 (37%)	0.39	1 (8%)	17 20	38, 48, 82, 109	0
All	All	586/666 (87%)	-0.02	33 (5%)	30 35	13, 36, 80, 132	6 (1%)

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	209	ALA	12.5
1	B	210	SER	6.4
1	A	370	LYS	5.0
1	B	253	LEU	4.7
1	A	254	VAL	4.5
1	A	267	PHE	4.5
1	B	211	ASN	4.4
1	A	210	SER	3.8
1	B	464	GLU	3.5
1	B	261	PHE	3.5
1	B	468	THR	3.4
2	C	30	TYR	3.3
1	B	470	GLY	3.3
1	A	464	GLU	3.2
1	A	265	ILE	3.2
1	A	376	ILE	3.2
1	B	465	LYS	3.2
1	A	219	TYR	3.0
1	A	271	TYR	2.9
1	B	409[A]	GLN	2.9
1	A	484	GLU	2.9
1	B	295	TYR	2.7
1	A	253	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	266	THR	2.6
1	B	214	MET	2.5
1	B	219	TYR	2.5
1	A	270	LEU	2.5
1	B	367	LYS	2.4
1	A	252	ASN	2.4
1	A	463	ALA	2.4
1	B	262	HIS	2.3
1	B	469	ALA	2.2
1	A	468	THR	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.