



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 9, 2020 – 08:49 AM BST

PDB ID : 2P28
Title : Structure of the PHE2 and PHE3 fragments of the integrin beta2 subunit
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Deposited on : 2007-03-07
Resolution : 2.20 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
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) : 2.13.1

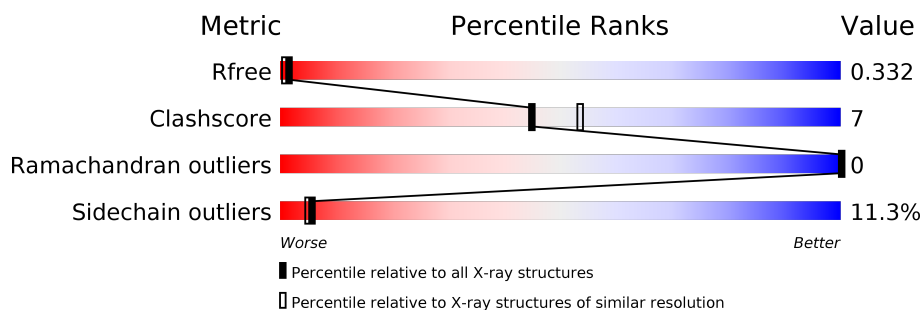
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)

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 ≥ 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	100	
2	B	217	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NAG	A	401	X	-	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2569 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 Integrin beta-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	96	Total	C	N	O	S	0	0	0
			740	453	133	145	9			

- Molecule 2 is a protein called Integrin beta-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	214	Total	C	N	O	S	0	0	0
			1615	978	299	311	27			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	553	HIS	-	expression tag	UNP P05107
B	554	HIS	-	expression tag	UNP P05107
B	555	HIS	-	expression tag	UNP P05107
B	556	HIS	-	expression tag	UNP P05107

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			15	8	1	6		


- Molecule 4 is water.

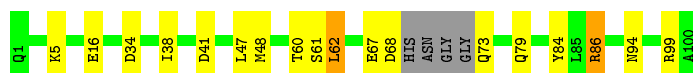
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	46	Total	O	0	0
			46	46		
4	B	153	Total	O	0	0
			153	153		

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.

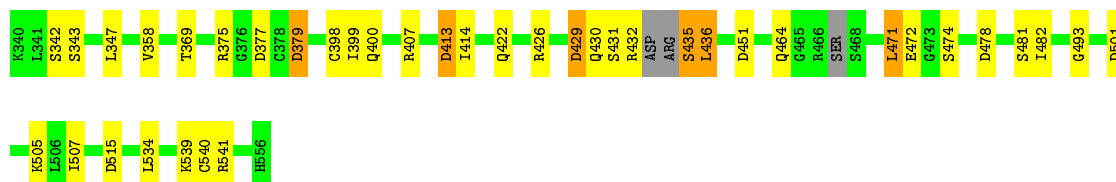
- Molecule 1: Integrin beta-2

Chain A: 



- Molecule 2: Integrin beta-2

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	52.26 Å 52.26 Å 423.92 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	25.00 – 2.20 24.97 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.3 (25.00-2.20) 99.3 (24.97-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.66 (at 2.19 Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.261 , 0.308 0.302 , 0.332	Depositor DCC
R_{free} test set	964 reflections (5.15%)	wwPDB-VP
Wilson B-factor (Å ²)	46.8	Xtriage
Anisotropy	0.039	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 49.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	2569	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.91% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAG

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	0.41	0/752	0.79	1/1014 (0.1%)
2	B	0.47	1/1641 (0.1%)	0.77	8/2208 (0.4%)
All	All	0.46	1/2393 (0.0%)	0.78	9/3222 (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
2	B	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	540	CYS	CB-SG	-5.18	1.73	1.81

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	377	ASP	CB-CG-OD2	6.68	124.31	118.30
1	A	68	ASP	CB-CG-OD2	6.63	124.27	118.30
2	B	515	ASP	CB-CG-OD2	6.01	123.71	118.30
2	B	451	ASP	CB-CG-OD2	5.59	123.33	118.30
2	B	413	ASP	CB-CG-OD2	5.52	123.27	118.30
2	B	501	ASP	CB-CG-OD2	5.27	123.04	118.30
2	B	478	ASP	CB-CG-OD2	5.24	123.02	118.30
2	B	379	ASP	CB-CG-OD2	5.14	122.93	118.30
2	B	429	ASP	CB-CG-OD2	5.12	122.91	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	431	SER	Peptide
2	B	435	SER	Peptide

5.2 Too-close contacts

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	740	0	717	14	0
2	B	1615	0	1500	17	0
3	A	15	0	15	6	0
4	A	46	0	0	1	0
4	B	153	0	0	3	1
All	All	2569	0	2232	30	1

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 7.

All (30) 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:B:435:SER:HB2	2:B:436:LEU:CA	1.94	0.94
2:B:435:SER:HB2	2:B:436:LEU:CB	2.07	0.83
2:B:436:LEU:O	2:B:436:LEU:HG	1.86	0.75
1:A:94:ASN:HD21	3:A:401:NAG:C1	2.01	0.73
1:A:73:GLN:N	1:A:79:GLN:OE1	2.23	0.72
2:B:435:SER:HB2	2:B:436:LEU:HA	1.73	0.69
2:B:435:SER:HB2	2:B:436:LEU:HB2	1.73	0.69
2:B:541:ARG:NH2	4:B:662:HOH:O	2.26	0.68
2:B:435:SER:CB	2:B:436:LEU:CA	2.75	0.61
2:B:505:LYS:HE2	2:B:507:ILE:HD11	1.83	0.59
1:A:94:ASN:HD21	3:A:401:NAG:C2	2.20	0.55
1:A:86:ARG:HD3	4:A:402:HOH:O	2.07	0.53
2:B:471:LEU:O	2:B:474:SER:HB2	2.13	0.49
1:A:16:GLU:HG2	2:B:398:CYS:SG	2.53	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:94:ASN:HD21	3:A:401:NAG:H1	1.78	0.48
1:A:94:ASN:HD21	3:A:401:NAG:H2	1.78	0.48
2:B:472:GLU:HG2	2:B:493:GLY:HA2	1.95	0.47
1:A:62:LEU:HD13	1:A:84:TYR:HB2	1.95	0.47
2:B:369:THR:HG22	4:B:590:HOH:O	2.14	0.47
1:A:73:GLN:HA	1:A:73:GLN:NE2	2.30	0.47
2:B:505:LYS:CE	2:B:507:ILE:HD11	2.45	0.46
2:B:471:LEU:N	2:B:471:LEU:CD1	2.77	0.45
1:A:62:LEU:CD1	1:A:84:TYR:HB2	2.45	0.45
1:A:94:ASN:OD1	3:A:401:NAG:H1	2.17	0.45
1:A:60:THR:HG22	1:A:61:SER:O	2.18	0.44
1:A:34:ASP:HB3	1:A:38:ILE:HD13	1.99	0.43
2:B:413:ASP:O	4:B:578:HOH:O	2.21	0.42
2:B:471:LEU:O	2:B:474:SER:N	2.52	0.42
1:A:94:ASN:ND2	3:A:401:NAG:C1	2.78	0.42
2:B:471:LEU:HA	2:B:471:LEU:HD12	1.81	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:557:HOH:O	4:B:594:HOH:O[8_665]	1.84	0.36

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	92/100 (92%)	88 (96%)	4 (4%)	0	100	100
2	B	208/217 (96%)	198 (95%)	10 (5%)	0	100	100
All	All	300/317 (95%)	286 (95%)	14 (5%)	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	83/85 (98%)	75 (90%)	8 (10%)	8	8
2	B	183/189 (97%)	161 (88%)	22 (12%)	5	4
All	All	266/274 (97%)	236 (89%)	30 (11%)	6	5

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	LYS
1	A	41	ASP
1	A	47	LEU
1	A	48	MET
1	A	62	LEU
1	A	67	GLU
1	A	86	ARG
1	A	99	ARG
2	B	342	SER
2	B	343	SER
2	B	347	LEU
2	B	358	VAL
2	B	375	ARG
2	B	379	ASP
2	B	399	ILE
2	B	400	GLN
2	B	407	ARG
2	B	414	ILE
2	B	422	GLN
2	B	426	ARG
2	B	429	ASP
2	B	430	GLN
2	B	432	ARG
2	B	436	LEU
2	B	464	GLN

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Mol	Chain	Res	Type
2	B	471	LEU
2	B	481	SER
2	B	482	ILE
2	B	534	LEU
2	B	539	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	79	GLN
1	A	94	ASN
2	B	349	HIS
2	B	382	GLN
2	B	402	GLN
2	B	422	GLN
2	B	464	GLN
2	B	498	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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	$\# Z > 2$
3	NAG	A	401	-	15,15,15	0.55	0	21,21,21	1.64	5 (23%)

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
3	NAG	A	401	-	1/1/6/7	4/6/26/26	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	A	401	NAG	O5-C1-C2	-4.44	105.05	109.52
3	A	401	NAG	C3-C4-C5	3.10	115.77	110.24
3	A	401	NAG	O5-C5-C4	2.29	113.85	109.69
3	A	401	NAG	C1-C2-N2	2.11	113.17	110.73
3	A	401	NAG	C1-C2-C3	-2.03	107.78	110.54

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	401	NAG	C1

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	401	NAG	O7-C7-N2-C2
3	A	401	NAG	C8-C7-N2-C2
3	A	401	NAG	O5-C5-C6-O6
3	A	401	NAG	C4-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	401	NAG	6	0

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.