



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2018 – 11:47 pm GMT

PDB ID : 2GOX
Title : Crystal structure of Efb-C / C3d Complex
Authors : Hammel, M.; Geisbrecht, B.V.
Deposited on : 2006-04-14
Resolution : 2.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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
Xtriage (Phenix) : 1.13
EDS : trunk30967
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk30967

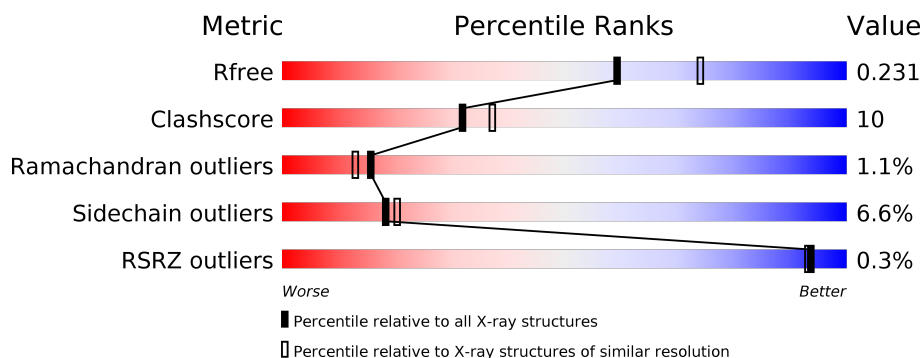
1 Overall quality at a glance

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}	111664	4343 (2.20-2.20)
Clashscore	122126	5027 (2.20-2.20)
Ramachandran outliers	120053	4952 (2.20-2.20)
Sidechain outliers	120020	4953 (2.20-2.20)
RSRZ outliers	108989	4245 (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. 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	297	<div> <div>84%</div> <div>14%</div> <div>•</div> </div>
1	C	297	<div> <div>78%</div> <div>19%</div> <div>•</div> </div>
2	B	65	<div> <div>68%</div> <div>28%</div> <div>5%</div> </div>
2	D	65	<div> <div>3%</div> <div>71%</div> <div>26%</div> <div>••</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5991 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 Complement C3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	297	Total	C	N	O	S	0	0	0
			2327	1492	393	433	9			
1	C	297	Total	C	N	O	S	0	0	0
			2327	1492	393	433	9			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	991	GLY	-	EXPRESSION TAG	UNP P01024
A	992	SER	-	EXPRESSION TAG	UNP P01024
A	993	ARG	-	EXPRESSION TAG	UNP P01024
A	994	SER	-	EXPRESSION TAG	UNP P01024
A	995	THR	-	EXPRESSION TAG	UNP P01024
A	1010	ALA	CYS	ENGINEERED	UNP P01024
C	991	GLY	-	EXPRESSION TAG	UNP P01024
C	992	SER	-	EXPRESSION TAG	UNP P01024
C	993	ARG	-	EXPRESSION TAG	UNP P01024
C	994	SER	-	EXPRESSION TAG	UNP P01024
C	995	THR	-	EXPRESSION TAG	UNP P01024
C	1010	ALA	CYS	ENGINEERED	UNP P01024

- Molecule 2 is a protein called Fibrinogen-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	65	Total	C	N	O	S	0	0	0
			513	321	95	96	1			
2	D	65	Total	C	N	O	S	0	0	0
			507	318	92	96	1			

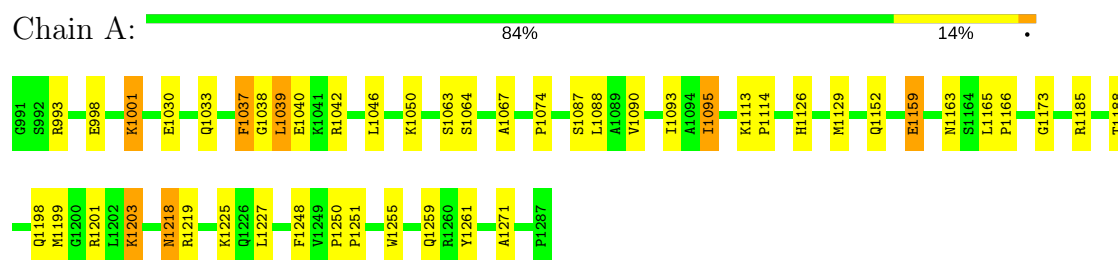
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	145	Total 145	O 145	0	0
3	B	17	Total 17	O 17	0	0
3	C	139	Total 139	O 139	0	0
3	D	16	Total 16	O 16	0	0

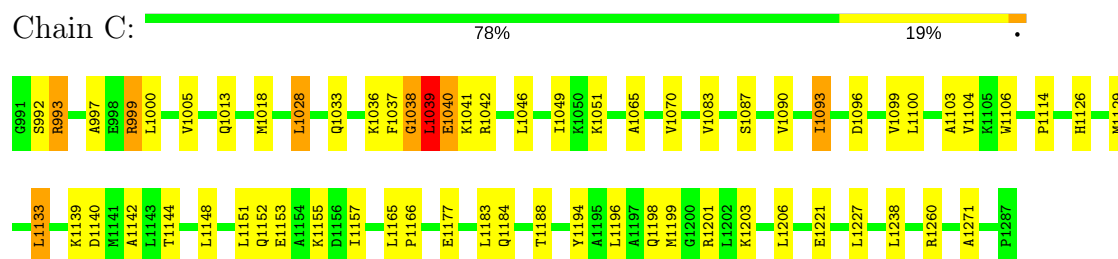
3 Residue-property plots [i](#)

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 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.

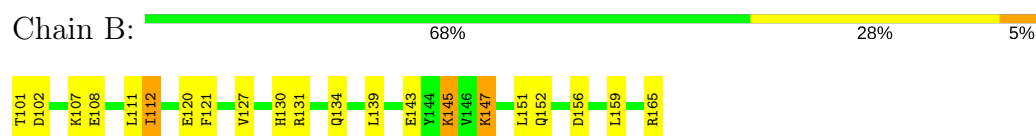
• Molecule 1: Complement C3



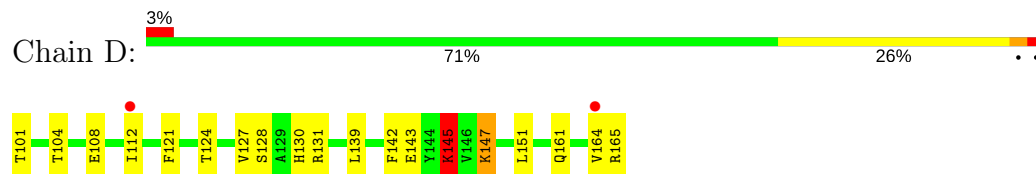
• Molecule 1: Complement C3



• Molecule 2: Fibrinogen-binding protein



• Molecule 2: Fibrinogen-binding protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	90.94Å 90.94Å 122.24Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.20 45.47 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.8 (50.00-2.20) 98.8 (45.47-2.20)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.98 (at 2.20Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.181 , 0.231 0.180 , 0.231	Depositor DCC
R_{free} test set	2519 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	37.1	Xtriage
Anisotropy	0.114	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 41.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.468 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5991	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.94% 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	1.14	0/2376	0.93	1/3219 (0.0%)
1	C	1.17	4/2376 (0.2%)	0.95	2/3219 (0.1%)
2	B	0.92	2/516 (0.4%)	0.82	1/691 (0.1%)
2	D	0.85	0/510	0.79	0/684
All	All	1.11	6/5778 (0.1%)	0.92	4/7813 (0.1%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	1221	GLU	CG-CD	7.12	1.62	1.51
2	B	145	LYS	CD-CE	6.93	1.68	1.51
2	B	145	LYS	CE-NZ	6.31	1.64	1.49
1	C	1153	GLU	CB-CG	6.01	1.63	1.52
1	C	1103	ALA	CA-CB	5.21	1.63	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	1260	ARG	NE-CZ-NH1	5.53	123.06	120.30
1	A	1201	ARG	NE-CZ-NH2	-5.38	117.61	120.30
2	B	145	LYS	CD-CE-NZ	-5.12	99.94	111.70
1	C	1018	MET	CG-SD-CE	-5.11	92.03	100.20

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	2327	0	2324	36	0
1	C	2327	0	2324	48	0
2	B	513	0	532	16	0
2	D	507	0	521	19	0
3	A	145	0	0	6	0
3	B	17	0	0	0	0
3	C	139	0	0	14	0
3	D	16	0	0	1	0
All	All	5991	0	5701	109	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 10.

The worst 5 of 109 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:1039:LEU:HD11	2:B:165:ARG:H	1.19	1.02
2:B:134:GLN:HE22	2:B:152:GLN:HE22	1.25	0.84
2:D:101:THR:HA	2:D:104:THR:HB	1.59	0.83
1:C:1201:ARG:HD2	3:C:168:HOH:O	1.79	0.81
1:A:1037:PHE:CZ	3:A:306:HOH:O	2.34	0.81

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	295/297 (99%)	287 (97%)	6 (2%)	2 (1%)	24	23
1	C	295/297 (99%)	286 (97%)	5 (2%)	4 (1%)	12	9
2	B	63/65 (97%)	60 (95%)	2 (3%)	1 (2%)	11	8
2	D	63/65 (97%)	61 (97%)	1 (2%)	1 (2%)	11	8

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	716/724 (99%)	694 (97%)	14 (2%)	8 (1%)	16 13

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	1036	LYS
1	A	1037	PHE
2	B	145	LYS
1	C	1037	PHE
1	C	1039	LEU

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	243/245 (99%)	229 (94%)	14 (6%)	22 26
1	C	243/245 (99%)	230 (95%)	13 (5%)	25 30
2	B	55/59 (93%)	49 (89%)	6 (11%)	7 6
2	D	54/59 (92%)	48 (89%)	6 (11%)	7 6
All	All	595/608 (98%)	556 (93%)	39 (7%)	18 20

5 of 39 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	112	ILE
1	C	999	ARG
2	D	143	GLU
2	B	120	GLU
2	B	147	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	1013	GLN
1	C	1033	GLN
1	C	1257	ASN
2	B	134	GLN
2	B	161	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 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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	297/297 (100%)	-0.32	0 100 100	27, 36, 59, 72	0
1	C	297/297 (100%)	-0.28	0 100 100	27, 37, 60, 68	0
2	B	65/65 (100%)	0.14	0 100 100	44, 59, 76, 87	0
2	D	65/65 (100%)	0.11	2 (3%) 49 46	44, 58, 81, 88	0
All	All	724/724 (100%)	-0.22	2 (0%) 93 93	27, 39, 66, 88	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	112	ILE	2.4
2	D	164	VAL	2.1

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 carbohydrates 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.