



Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 03:29 pm BST

PDB ID : 2BYV
Title : Structure of the cAMP responsive exchange factor Epac2 in its auto- inhibited state
Authors : Rehmann, H.; Wittinghofer, A.; Bos, J.L.
Deposited on : 2005-08-08
Resolution : 2.70 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
Xtriage (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

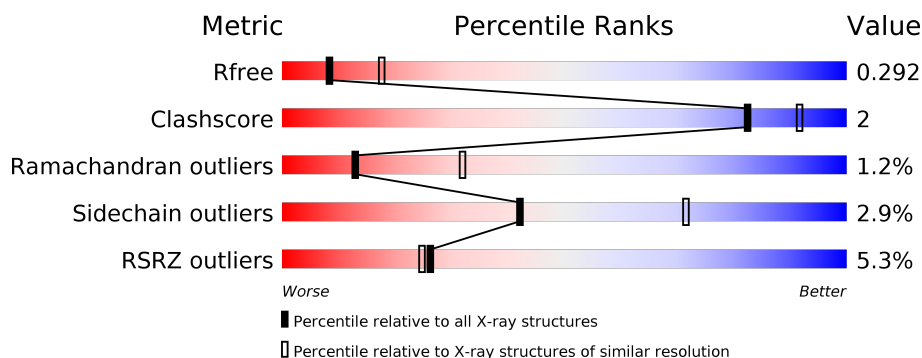
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 $\leq 5\%$. 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	E	999	<div> <div>5%</div> <div> <div></div> <div>83%</div> <div>8%</div> <div>8%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7430 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 RAP GUANINE NUCLEOTIDE EXCHANGE FACTOR 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	E	922	Total	C	N	O	S	0	0	0
			7364	4677	1274	1369	44			

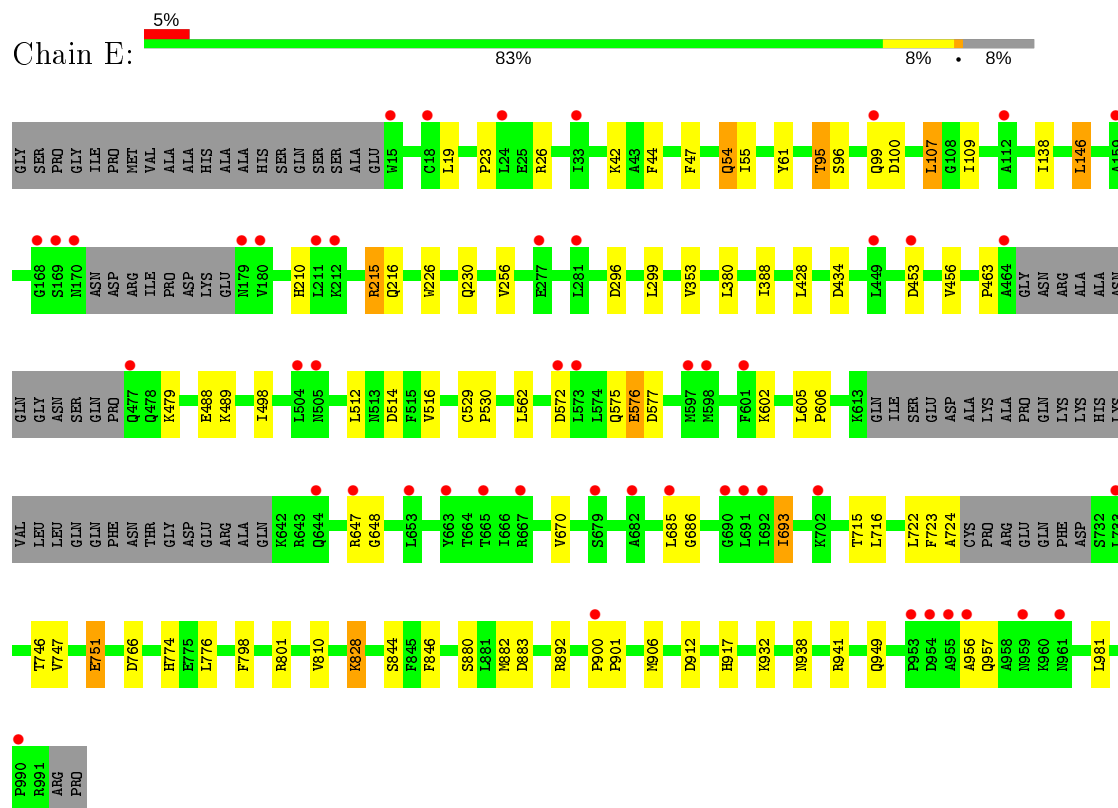
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	E	66	Total	O	0	0
			66	66		

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: RAP GUANINE NUCLEOTIDE EXCHANGE FACTOR 4



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	76.41Å 97.04Å 172.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.88 – 2.70 29.86 – 2.70	Depositor EDS
% Data completeness (in resolution range)	100.0 (29.88-2.70) 99.8 (29.86-2.70)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.58 (at 2.68Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.245 , 0.297 0.242 , 0.292	Depositor DCC
R_{free} test set	1791 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	61.0	Xtriage
Anisotropy	0.191	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 43.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	7430	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.28% 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	E	0.34	0/7511	0.49	1/10166 (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	E	107	LEU	CA-CB-CG	5.29	127.47	115.30

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	E	7364	0	7303	36	0
2	E	66	0	0	0	0
All	All	7430	0	7303	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 2.

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:E:693:ILE:HA	1:E:723:PHE:O	1.96	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:23:PRO:HA	1:E:26:ARG:HE	1.60	0.66
1:E:798:PHE:CE2	1:E:906:MET:HG3	2.30	0.65
1:E:798:PHE:HE2	1:E:906:MET:HG3	1.63	0.63
1:E:19:LEU:HB3	1:E:61:TYR:HB2	1.79	0.63
1:E:901:PRO:HG3	1:E:949:GLN:HB2	1.87	0.57
1:E:353:VAL:HG11	1:E:434:ASP:HB3	1.88	0.56
1:E:693:ILE:H	1:E:724:ALA:HA	1.71	0.55
1:E:602:LYS:O	1:E:606:PRO:HD3	2.08	0.52
1:E:54:GLN:HB3	1:E:146:LEU:HD11	1.93	0.51
1:E:846:PHE:CE2	1:E:882:MET:HG2	2.46	0.51
1:E:751:GLU:HA	1:E:828:LYS:HD3	1.92	0.51
1:E:766:ASP:OD2	1:E:844:SER:OG	2.26	0.50
1:E:44:PHE:HA	1:E:47:PHE:CD1	2.47	0.49
1:E:226:TRP:CE2	1:E:230:GLN:HG3	2.48	0.49
1:E:751:GLU:HA	1:E:828:LYS:CD	2.42	0.49
1:E:498:ILE:HG12	1:E:512:LEU:HD11	1.96	0.48
1:E:55:ILE:HG23	1:E:138:ILE:HD11	1.96	0.47
1:E:529:CYS:HB2	1:E:530:PRO:HD3	1.96	0.47
1:E:299:LEU:HD13	1:E:880:SER:HB2	1.96	0.47
1:E:380:LEU:HD11	1:E:428:LEU:HD13	1.97	0.46
1:E:605:LEU:N	1:E:606:PRO:HD2	2.31	0.46
1:E:514:ASP:OD1	1:E:941:ARG:NH2	2.47	0.44
1:E:456:VAL:HG13	1:E:489:LYS:HG2	2.00	0.43
1:E:892:ARG:NH2	1:E:912:ASP:OD2	2.52	0.43
1:E:99:GLN:HE21	1:E:99:GLN:HB2	1.68	0.42
1:E:648:GLY:HA2	1:E:670:VAL:HB	2.01	0.42
1:E:810:VAL:HG12	1:E:981:LEU:HD22	2.01	0.42
1:E:917:HIS:HA	1:E:932:LYS:HE3	2.00	0.42
1:E:512:LEU:HD22	1:E:562:LEU:HD13	2.00	0.42
1:E:95:THR:HG22	1:E:96:SER:H	1.85	0.42
1:E:716:LEU:HD11	1:E:722:LEU:HD13	2.02	0.41
1:E:880:SER:O	1:E:883:ASP:HB2	2.21	0.41
1:E:575:GLN:C	1:E:577:ASP:H	2.25	0.41
1:E:42:LYS:HB3	1:E:109:ILE:HG22	2.01	0.40
1:E:774:HIS:HD2	1:E:776:LEU:H	1.69	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	E	912/999 (91%)	864 (95%)	37 (4%)	11 (1%)	13	32

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	216	GLN
1	E	956	ALA
1	E	463	PRO
1	E	215	ARG
1	E	576	GLU
1	E	957	GLN
1	E	685	LEU
1	E	693	ILE
1	E	747	VAL
1	E	900	PRO
1	E	686	GLY

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	E	805/882 (91%)	782 (97%)	23 (3%)	42	71

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	54	GLN
1	E	95	THR
1	E	100	ASP
1	E	107	LEU
1	E	146	LEU
1	E	210	HIS
1	E	215	ARG
1	E	256	VAL
1	E	296	ASP
1	E	388	ILE
1	E	453	ASP
1	E	479	LYS
1	E	488	GLU
1	E	516	VAL
1	E	572	ASP
1	E	576	GLU
1	E	647	ARG
1	E	715	THR
1	E	746	THR
1	E	751	GLU
1	E	801	ARG
1	E	828	LYS
1	E	938	ASN

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

Mol	Chain	Res	Type
1	E	99	GLN
1	E	202	HIS
1	E	424	ASN
1	E	478	GLN
1	E	519	HIS
1	E	661	HIS
1	E	774	HIS
1	E	917	HIS
1	E	986	HIS

5.3.3 RNA ⓘ

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 ⓘ

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	E	922/999 (92%)	0.32	49 (5%) 26 25	36, 59, 95, 106	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	956	ALA	6.3
1	E	573	LEU	5.3
1	E	653	LEU	4.8
1	E	180	VAL	4.7
1	E	572	ASP	4.2
1	E	179	ASN	4.2
1	E	691	LEU	4.0
1	E	690	GLY	3.8
1	E	464	ALA	3.8
1	E	685	LEU	3.7
1	E	667	ARG	3.7
1	E	170	ASN	3.3
1	E	900	PRO	3.3
1	E	169	SER	3.3
1	E	955	ALA	3.2
1	E	598	MET	3.1
1	E	477	GLN	3.0
1	E	647	ARG	3.0
1	E	702	LYS	2.9
1	E	692	ILE	2.9
1	E	961	ASN	2.9
1	E	954	ASP	2.6
1	E	959	ASN	2.5
1	E	504	LEU	2.5
1	E	24	LEU	2.5
1	E	99	GLN	2.4
1	E	663	TYR	2.4

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Mol	Chain	Res	Type	RSRZ
1	E	168	GLY	2.4
1	E	112	ALA	2.4
1	E	953	PRO	2.3
1	E	505	ASN	2.3
1	E	644	GLN	2.3
1	E	211	LEU	2.2
1	E	159	ALA	2.2
1	E	33	ILE	2.2
1	E	449	LEU	2.2
1	E	15	TRP	2.2
1	E	597	MET	2.2
1	E	679	SER	2.1
1	E	281	LEU	2.1
1	E	18	CYS	2.1
1	E	212	LYS	2.1
1	E	601	PHE	2.1
1	E	682	ALA	2.1
1	E	453	ASP	2.1
1	E	733	LEU	2.0
1	E	990	PRO	2.0
1	E	665	THR	2.0
1	E	277	GLU	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 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.