



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 06:46 am GMT

PDB ID : 1EE4
Title : CRYSTAL STRUCTURE OF YEAST KARYOPHERIN (IMPORTIN) ALPHA IN A COMPLEX WITH A C-MYC NLS PEPTIDE
Authors : Conti, E.
Deposited on : 2000-01-30
Resolution : 2.10 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

<http://wwpdb.org/validation/2016/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
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

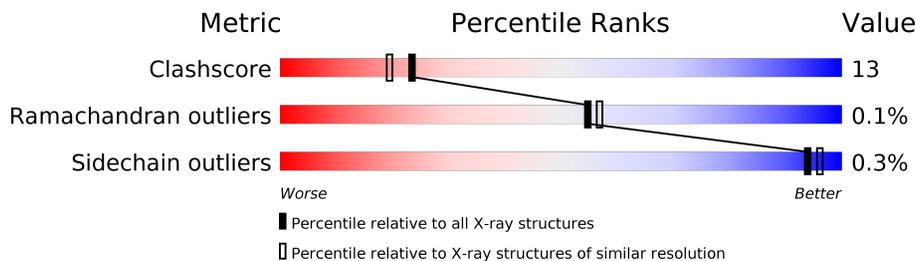
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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))
Clashscore	112137	4788 (2.10-2.10)
Ramachandran outliers	110173	4740 (2.10-2.10)
Sidechain outliers	110143	4741 (2.10-2.10)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	423	
1	B	423	
2	C	9	
2	D	9	
2	E	9	
2	F	9	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6991 atoms, of which 174 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 KARYOPHERIN ALPHA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	423	3248	2012	88	528	605	15	5	0	0
1	B	423	3236	2007	86	529	600	14	6	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	397	ASP	TYR	ENGINEERED	UNP Q02821
B	397	ASP	TYR	ENGINEERED	UNP Q02821

- Molecule 2 is a protein called MYC PROTO-ONCOGENE PROTEIN.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	C	9	69	44	14	11	0	0	0
2	D	5	37	23	9	5	0	0	0
2	E	9	69	44	14	11	0	0	0
2	F	4	32	20	8	4	0	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	122	Total	O	0	0
			122	122		
3	B	140	Total	O	0	0
			140	140		
3	C	14	Total	O	0	0
			14	14		

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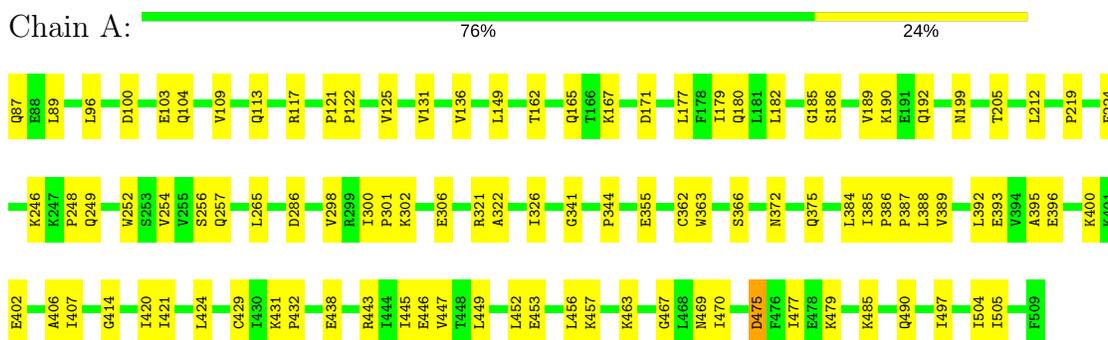
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	D	4	Total O 4 4	0	0
3	E	17	Total O 17 17	0	0
3	F	3	Total O 3 3	0	0

3 Residue-property plots [i](#)

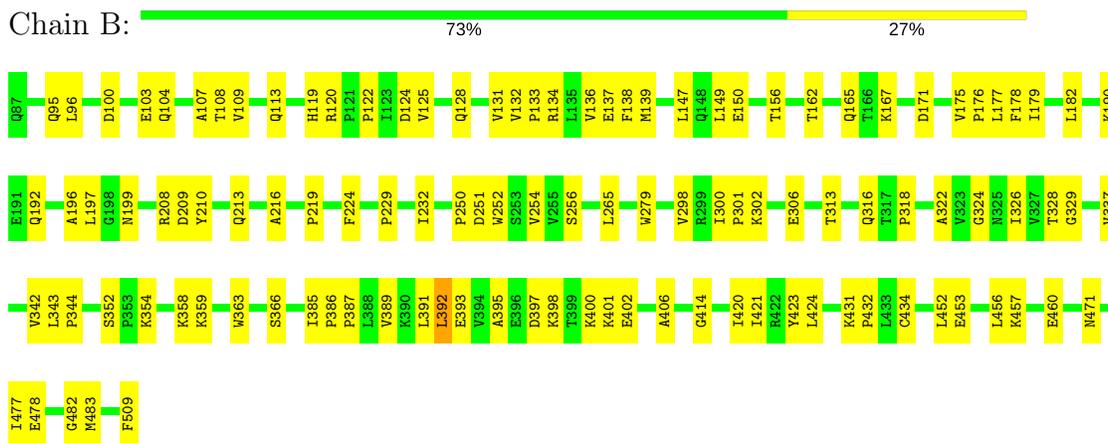
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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.

Note EDS was not executed.

- Molecule 1: KARYOPHERIN ALPHA



- Molecule 1: KARYOPHERIN ALPHA



- Molecule 2: MYC PROTO-ONCOGENE PROTEIN



- Molecule 2: MYC PROTO-ONCOGENE PROTEIN



- Molecule 2: MYC PROTO-ONCOGENE PROTEIN



- Molecule 2: MYC PROTO-ONCOGENE PROTEIN



4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	42.68Å 85.85Å 117.50Å 90.00° 93.42° 90.00°	Depositor
Resolution (Å)	30.00 – 2.10	Depositor
% Data completeness (in resolution range)	(Not available) (30.00-2.10)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.246 , 0.277	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	6991	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

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	0.28	0/3211	0.57	0/4386
1	B	0.28	0/3201	0.57	0/4376
2	C	0.30	0/69	0.70	0/90
2	D	0.22	0/36	0.53	0/46
2	E	0.26	0/69	0.68	0/90
2	F	0.21	0/31	0.55	0/39
All	All	0.28	0/6617	0.57	0/9027

There are no bond length outliers.

There are no bond angle outliers.

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	3160	88	3115	70	0
1	B	3150	86	3112	87	0
2	C	69	0	80	7	0
2	D	37	0	38	2	0
2	E	69	0	80	4	0
2	F	32	0	36	1	0
3	A	122	0	0	5	0
3	B	140	0	0	3	0
3	C	14	0	0	2	0
3	D	4	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	E	17	0	0	2	0
3	F	3	0	0	0	0
All	All	6817	174	6461	165	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 13.

The worst 5 of 165 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:87:GLN:HA	3:A:592:HOH:O	1.83	0.78
1:A:100:ASP:O	1:A:104:GLN:HG3	1.87	0.75
1:B:478:GLU:CD	1:B:483:MET:HE3	2.07	0.75
1:A:355:GLU:HG2	1:A:396:GLU:OE1	1.86	0.75
1:A:122:PRO:O	1:A:125:VAL:HG12	1.88	0.72

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	421/423 (100%)	413 (98%)	7 (2%)	1 (0%)	51	52
1	B	421/423 (100%)	415 (99%)	6 (1%)	0	100	100
2	C	7/9 (78%)	7 (100%)	0	0	100	100
2	D	3/9 (33%)	3 (100%)	0	0	100	100
2	E	7/9 (78%)	7 (100%)	0	0	100	100
2	F	2/9 (22%)	2 (100%)	0	0	100	100
All	All	861/882 (98%)	847 (98%)	13 (2%)	1 (0%)	55	57

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	467	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	A	326/365 (89%)	325 (100%)	1 (0%)	94	96
1	B	326/365 (89%)	325 (100%)	1 (0%)	94	96
2	C	7/7 (100%)	7 (100%)	0	100	100
2	D	3/7 (43%)	3 (100%)	0	100	100
2	E	7/7 (100%)	7 (100%)	0	100	100
2	F	3/7 (43%)	3 (100%)	0	100	100
All	All	672/758 (89%)	670 (100%)	2 (0%)	94	96

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	475	ASP
1	B	392	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	490	GLN
1	B	95	GLN
1	B	213	GLN
1	A	289	GLN
1	B	128	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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.