



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 24, 2023 – 01:15 AM EDT

PDB ID : 5SV7
Title : The Crystal structure of a chaperone
Authors : Wang, P.; Li, J.; Sha, B.
Deposited on : 2016-08-04
Resolution : 3.21 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 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 : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.35.1
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) : 2.35.1

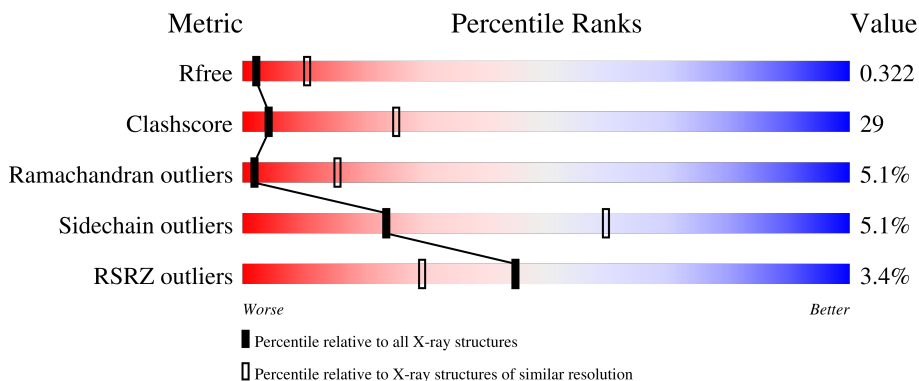
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.21 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	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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 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	326	
1	B	326	
1	C	326	
1	D	326	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6602 atoms, of which 0 are hydrogens and 0 are deuteriums.

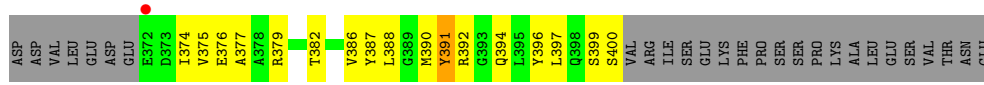
In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Eukaryotic translation initiation factor 2-alpha kinase 3.

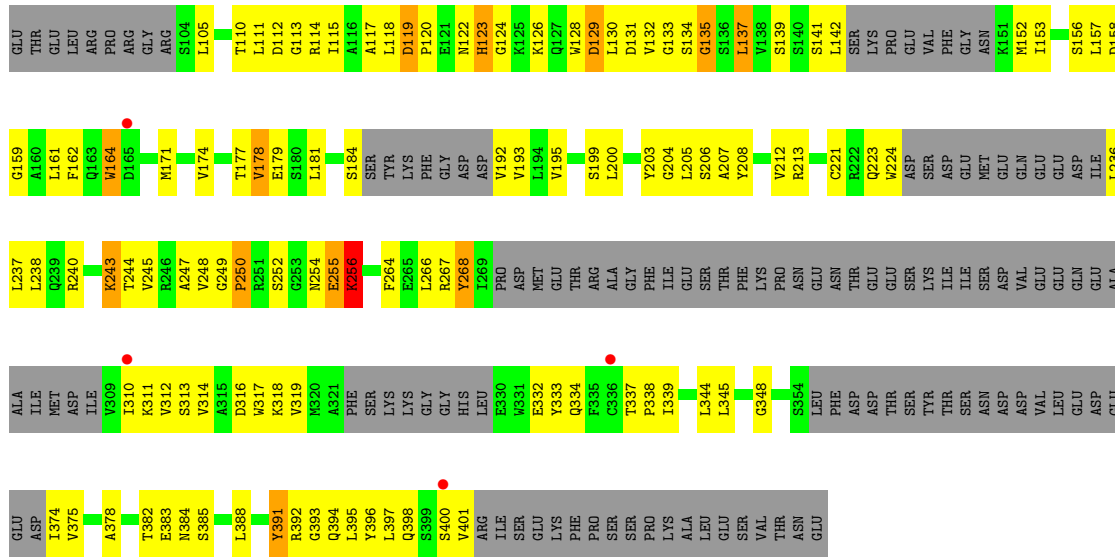
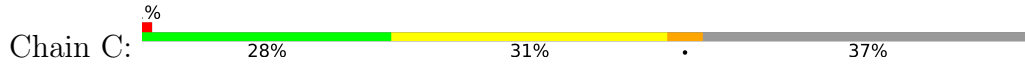
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	203	Total 1584	C 1010	N 269	O 298	S 7	0	0	0
1	B	224	Total 1751	C 1122	N 293	O 329	S 7	0	0	0
1	C	206	Total 1608	C 1031	N 271	O 299	S 7	0	0	0
1	D	209	Total 1630	C 1040	N 273	O 310	S 7	0	0	0

- Molecule 2 is water.

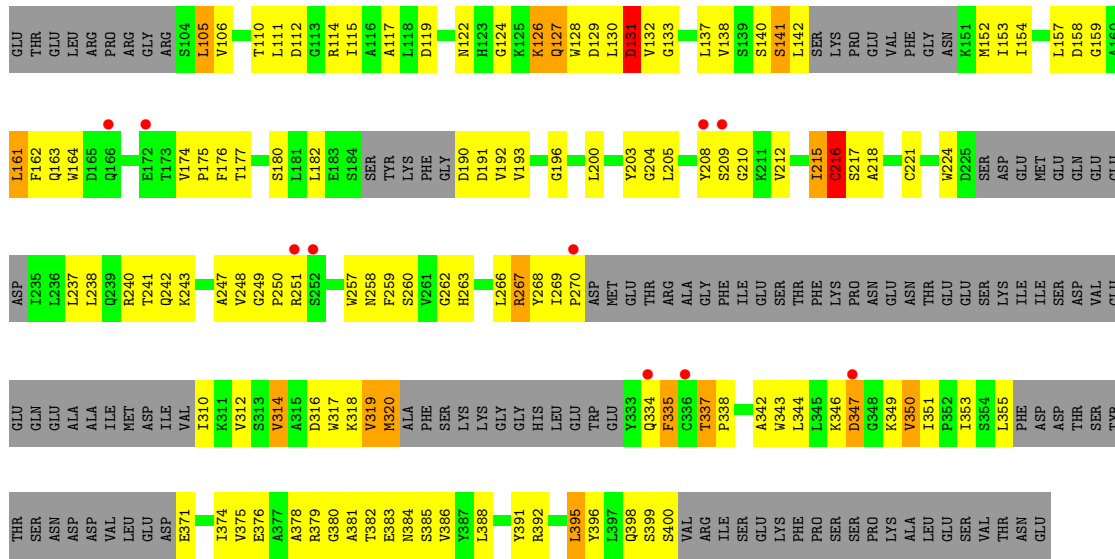
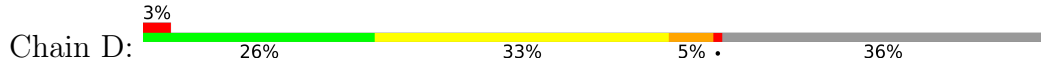
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	9	Total 9	O 9	0	0
2	B	3	Total 3	O 3	0	0
2	C	6	Total 6	O 6	0	0
2	D	11	Total 11	O 11	0	0



● Molecule 1: Eukaryotic translation initiation factor 2-alpha kinase 3



● Molecule 1: Eukaryotic translation initiation factor 2-alpha kinase 3



4 Data and refinement statistics i

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	163.91Å 163.91Å 63.08Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	37.85 – 3.21 37.85 – 3.21	Depositor EDS
% Data completeness (in resolution range)	98.0 (37.85-3.21) 98.3 (37.85-3.21)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.25 (at 3.18Å)	Xtrriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.271 , 0.322 0.271 , 0.322	Depositor DCC
R_{free} test set	1578 reflections (5.18%)	wwPDB-VP
Wilson B-factor (Å ²)	32.1	Xtrriage
Anisotropy	0.000	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 37.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.37$	Xtrriage
Estimated twinning fraction	0.000 for -h,-k,l 0.034 for h,-h-k,-l 0.006 for -k,-h,-l	Xtrriage
F_o, F_c correlation	0.81	EDS
Total number of atoms	6602	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.90% 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	0.56	0/1610	0.86	1/2172 (0.0%)
1	B	0.63	3/1784 (0.2%)	0.78	2/2409 (0.1%)
1	C	0.61	0/1636	0.95	1/2209 (0.0%)
1	D	0.63	1/1657 (0.1%)	0.91	3/2237 (0.1%)
All	All	0.61	4/6687 (0.1%)	0.87	7/9027 (0.1%)

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
1	A	0	6
1	B	0	2
1	C	0	1
1	D	0	4
All	All	0	13

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	332	GLU	CD-OE1	-8.04	1.16	1.25
1	B	216	CYS	CB-SG	-6.33	1.71	1.82
1	B	332	GLU	CD-OE2	-6.21	1.18	1.25
1	D	131	ASP	CA-CB	5.01	1.65	1.53

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	395	LEU	CA-CB-CG	7.84	133.34	115.30
1	D	200	LEU	CA-CB-CG	5.88	128.84	115.30
1	A	345	LEU	CA-CB-CG	5.87	128.81	115.30
1	B	219	LEU	CA-CB-CG	5.78	128.60	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	C	137	LEU	CA-CB-CG	5.64	128.26	115.30

There are no chirality outliers.

5 of 13 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	123	HIS	Peptide
1	A	203	TYR	Peptide
1	A	267	ARG	Peptide
1	A	335	PHE	Peptide
1	A	336	CYS	Peptide

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	1584	0	1586	89	0
1	B	1751	0	1749	105	0
1	C	1608	0	1615	102	0
1	D	1630	0	1629	112	0
2	A	9	0	0	1	0
2	B	3	0	0	0	0
2	C	6	0	0	1	0
2	D	11	0	0	0	0
All	All	6602	0	6579	384	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 29.

The worst 5 of 384 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:345:LEU:HG	1:A:349:LYS:HG3	1.38	1.05
1:B:104:SER:HB3	1:B:346:LYS:HA	1.53	0.89
1:A:157:LEU:HD11	1:A:398:GLN:HG2	1.57	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:203:TYR:O	1:A:238:LEU:N	2.09	0.86
1:C:120:PRO:HD2	1:C:123:HIS:HB2	1.58	0.85

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	189/326 (58%)	156 (82%)	24 (13%)	9 (5%)	2	17
1	B	212/326 (65%)	169 (80%)	33 (16%)	10 (5%)	2	17
1	C	192/326 (59%)	161 (84%)	20 (10%)	11 (6%)	1	14
1	D	195/326 (60%)	150 (77%)	35 (18%)	10 (5%)	2	15
All	All	788/1304 (60%)	636 (81%)	112 (14%)	40 (5%)	2	15

5 of 40 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	317	TRP
1	A	350	VAL
1	A	376	GLU
1	B	119	ASP
1	B	212	VAL

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	174/286 (61%)	165 (95%)	9 (5%)	23	59
1	B	192/286 (67%)	181 (94%)	11 (6%)	20	56
1	C	176/286 (62%)	166 (94%)	10 (6%)	20	56
1	D	180/286 (63%)	173 (96%)	7 (4%)	32	67
All	All	722/1144 (63%)	685 (95%)	37 (5%)	24	60

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	333	TYR
1	D	334	GLN
1	C	384	ASN
1	D	190	ASP
1	B	208	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	127	GLN
1	A	254	ASN
1	B	394	GLN
1	C	254	ASN
1	C	394	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 monosaccharides 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	203/326 (62%)	0.27	9 (4%) 34 21	27, 41, 65, 83	0
1	B	224/326 (68%)	0.22	6 (2%) 54 39	21, 38, 64, 72	0
1	C	206/326 (63%)	0.12	4 (1%) 66 53	9, 29, 55, 66	0
1	D	209/326 (64%)	0.29	10 (4%) 30 18	16, 31, 61, 73	0
All	All	842/1304 (64%)	0.23	29 (3%) 45 29	9, 36, 62, 83	0

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	209	SER	4.5
1	A	336	CYS	3.8
1	D	252	SER	3.6
1	D	172	GLU	3.1
1	A	384	ASN	3.0

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 monosaccharides 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.