

wwPDB X-ray Structure Validation Summary Report (i)

Dec 20, 2021 – 03:03 pm GMT

PDB ID	:	6T5H
Title	:	Human 14-3-3 sigma fused to the StARD1 peptide including phosphoserine-57
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Deposited on		
Resolution	:	2.04 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

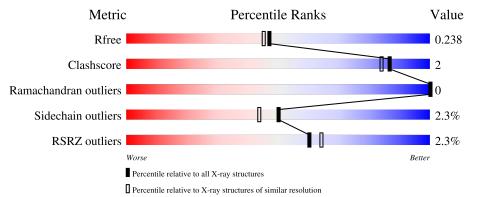
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.24
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.24

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 2.04 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)
RSRZ outliers	127900	1672 (2.04-2.04)

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 <=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	А	248	% 91%	• 6%					
1	В	248	3% 92%	5% • •					

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
2	PGE	В	301	-	-	-	Х



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4182 atoms, of which 47 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 14-3-3 protein sigma, Steroidogenic acute regulatory protein, mitochondrial.

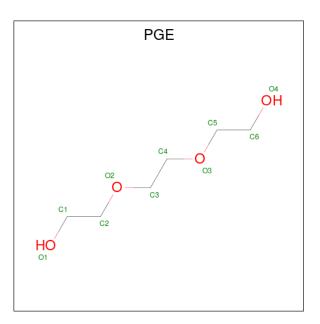
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
1	А	234	Total 1855	C 1157	11	0 371	-	S 10	0	1	0
1	В	241	Total 1900	C 1183		-	Р 1	S 10	0	0	0

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP P31947
А	-1	PRO	-	expression tag	UNP P31947
A	0	HIS	-	expression tag	UNP P31947
А	75	ALA	GLU	engineered mutation	UNP P31947
А	76	ALA	GLU	engineered mutation	UNP P31947
А	77	ALA	LYS	engineered mutation	UNP P31947
А	232	GLY	-	linker	UNP P31947
А	233	SER	-	linker	UNP P31947
А	234	GLY	-	linker	UNP P31947
А	235	SER	-	linker	UNP P31947
А	236	LEU	-	linker	UNP P31947
В	-2	GLY	-	expression tag	UNP P31947
В	-1	PRO	-	expression tag	UNP P31947
В	0	HIS	-	expression tag	UNP P31947
В	75	ALA	GLU	engineered mutation	UNP P31947
В	76	ALA	GLU	engineered mutation	UNP P31947
В	77	ALA	LYS	engineered mutation	UNP P31947
В	232	GLY	-	linker	UNP P31947
В	233	SER	-	linker	UNP P31947
В	234	GLY	-	linker	UNP P31947
В	235	SER	-	linker	UNP P31947
В	236	LEU	-	linker	UNP P31947

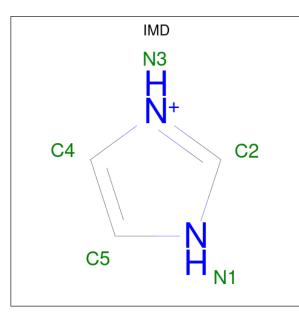
There are 22 discrepancies between the modelled and reference sequences:

• Molecule 2 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: $C_6H_{14}O_4$).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	$\begin{array}{cccc} \text{Total} \text{C} \text{H} \text{O} \\ 24 6 14 4 \end{array}$	0	0
2	А	1	Total C H O 24 6 14 4	0	0
2	В	1	Total C H O 24 6 14 4	0	0



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	А	1	Total 10	С 3	H5	N 2	0	0



• Molecule 4 is water.

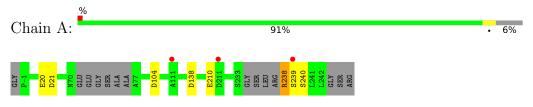
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	168	Total O 168 168	0	0
4	В	177	Total O 177 177	0	0



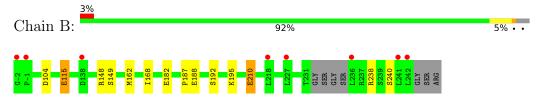
3 Residue-property plots (i)

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 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: 14-3-3 protein sigma, Steroidogenic acute regulatory protein, mitochondrial



• Molecule 1: 14-3-3 protein sigma, Steroidogenic acute regulatory protein, mitochondrial





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	90.17Å 78.35Å 76.06Å	Depositor
a, b, c, α , β , γ	90.00° 100.42° 90.00°	Depositor
Resolution (Å)	49.13 - 2.04	Depositor
Resolution (A)	58.72 - 2.04	EDS
% Data completeness	99.8 (49.13-2.04)	Depositor
(in resolution range)	99.8(58.72-2.04)	EDS
R _{merge}	0.11	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.80 (at 2.05 \text{\AA})$	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
D D	0.185 , 0.229	Depositor
R, R_{free}	0.191 , 0.238	DCC
R_{free} test set	1632 reflections (4.92%)	wwPDB-VP
Wilson B-factor $(Å^2)$	33.2	Xtriage
Anisotropy	0.498	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	(Not available), (Not available)	EDS
L-test for twinning ²	$ L > = 0.50, < L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4182	wwPDB-VP
Average B, all atoms $(Å^2)$	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 7.21% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: PGE, IMD, SEP

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		
	Ullain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.52	0/1873	0.59	0/2516	
1	В	0.51	0/1916	0.61	0/2576	
All	All	0.51	0/3789	0.60	0/5092	

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	А	1855	0	1835	10	0
1	В	1900	0	1879	10	0
2	А	20	28	28	5	0
2	В	10	14	14	2	0
3	А	5	5	5	0	0
4	А	168	0	0	1	0
4	В	177	0	0	0	0
All	All	4135	47	3761	16	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.



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:210:GLU:HB3	1:B:210:GLU:HG2	1.10	1.05
1:A:210:GLU:CB	1:B:210:GLU:HG2	1.96	0.95
1:A:210:GLU:HB3	1:B:210:GLU:CG	2.05	0.67
1:A:20:GLU:HB2	2:A:302:PGE:C4	2.28	0.63
1:B:115:GLU:HG3	1:B:168:ILE:HD12	1.83	0.60

The worst 5 of 16 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

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	А	228/248~(92%)	224 (98%)	4 (2%)	0	100	100	
1	В	236/248~(95%)	232~(98%)	4 (2%)	0	100	100	
All	All	464/496~(94%)	456 (98%)	8 (2%)	0	100	100	

There are no Ramachandran outliers to report.

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	А	198/205~(97%)	195~(98%)	3~(2%)	65 62		

Continued on next page...



	Chain	Analysed	Rotameric	Outliers	Percentiles
1	В	201/205 (98%)	195 (97%)	6 (3%)	41 34
All	All	399/410~(97%)	390~(98%)	9(2%)	50 44

Continued from previous page...

5 of 9 residues with a non-rotameric side chain are listed below:

Mol	Chain	Res	Type
1	В	210	GLU
1	В	238	ARG
1	В	104	ASP
1	В	115	GLU
1	В	192	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

2 non-standard protein/DNA/RNA residues are 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	B	Bond lengths			Bond ang	gles
WIOI	туре	Ullalli	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
1	SEP	А	240	1	8,9,10	1.34	2 (25%)	8,12,14	1.01	0
1	SEP	В	240	1	8,9,10	1.18	1 (12%)	8,12,14	1.74	3 (37%)

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
1	SEP	А	240	1	-	0/5/8/10	-
1	SEP	В	240	1	-	0/5/8/10	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	В	240	SEP	P-O3P	-2.55	1.45	1.54
1	А	240	SEP	P-OG	-2.35	1.52	1.60
1	А	240	SEP	P-O3P	-2.25	1.46	1.54

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^{o})$	$Ideal(^{o})$
1	В	240	SEP	OG-P-O1P	2.98	114.83	106.47
1	В	240	SEP	OG-CB-CA	2.60	110.68	108.14
1	В	240	SEP	O3P-P-O1P	-2.01	102.83	110.68

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

4 ligands are 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).

Т	Mol Type (Chain	Res	Link	Bond lengths			Bond angles			
	Type				Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2	
	2	PGE	А	302	-	9,9,9	0.18	0	8,8,8	0.29	0



Mol	Type	Chain	Res	Link	B	Bond lengths			Bond angles		
10101	туре	Chain	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2	
2	PGE	А	301	-	9,9,9	0.20	0	8,8,8	0.19	0	
3	IMD	А	303	-	$3,\!5,\!5$	0.39	0	$4,\!5,\!5$	0.72	0	
2	PGE	В	301	-	9,9,9	0.28	0	8,8,8	0.28	0	

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
2	PGE	А	302	-	-	3/7/7/7	-
2	PGE	А	301	-	-	1/7/7/7	-
3	IMD	А	303	-	-	-	0/1/1/1
2	PGE	В	301	-	-	2/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	В	301	PGE	O1-C1-C2-O2
2	В	301	PGE	O2-C3-C4-O3
2	А	302	PGE	O1-C1-C2-O2
2	А	301	PGE	O2-C3-C4-O3
2	А	302	PGE	C1-C2-O2-C3

There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	А	302	PGE	5	0
2	В	301	PGE	2	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 (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, 95^{th} 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	$\langle RSRZ \rangle$	#RSRZ>2	$OWAB(Å^2)$	Q<0.9
1	А	233/248~(93%)	-0.27	3 (1%) 77 79	27, 39, 68, 103	0
1	В	240/248~(96%)	-0.12	8 (3%) 46 50	28, 42, 69, 103	0
All	All	473/496~(95%)	-0.19	11 (2%) 60 64	27, 41, 69, 103	0

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	236	LEU	8.5
1	В	138	ASP	5.2
1	В	-1	PRO	4.0
1	В	241	LEU	3.6
1	А	239	SER	3.2

6.2 Non-standard residues in protein, DNA, RNA chains (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q < 0.9
1	SEP	А	240	10/11	0.97	0.12	41,48,57,59	0
1	SEP	В	240	10/11	0.99	0.10	29,36,53,54	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.



6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q<0.9
2	PGE	В	301	10/10	0.80	0.46	66,71,81,82	0
2	PGE	А	302	10/10	0.83	0.29	51,54,77,80	0
2	PGE	А	301	10/10	0.83	0.21	54,63,74,74	0
3	IMD	А	303	5/5	0.88	0.15	81,82,82,82	0

6.5 Other polymers (i)

There are no such residues in this entry.

