



wwPDB X-ray Structure Validation Summary Report

Feb 27, 2014 – 02:44 PM GMT

PDB ID : 4L0N
Title : Crystal structure of STK3 (MST2) SARAH domain
Authors : Chaikuad, A.; Krojer, T.; Newman, J.A.; Dixon-Clarke, S.; von Delft, F.; Arrowsmith, C.H.; Edwards, A.M.; Bountra, C.; Knapp, S.; Structural Genomics Consortium (SGC)
Deposited on : 2013-05-31
Resolution : 1.40 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

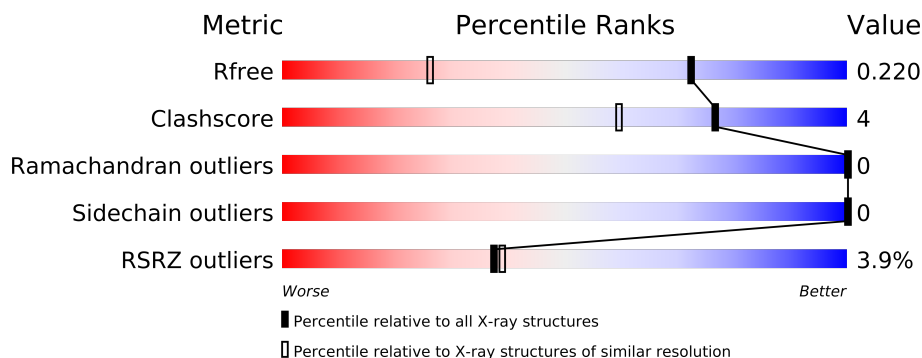
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 1.40 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}	66092	1097 (1.42-1.38)
Clashscore	79885	1246 (1.42-1.38)
Ramachandran outliers	78287	1206 (1.42-1.38)
Sidechain outliers	78261	1205 (1.42-1.38)
RSRZ outliers	66119	1097 (1.42-1.38)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	51	
1	B	51	
1	C	51	
1	D	51	
1	E	51	
1	F	51	
1	G	51	
1	H	51	
1	I	51	
1	J	51	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5292 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Serine/threonine-proteinkinase 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	51	Total	C	N	O	S	0	6	0
			463	293	79	85	6			
1	B	51	Total	C	N	O	S	0	3	0
			447	281	77	84	5			
1	C	51	Total	C	N	O	S	0	2	0
			438	276	74	82	6			
1	D	51	Total	C	N	O	S	0	6	0
			461	292	77	85	7			
1	E	51	Total	C	N	O	S	0	7	0
			468	294	79	89	6			
1	F	51	Total	C	N	O	S	0	2	0
			434	272	73	83	6			
1	G	51	Total	C	N	O	S	0	11	0
			492	313	82	91	6			
1	H	51	Total	C	N	O	S	0	1	0
			430	270	74	80	6			
1	I	51	Total	C	N	O	S	0	4	0
			451	285	77	82	7			
1	J	48	Total	C	N	O	S	0	2	0
			409	255	76	74	4			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	SER	-	EXPRESSION TAG	UNP Q13188
A	0	MET	-	EXPRESSION TAG	UNP Q13188
B	-1	SER	-	EXPRESSION TAG	UNP Q13188
B	0	MET	-	EXPRESSION TAG	UNP Q13188
C	-1	SER	-	EXPRESSION TAG	UNP Q13188
C	0	MET	-	EXPRESSION TAG	UNP Q13188
D	-1	SER	-	EXPRESSION TAG	UNP Q13188
D	0	MET	-	EXPRESSION TAG	UNP Q13188
E	-1	SER	-	EXPRESSION TAG	UNP Q13188

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Chain	Residue	Modelled	Actual	Comment	Reference
E	0	MET	-	EXPRESSION TAG	UNP Q13188
F	-1	SER	-	EXPRESSION TAG	UNP Q13188
F	0	MET	-	EXPRESSION TAG	UNP Q13188
G	-1	SER	-	EXPRESSION TAG	UNP Q13188
G	0	MET	-	EXPRESSION TAG	UNP Q13188
H	-1	SER	-	EXPRESSION TAG	UNP Q13188
H	0	MET	-	EXPRESSION TAG	UNP Q13188
I	-1	SER	-	EXPRESSION TAG	UNP Q13188
I	0	MET	-	EXPRESSION TAG	UNP Q13188
J	434	SER	-	EXPRESSION TAG	UNP Q13188
J	435	MET	-	EXPRESSION TAG	UNP Q13188

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	84	Total O 84 84	0	0
2	B	78	Total O 78 78	0	0
2	C	85	Total O 85 85	0	0
2	D	105	Total O 105 105	0	0
2	E	84	Total O 84 84	0	0
2	F	86	Total O 86 86	0	0
2	G	72	Total O 72 72	0	0
2	H	58	Total O 58 58	0	0
2	I	80	Total O 80 80	0	0
2	J	67	Total O 67 67	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Serine/threonine-proteinkinase 3

Chain A: 



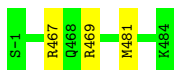
- Molecule 1: Serine/threonine-proteinkinase 3

Chain B: 



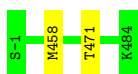
- Molecule 1: Serine/threonine-proteinkinase 3

Chain C: 



- Molecule 1: Serine/threonine-proteinkinase 3

Chain D: 



- Molecule 1: Serine/threonine-proteinkinase 3

Chain E: 



- Molecule 1: Serine/threonine-proteinkinase 3

Chain F: 



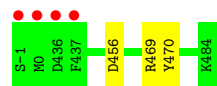
- Molecule 1: Serine/threonine-proteinkinase 3

Chain G: 



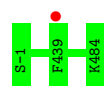
- Molecule 1: Serine/threonine-proteinkinase 3

Chain H: 



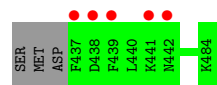
- Molecule 1: Serine/threonine-proteinkinase 3

Chain I: 



- Molecule 1: Serine/threonine-proteinkinase 3

Chain J: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	61.32Å 61.32Å 301.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.66 – 1.40 30.66 – 1.40	Depositor EDS
% Data completeness (in resolution range)	99.5 (30.66-1.40) 99.6 (30.66-1.40)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.84 (at 1.40Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.160 , 0.207 0.174 , 0.220	Depositor DCC
R_{free} test set	5733 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	16.7	Xtriage
Anisotropy	0.162	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 47.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	3 of 114370 reflections (0.003%)	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5292	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 27.58 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 2.1456e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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	0.89	0/485	0.93	1/641 (0.2%)
1	B	0.93	0/460	1.02	3/610 (0.5%)
1	C	0.92	0/448	0.94	1/594 (0.2%)
1	D	0.90	0/483	0.92	2/640 (0.3%)
1	E	0.93	0/493	0.87	0/653
1	F	0.84	0/444	0.81	0/591
1	G	0.83	0/513	0.91	1/682 (0.1%)
1	H	0.87	0/437	0.85	0/579
1	I	0.78	0/467	0.84	0/618
1	J	0.82	0/418	0.83	0/555
All	All	0.87	0/4648	0.90	8/6163 (0.1%)

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	458[A]	MET	CG-SD-CE	6.86	111.17	100.20
1	D	458[B]	MET	CG-SD-CE	6.86	111.17	100.20
1	B	481	MET	CG-SD-CE	-6.73	89.43	100.20
1	A	474	ARG	NE-CZ-NH1	-6.33	117.14	120.30
1	B	467[A]	ARG	NE-CZ-NH2	-6.00	117.30	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Close contacts

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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the

chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	463	0	0	2	0
1	B	447	0	0	1	0
1	C	438	0	0	2	0
1	D	461	0	0	1	0
1	E	468	0	0	1	0
1	F	434	0	0	3	0
1	G	492	0	0	6	0
1	H	430	0	0	4	0
1	I	451	0	0	0	0
1	J	409	0	0	0	0
2	A	84	0	0	2	0
2	B	78	0	0	0	0
2	C	85	0	0	2	0
2	D	105	0	0	1	0
2	E	84	0	0	1	0
2	F	86	0	0	0	0
2	G	72	0	0	2	0
2	H	58	0	0	3	0
2	I	80	0	0	0	0
2	J	67	0	0	0	0
All	All	5292	0	0	17	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 4.

The worst 5 of 17 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:469:ARG:NH1	2:C:569:HOH:O	2.31	0.63
2:E:577:HOH:O	1:F:458[A]:MET:SD	2.57	0.59
1:H:469:ARG:NH1	2:H:558:HOH:O	2.37	0.56
1:G:436[A]:ASP:C	1:G:438[A]:ASP:N	2.64	0.51
1:E:470:TYR:OH	1:F:462:GLU:OE2	2.29	0.50

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	55/51 (108%)	55 (100%)	0	0	100	100
1	B	52/51 (102%)	52 (100%)	0	0	100	100
1	C	51/51 (100%)	51 (100%)	0	0	100	100
1	D	55/51 (108%)	55 (100%)	0	0	100	100
1	E	55/51 (108%)	55 (100%)	0	0	100	100
1	F	51/51 (100%)	51 (100%)	0	0	100	100
1	G	59/51 (116%)	55 (93%)	4 (7%)	0	100	100
1	H	50/51 (98%)	50 (100%)	0	0	100	100
1	I	53/51 (104%)	53 (100%)	0	0	100	100
1	J	48/51 (94%)	48 (100%)	0	0	100	100
All	All	529/510 (104%)	525 (99%)	4 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	53/47 (113%)	53 (100%)	0	100	100
1	B	50/47 (106%)	50 (100%)	0	100	100
1	C	49/47 (104%)	49 (100%)	0	100	100
1	D	53/47 (113%)	53 (100%)	0	100	100
1	E	54/47 (115%)	54 (100%)	0	100	100
1	F	48/47 (102%)	48 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	52/47 (111%)	52 (100%)	0	100	100
1	H	47/47 (100%)	47 (100%)	0	100	100
1	I	51/47 (108%)	51 (100%)	0	100	100
1	J	43/47 (92%)	43 (100%)	0	100	100
All	All	500/470 (106%)	500 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	A	51/51 (100%)	-0.28	0 100 100	12, 19, 25, 30	0
1	B	51/51 (100%)	-0.13	2 (3%) 37 39	12, 19, 32, 40	0
1	C	51/51 (100%)	-0.13	0 100 100	12, 18, 25, 30	0
1	D	51/51 (100%)	-0.18	0 100 100	11, 15, 24, 34	0
1	E	51/51 (100%)	-0.29	0 100 100	14, 20, 25, 31	0
1	F	51/51 (100%)	0.14	3 (5%) 22 21	13, 18, 33, 55	0
1	G	51/51 (100%)	0.09	5 (9%) 8 8	16, 22, 34, 40	0
1	H	51/51 (100%)	0.08	4 (7%) 13 12	13, 20, 42, 61	0
1	I	51/51 (100%)	-0.16	1 (1%) 62 66	13, 18, 30, 32	0
1	J	48/51 (94%)	0.45	5 (10%) 7 6	18, 25, 40, 54	0
All	All	507/510 (99%)	-0.05	20 (3%) 37 39	11, 19, 33, 61	0

The worst 5 of 20 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	437	PHE	6.2
1	J	438	ASP	5.7
1	J	442	ASN	5.6
1	J	439	PHE	5.5
1	G	442	ASN	3.7

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.