



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 03:17 PM GMT

PDB ID : 1FC3
Title : THE CRYSTAL STRUCTURE OF TRANS-ACTIVATION DOMAIN OF
THE SPORULATION RESPONSE REGULATOR, SPO0A
Authors : Lewis, R.J.; Krzywda, S.; Wilkinson, A.J.
Deposited on : 2000-07-17
Resolution : 2.00 Å(reported)

This is a full wwPDB validation 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>

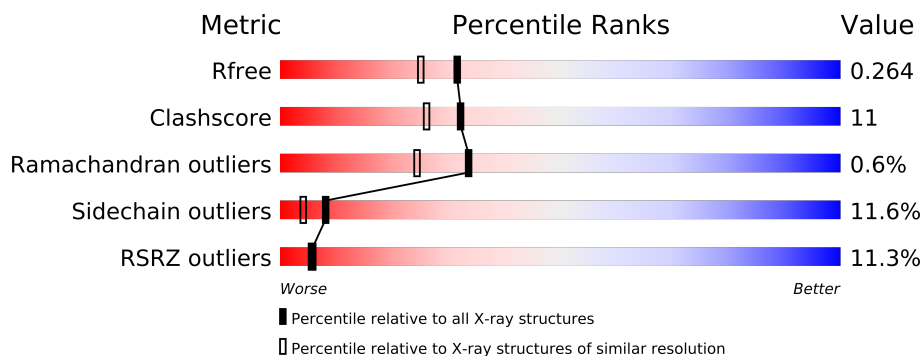
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.00 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	4888 (2.00-2.00)
Clashscore	79885	6188 (2.00-2.00)
Ramachandran outliers	78287	6102 (2.00-2.00)
Sidechain outliers	78261	6100 (2.00-2.00)
RSRZ outliers	66119	4890 (2.00-2.00)

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	120	
1	B	120	
1	C	120	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2983 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 SPO0A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	119	Total	C	N	O	S	31	3	0
			940	602	163	173	2			
1	B	101	Total	C	N	O	S	29	2	0
			804	516	141	144	3			
1	C	116	Total	C	N	O	S	34	4	0
			920	587	157	174	2			

- Molecule 2 is water.

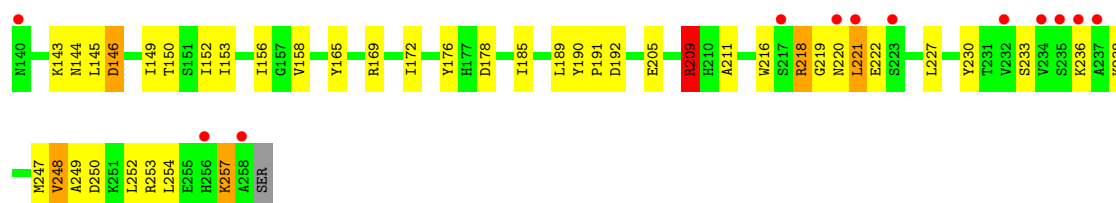
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	92	Total	O	0	0
			92	92		
2	B	95	Total	O	0	0
			95	95		
2	C	132	Total	O	0	0
			132	132		

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.

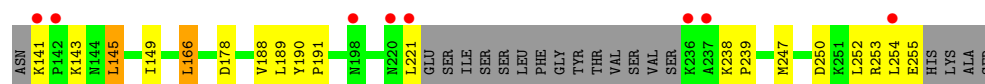
• Molecule 1: SPO0A

Chain A: 



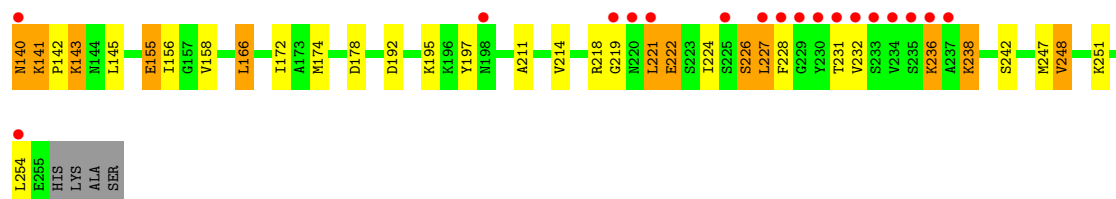
• Molecule 1: SPO0A

Chain B: 



• Molecule 1: SPO0A

Chain C: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	43.12Å 53.41Å 53.72Å 90.82° 111.73° 111.32°	Depositor
Resolution (Å)	20.00 – 2.00 19.42 – 1.99	Depositor EDS
% Data completeness (in resolution range)	87.6 (20.00-2.00) 87.6 (19.42-1.99)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.25 (at 1.99Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.196 , 0.258 0.216 , 0.264	Depositor DCC
R_{free} test set	1235 reflections (5.05%)	DCC
Wilson B-factor (Å ²)	28.4	Xtriage
Anisotropy	0.548	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 61.2	EDS
Estimated twinning fraction	0.020 for -h,-l,-k	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 24464 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2983	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.76% of the height of the origin peak. No significant pseudotranslation is detected.*

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	0.92	2/973 (0.2%)	1.16	12/1316 (0.9%)
1	B	0.84	1/828 (0.1%)	0.97	4/1117 (0.4%)
1	C	0.99	4/957 (0.4%)	1.07	5/1295 (0.4%)
All	All	0.92	7/2758 (0.3%)	1.07	21/3728 (0.6%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	195	LYS	CD-CE	11.00	1.78	1.51
1	C	222	GLU	CA-CB	-9.36	1.33	1.53
1	A	236	LYS	CB-CG	8.50	1.75	1.52
1	C	143	LYS	CD-CE	6.47	1.67	1.51
1	C	232	VAL	CA-CB	5.37	1.66	1.54
1	B	255	GLU	CA-CB	5.30	1.65	1.53
1	A	247	MET	CG-SD	5.26	1.94	1.81

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	209	ARG	NE-CZ-NH2	-13.67	113.47	120.30
1	A	209	ARG	NE-CZ-NH1	9.85	125.22	120.30
1	C	178	ASP	CB-CG-OD2	6.89	124.50	118.30
1	A	236	LYS	CA-CB-CG	-6.52	99.05	113.40
1	A	250	ASP	CB-CG-OD2	6.51	124.16	118.30
1	A	219	GLY	O-C-N	5.75	131.89	122.70
1	A	209	ARG	CG-CD-NE	-5.73	99.76	111.80
1	B	250	ASP	CB-CG-OD2	5.70	123.43	118.30
1	C	222	GLU	CB-CA-C	5.61	121.62	110.40
1	C	219	GLY	N-CA-C	-5.60	99.11	113.10
1	B	166	LEU	CB-CG-CD2	5.55	120.44	111.00
1	C	222	GLU	N-CA-CB	-5.49	100.71	110.60
1	A	248	VAL	CG1-CB-CG2	5.47	119.65	110.90
1	A	218	ARG	CD-NE-CZ	-5.33	116.13	123.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	178	ASP	CB-CG-OD2	5.32	123.09	118.30
1	A	178	ASP	CB-CG-OD2	5.27	123.05	118.30
1	C	174	MET	CG-SD-CE	-5.20	91.88	100.20
1	A	146	ASP	CB-CG-OD1	5.19	122.97	118.30
1	B	255	GLU	N-CA-CB	-5.15	101.33	110.60
1	A	218	ARG	CA-CB-CG	-5.09	102.19	113.40
1	A	192	ASP	CB-CG-OD2	5.05	122.84	118.30

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	940	0	975	28	0
1	B	804	0	841	7	1
1	C	920	0	945	25	1
2	A	92	0	0	1	1
2	B	95	0	0	0	1
2	C	132	0	0	1	0
All	All	2983	0	2761	59	2

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 11.

All (59) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:152[B]:ILE:HD11	1:A:227:LEU:HD22	1.52	0.92
1:A:176:TYR:HA	1:A:253:ARG:HH21	1.34	0.92
1:A:221:LEU:O	1:A:221:LEU:HD12	1.75	0.86
1:C:140:ASN:N	1:C:140:ASN:HD22	1.76	0.84
1:C:227:LEU:CD1	1:C:251:LYS:HE2	2.07	0.84
1:C:227:LEU:HD11	1:C:251:LYS:HE2	1.60	0.82
1:A:152[A]:ILE:HD12	1:A:252:LEU:HD21	1.63	0.80

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:152[A]:ILE:CD1	1:A:252:LEU:HD21	2.19	0.72
1:C:140:ASN:ND2	1:C:140:ASN:N	2.33	0.71
1:A:221:LEU:O	1:A:221:LEU:CD1	2.40	0.69
1:C:224:ILE:O	1:C:224:ILE:HG22	1.95	0.67
1:C:238:LYS:HD2	2:C:312:HOH:O	1.94	0.66
1:B:149:ILE:HG12	1:B:252:LEU:HD11	1.78	0.65
1:A:152[B]:ILE:CD1	1:A:227:LEU:HD22	2.25	0.61
1:C:156:ILE:HD11	1:C:228:PHE:HE2	1.66	0.60
1:A:221:LEU:CG	1:A:221:LEU:O	2.49	0.60
1:C:224:ILE:CG2	1:C:224:ILE:O	2.50	0.59
1:A:221:LEU:HD12	1:A:233:SER:OG	2.02	0.58
1:C:141:LYS:N	1:C:142:PRO:CD	2.67	0.58
1:A:205:GLU:OE1	1:A:209:ARG:HD3	2.04	0.57
1:A:257:LYS:HE3	2:A:281:HOH:O	2.03	0.57
1:A:176:TYR:HA	1:A:253:ARG:NH2	2.12	0.57
1:C:172:ILE:HG21	1:C:248:VAL:HG22	1.85	0.57
1:C:227:LEU:HD12	1:C:251:LYS:HE2	1.83	0.57
1:C:156:ILE:HD11	1:C:228:PHE:CE2	2.40	0.56
1:A:209:ARG:NH2	1:C:192:ASP:OD2	2.37	0.56
1:A:249:ALA:HB1	1:A:253:ARG:HH22	1.72	0.55
1:C:214:VAL:O	1:C:218:ARG:HG3	2.07	0.55
1:A:230:TYR:O	1:A:233:SER:HB3	2.10	0.52
1:C:141:LYS:N	1:C:142:PRO:HD3	2.25	0.51
1:A:249:ALA:HB1	1:A:253:ARG:NH2	2.25	0.51
1:C:166:LEU:HD11	1:C:197:TYR:CZ	2.45	0.51
1:A:150:THR:HG23	1:A:165:TYR:OH	2.11	0.50
1:C:221:LEU:O	1:C:221:LEU:HD12	2.12	0.50
1:A:146:ASP:OD2	1:A:169:ARG:NH2	2.31	0.49
1:A:149:ILE:O	1:A:152[B]:ILE:HG22	2.13	0.49
1:B:145:LEU:HD21	1:B:252:LEU:HD13	1.95	0.48
1:A:190:TYR:HB2	1:A:191:PRO:HD3	1.95	0.47
1:C:155[A]:GLU:HG2	1:C:227:LEU:CD2	2.45	0.47
1:C:227:LEU:HD12	1:C:251:LYS:CE	2.46	0.46
1:C:158:VAL:HG13	1:C:211:ALA:HB1	1.97	0.46
1:A:189:LEU:C	1:A:189:LEU:HD23	2.36	0.46
1:A:158:VAL:HG13	1:A:211:ALA:HB1	1.99	0.45
1:C:156:ILE:CD1	1:C:228:PHE:HE2	2.30	0.44
1:A:221:LEU:HG	1:A:221:LEU:O	2.15	0.43
1:A:172:ILE:HG21	1:A:248:VAL:HG22	2.00	0.43
1:A:152[B]:ILE:HG23	1:A:153:ILE:N	2.34	0.43
1:C:238:LYS:O	1:C:238:LYS:HG2	2.18	0.43
1:C:166:LEU:HD11	1:C:197:TYR:CE2	2.53	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:141:LYS:H	1:C:142:PRO:HD3	1.84	0.42
1:C:226:SER:O	1:C:226:SER:OG	2.39	0.41
1:B:190:TYR:N	1:B:191:PRO:CD	2.83	0.41
1:A:144:ASN:HA	1:A:144:ASN:HD22	1.62	0.41
1:B:188:VAL:C	1:B:191:PRO:HD2	2.41	0.41
1:A:185:ILE:HD13	1:A:185:ILE:HG21	1.85	0.40
1:B:190:TYR:HB2	1:B:191:PRO:HD3	2.02	0.40
1:B:238:LYS:HG3	1:B:239:PRO:HD2	2.04	0.40
1:B:189:LEU:HD23	1:B:189:LEU:C	2.41	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:343:HOH:O	2:B:349:HOH:O[1_455]	0.11	2.09
1:B:254:LEU:O	1:C:236:LYS:CB[1_766]	2.17	0.03

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	120/120 (100%)	114 (95%)	5 (4%)	1 (1%)	27	17
1	B	99/120 (82%)	95 (96%)	4 (4%)	0	100	100
1	C	118/120 (98%)	110 (93%)	7 (6%)	1 (1%)	27	17
All	All	337/360 (94%)	319 (95%)	16 (5%)	2 (1%)	33	24

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	254	LEU
1	A	220	ASN

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	104/102 (102%)	94 (90%)	10 (10%)	12	6
1	B	87/102 (85%)	79 (91%)	8 (9%)	13	7
1	C	103/102 (101%)	85 (82%)	18 (18%)	3	1
All	All	294/306 (96%)	258 (88%)	36 (12%)	8	4

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	143	LYS
1	A	145	LEU
1	A	209	ARG
1	A	216	TRP
1	A	218	ARG
1	A	221	LEU
1	A	222	GLU
1	A	238	LYS
1	A	254	LEU
1	A	257	LYS
1	B	141	LYS
1	B	143	LYS
1	B	145	LEU
1	B	166	LEU
1	B	221	LEU
1	B	247[A]	MET
1	B	247[B]	MET
1	B	253	ARG
1	C	140	ASN
1	C	141	LYS
1	C	143	LYS
1	C	145	LEU
1	C	155[A]	GLU
1	C	155[B]	GLU
1	C	166	LEU
1	C	221	LEU
1	C	222	GLU

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Mol	Chain	Res	Type
1	C	226	SER
1	C	227	LEU
1	C	231	THR
1	C	236	LYS
1	C	238	LYS
1	C	242[A]	SER
1	C	242[B]	SER
1	C	247	MET
1	C	248	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	140	ASN
1	A	144	ASN

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	118/120 (98%)	0.34	12 (10%) 7 7	23, 28, 42, 60	6 (5%)
1	B	101/120 (84%)	0.28	8 (7%) 13 12	25, 28, 44, 49	7 (6%)
1	C	116/120 (96%)	0.59	18 (15%) 3 3	22, 28, 52, 53	10 (8%)
All	All	335/360 (93%)	0.41	38 (11%) 6 5	22, 28, 51, 60	23 (6%)

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	232	VAL	6.7
1	A	217	SER	5.7
1	C	230	TYR	5.3
1	B	142	PRO	5.2
1	C	229	GLY	5.1
1	C	235	SER	4.8
1	C	237	ALA	4.8
1	A	235	SER	4.7
1	C	233	SER	4.7
1	B	220	ASN	4.6
1	C	140	ASN	4.5
1	B	221	LEU	4.5
1	C	220	ASN	4.2
1	C	254	LEU	4.1
1	A	237	ALA	4.0
1	C	231	THR	3.9
1	C	236	LYS	3.8
1	B	236	LYS	3.7
1	C	225	SER	3.7
1	A	234	VAL	3.7
1	B	254	LEU	3.6
1	C	219	GLY	3.6
1	A	140	ASN	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	236	LYS	3.3
1	B	198	ASN	2.9
1	A	223	SER	2.9
1	C	221	LEU	2.7
1	B	141	LYS	2.7
1	C	228	PHE	2.7
1	A	258	ALA	2.6
1	B	237	ALA	2.4
1	A	232	VAL	2.4
1	A	256	HIS	2.4
1	A	221	LEU	2.3
1	C	198	ASN	2.2
1	C	234	VAL	2.2
1	C	227	LEU	2.1
1	A	220	ASN	2.1

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.