



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 30, 2020 – 12:51 PM BST

PDB ID : 3N70
Title : The Crystal Structure of the P-loop NTPase domain of the Sigma-54 transport activator from E. coli to 2.8Å
Authors : Stein, A.J.; Mulligan, R.; Volkart, L.; Freeman, L.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)
Deposited on : 2010-05-26
Resolution : 2.80 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13
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) : 2.13

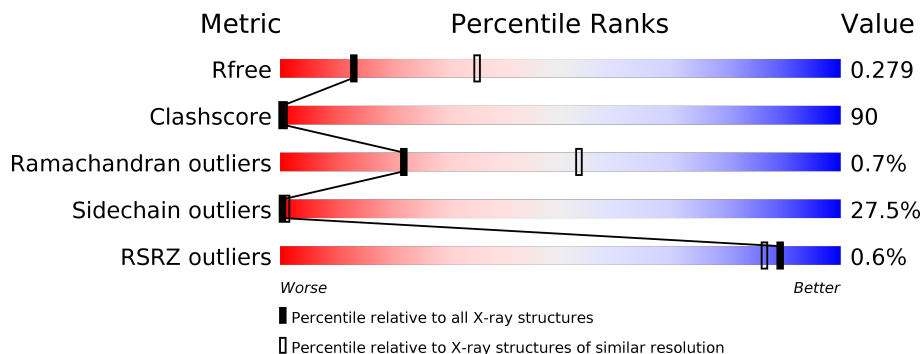
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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 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	145	
1	B	145	
1	C	145	
1	D	145	
1	E	145	
1	F	145	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	G	145	
1	H	145	

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	SO4	C	2	-	-	X	-
2	SO4	D	4	-	-	X	-
2	SO4	F	7	-	-	X	-
2	SO4	G	6	-	-	X	-
2	SO4	H	8	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7146 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 Transport activator.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	N	O	S				Se
1	A	142	Total 1060	C 672	N 190	O 195	S 2	Se 1	0	0	0
1	B	108	Total 734	C 464	N 129	O 138	S 1	Se 2	0	0	0
1	C	132	Total 959	C 615	N 169	O 171	S 2	Se 2	0	0	0
1	D	116	Total 833	C 535	N 149	O 148	S 1	Se 1	0	0	0
1	E	137	Total 1026	C 659	N 183	O 180	S 2	Se 2	0	0	0
1	F	105	Total 719	C 455	N 128	O 133	S 2	Se 1	0	0	0
1	G	128	Total 936	C 591	N 170	O 171	S 2	Se 2	0	0	0
1	H	122	Total 834	C 526	N 154	O 152	S 1	Se 1	0	0	0

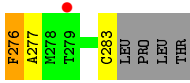
- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



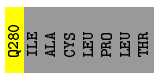
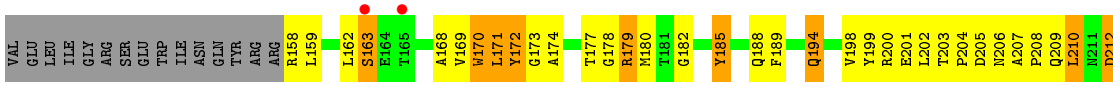
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	F	1	Total	O	S	0	0
			5	4	1		
2	G	1	Total	O	S	0	0
			5	4	1		
2	H	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is water.

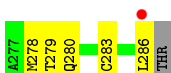
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total	O	0	0
			3	3		
3	E	2	Total	O	0	0
			2	2		



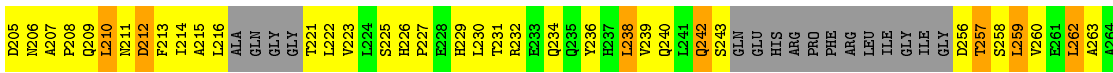
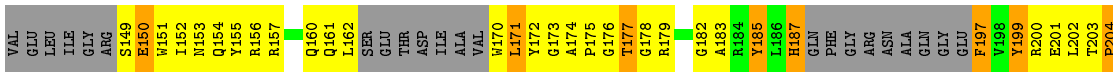
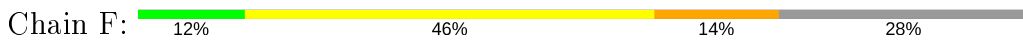
• Molecule 1: Transport activator



• Molecule 1: Transport activator



• Molecule 1: Transport activator



• Molecule 1: Transport activator



4 Data and refinement statistics

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α , β , γ	77.61Å 77.61Å 215.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.88 – 2.80 48.88 – 2.80	Depositor EDS
% Data completeness (in resolution range)	92.3 (48.88-2.80) 99.9 (48.88-2.80)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.25 (at 2.81Å)	Xtriage
Refinement program	PHENIX 1.5_2	Depositor
R, R_{free}	0.229 , 0.280 0.261 , 0.279	Depositor DCC
R_{free} test set	1574 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	67.2	Xtriage
Anisotropy	0.015	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 71.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.467 for h,-k,-l	Xtriage
Reported twinning fraction	0.496 for h,-k,-l	Depositor
Outliers	0 of 31209 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	7146	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.02% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	0.50	0/1082	0.58	1/1474 (0.1%)
1	B	0.55	0/744	0.55	0/1014
1	C	0.47	0/978	0.57	0/1331
1	D	0.39	0/850	0.49	0/1158
1	E	0.47	0/1048	0.50	0/1426
1	F	0.55	0/731	0.54	0/998
1	G	0.49	0/953	0.49	0/1294
1	H	0.49	0/850	0.55	0/1162
All	All	0.49	0/7236	0.53	1/9857 (0.0%)

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	H	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	238	LEU	CA-CB-CG	-5.17	103.41	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	H	250	ARG	Sidechain

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	1060	0	975	124	1
1	B	734	0	611	166	0
1	C	959	0	861	161	4
1	D	833	0	740	152	3
1	E	1026	0	936	165	2
1	F	719	0	575	213	0
1	G	936	0	843	161	2
1	H	834	0	710	129	0
2	A	5	0	0	1	0
2	B	5	0	0	0	0
2	C	5	0	0	2	0
2	D	5	0	0	2	0
2	E	5	0	0	0	0
2	F	5	0	0	4	0
2	G	5	0	0	3	0
2	H	5	0	0	3	0
3	A	3	0	0	0	0
3	E	2	0	0	0	0
All	All	7146	0	6251	1203	6

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 90.

The worst 5 of 1203 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:F:199:TYR:HB2	1:F:223:VAL:CG1	1.31	1.55
1:F:187:HIS:CD2	1:F:197:PHE:HB2	1.54	1.42
1:F:278:MSE:HE1	1:G:263:ALA:CB	1.47	1.42
1:A:204:PRO:HD2	1:B:267:HIS:ND1	1.38	1.38
1:C:195:GLY:HA3	1:C:219:GLY:C	1.42	1.36

The worst 5 of 6 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	Interatomic distance (Å)	Clash overlap (Å)
1:C:196:GLU:OE1	1:D:200:ARG:NH2[3_554]	0.86	1.34
1:A:160:GLN:NE2	1:C:164:GLU:OE2[4_555]	1.51	0.69
1:C:196:GLU:CD	1:D:200:ARG:NH2[3_554]	1.92	0.28
1:E:185:TYR:OH	1:G:160:GLN:CG[3_544]	1.95	0.25
1:C:196:GLU:OE1	1:D:200:ARG:CZ[3_554]	2.06	0.14

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	140/145 (97%)	134 (96%)	6 (4%)	0	100	100
1	B	98/145 (68%)	92 (94%)	5 (5%)	1 (1%)	15	44
1	C	128/145 (88%)	121 (94%)	6 (5%)	1 (1%)	19	49
1	D	112/145 (77%)	109 (97%)	2 (2%)	1 (1%)	17	46
1	E	131/145 (90%)	123 (94%)	6 (5%)	2 (2%)	10	33
1	F	95/145 (66%)	90 (95%)	3 (3%)	2 (2%)	7	23
1	G	124/145 (86%)	123 (99%)	1 (1%)	0	100	100
1	H	120/145 (83%)	118 (98%)	2 (2%)	0	100	100
All	All	948/1160 (82%)	910 (96%)	31 (3%)	7 (1%)	22	53

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	265	SER
1	E	273	TYR
1	F	177	THR
1	B	175	PRO
1	E	270	ALA

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	98/120 (82%)	67 (68%)	31 (32%)	0	0
1	B	57/120 (48%)	39 (68%)	18 (32%)	0	0
1	C	83/120 (69%)	67 (81%)	16 (19%)	1	4
1	D	70/120 (58%)	50 (71%)	20 (29%)	0	1
1	E	92/120 (77%)	65 (71%)	27 (29%)	0	1
1	F	55/120 (46%)	35 (64%)	20 (36%)	0	0
1	G	83/120 (69%)	69 (83%)	14 (17%)	2	6
1	H	65/120 (54%)	45 (69%)	20 (31%)	0	0
All	All	603/960 (63%)	437 (72%)	166 (28%)	0	1

5 of 166 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	214	ILE
1	E	201	GLU
1	H	203	THR
1	D	237	HIS
1	D	279	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	244	GLN
1	D	235	GLN
1	G	280	GLN
1	D	192	ASN
1	D	194	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](#)

8 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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	SO4	E	5	-	4,4,4	0.23	0	6,6,6	0.40	0
2	SO4	F	7	-	4,4,4	0.14	0	6,6,6	0.26	0
2	SO4	A	1	-	4,4,4	0.13	0	6,6,6	0.25	0
2	SO4	D	4	-	4,4,4	0.10	0	6,6,6	0.32	0
2	SO4	C	2	-	4,4,4	0.14	0	6,6,6	0.15	0
2	SO4	G	6	-	4,4,4	0.15	0	6,6,6	0.09	0
2	SO4	B	3	-	4,4,4	0.19	0	6,6,6	0.16	0
2	SO4	H	8	-	4,4,4	0.10	0	6,6,6	0.15	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	7	SO4	4	0
2	A	1	SO4	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	4	SO4	2	0
2	C	2	SO4	2	0
2	G	6	SO4	3	0
2	H	8	SO4	3	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, 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	140/145 (96%)	-0.07	1 (0%) 87 84	49, 59, 68, 76	0
1	B	106/145 (73%)	-0.36	1 (0%) 84 80	55, 68, 75, 78	0
1	C	130/145 (89%)	-0.13	1 (0%) 86 81	52, 65, 84, 89	0
1	D	114/145 (78%)	-0.04	2 (1%) 68 61	56, 66, 86, 95	0
1	E	135/145 (93%)	-0.18	1 (0%) 87 84	45, 59, 72, 83	0
1	F	103/145 (71%)	-0.30	0 100 100	60, 69, 99, 106	0
1	G	126/145 (86%)	-0.15	0 100 100	50, 60, 77, 86	0
1	H	121/145 (83%)	-0.18	0 100 100	52, 63, 83, 89	0
All	All	975/1160 (84%)	-0.17	6 (0%) 89 86	45, 64, 83, 106	0

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	220	GLY	2.5
1	D	165	THR	2.3
1	E	286	LEU	2.3
1	C	279	THR	2.1
1	D	163	SER	2.1

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](#)

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, 95th 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	B-factors(Å ²)	Q<0.9
2	SO4	F	7	5/5	0.90	0.12	83,86,92,95	0
2	SO4	D	4	5/5	0.94	0.12	70,73,75,77	0
2	SO4	H	8	5/5	0.94	0.14	81,82,87,87	0
2	SO4	G	6	5/5	0.95	0.17	62,62,64,67	0
2	SO4	C	2	5/5	0.97	0.12	80,80,83,86	0
2	SO4	B	3	5/5	0.98	0.13	71,73,77,78	0
2	SO4	A	1	5/5	0.99	0.12	56,57,60,61	0
2	SO4	E	5	5/5	0.99	0.11	45,45,48,49	0

6.5 Other polymers [i](#)

There are no such residues in this entry.