



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 15, 2023 – 09:59 AM EDT

PDB ID : 8DN7
Title : The crystal structure of the Pisum sativum Toc75 POTRA domains in complex with fab ax9
Authors : Srinivasan, K.; Noinaj, N.
Deposited on : 2022-07-10
Resolution : 2.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 : 2.36
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) : 2.36

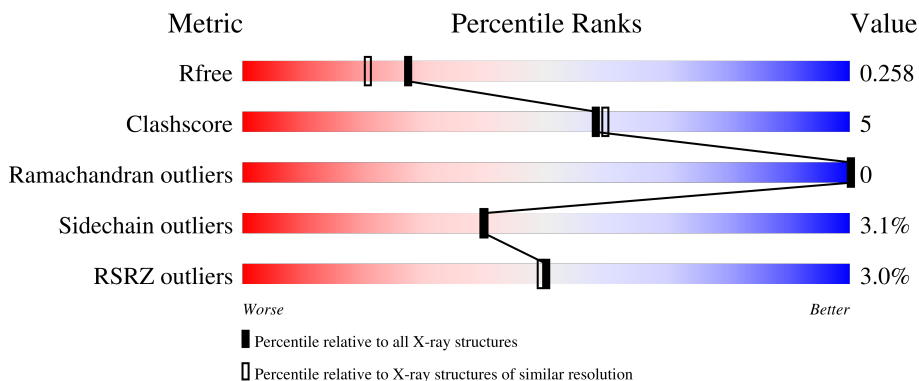
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (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 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	C	313	
1	E	313	
2	A	245	
2	D	245	
3	B	217	

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Mol	Chain	Length	Quality of chain
3	H	217	 <p>5% 86% 12% ..</p>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 8891 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 Protein TOC75, chloroplastic.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	E	112	902	560	170	164	8	0	0	0
1	C	118	962	594	179	181	8	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	0	GLY	-	expression tag	UNP Q43715
E	1	ALA	-	expression tag	UNP Q43715
E	2	MET	-	expression tag	UNP Q43715
E	3	GLY	-	expression tag	UNP Q43715
C	0	GLY	-	expression tag	UNP Q43715
C	1	ALA	-	expression tag	UNP Q43715
C	2	MET	-	expression tag	UNP Q43715
C	3	GLY	-	expression tag	UNP Q43715

- Molecule 2 is a protein called fabax9 Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	D	224	1688	1073	274	335	6	0	1	0
2	A	223	1671	1062	270	334	5	0	0	0

- Molecule 3 is a protein called fabax9 Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	B	214	1618	1012	269	332	5	0	2	0
3	H	215	1628	1017	272	333	6	0	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	30	Total 30	O 30	0	0
4	C	57	Total 57	O 57	0	0
4	D	83	Total 83	O 83	0	0
4	A	102	Total 102	O 102	0	0
4	B	79	Total 79	O 79	0	0
4	H	71	Total 71	O 71	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	43.21Å 43.43Å 169.61Å 94.20° 94.21° 104.44°	Depositor
Resolution (Å)	41.66 – 2.00 41.66 – 2.00	Depositor EDS
% Data completeness (in resolution range)	85.5 (41.66-2.00) 85.4 (41.66-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.20 (at 2.00Å)	Xtrriage
Refinement program	PHENIX 1.20_4459	Depositor
R, R_{free}	0.211 , 0.259 0.210 , 0.258	Depositor DCC
R_{free} test set	1953 reflections (2.83%)	wwPDB-VP
Wilson B-factor (Å ²)	31.7	Xtrriage
Anisotropy	0.292	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 46.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	0.059 for k,h,-h-k-l 0.047 for -k,-h,-l 0.018 for -h,-k,h+k+l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8891	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.07% 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	C	0.28	0/976	0.54	0/1308
1	E	0.27	0/915	0.57	0/1226
2	A	0.28	0/1717	0.55	0/2347
2	D	0.27	0/1737	0.55	0/2370
3	B	0.27	0/1659	0.53	0/2261
3	H	0.27	0/1663	0.54	0/2262
All	All	0.27	0/8667	0.54	0/11774

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	C	962	0	954	15	0
1	E	902	0	886	18	0
2	A	1671	0	1570	10	1
2	D	1688	0	1609	13	0
3	B	1618	0	1547	17	1
3	H	1628	0	1566	17	0
4	A	102	0	0	1	0
4	B	79	0	0	2	0
4	C	57	0	0	2	0
4	D	83	0	0	0	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	E	30	0	0	1	1
4	H	71	0	0	0	0
All	All	8891	0	8132	80	2

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 5.

All (80) 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)
3:H:192:HIS:O	3:H:214:ARG:NH1	2.14	0.81
1:C:184:SER:OG	4:C:401:HOH:O	2.01	0.79
1:C:139:GLU:OE2	2:A:101:ARG:NH2	2.24	0.71
3:B:31:SER:O	3:B:67:ARG:NH1	2.29	0.65
2:D:43:ALA:HB3	2:D:46:LYS:HD3	1.81	0.63
1:E:123:GLY:HA2	1:E:225:VAL:HG12	1.79	0.63
2:D:204:SER:HA	2:D:207:THR:HG22	1.79	0.62
3:H:4:GLN:HB2	3:H:27:SER:HB2	1.81	0.62
1:E:182:ARG:NH1	2:D:61:THR:H	2.01	0.59
1:C:139:GLU:CD	2:A:101:ARG:HH22	2.07	0.58
3:H:125:ASP:N	3:H:125:ASP:OD1	2.37	0.56
1:E:113:ARG:HD3	1:E:183:VAL:HG13	1.88	0.56
1:E:113:ARG:O	1:E:113:ARG:NH1	2.39	0.56
2:D:135:PRO:HB3	2:D:161:TYR:HB3	1.87	0.56
1:E:125:MET:HA	1:E:156:ARG:HH22	1.71	0.56
1:C:198:TRP:CZ2	1:C:202:GLU:HG3	2.40	0.55
3:H:152:LYS:HD3	3:H:155:ASN:HA	1.89	0.55
1:C:123:GLY:HA2	1:C:225:VAL:HG12	1.89	0.54
2:D:142:PRO:HG2	2:D:229:PRO:HG3	1.89	0.53
3:H:146:GLU:N	3:H:146:GLU:OE1	2.41	0.53
3:B:38:GLN:CB	3:B:48:LEU:HD21	2.39	0.53
1:C:147:ARG:HD3	1:C:151:ARG:CZ	2.40	0.52
3:B:111:ARG:HG2	3:B:112:THR:H	1.75	0.52
3:B:84:PHE:HB3	3:B:109:ILE:HD12	1.92	0.51
2:A:162:PHE:HB2	2:A:191:LEU:HD22	1.93	0.51
1:E:116:ARG:HH11	1:E:117:PHE:H	1.58	0.51
3:B:145:ARG:NH2	4:B:308:HOH:O	2.42	0.51
3:H:28:GLN:O	3:H:29:SER:OG	2.22	0.51
1:E:182:ARG:HH12	2:D:61:THR:H	1.59	0.50
1:E:116:ARG:NH1	1:E:117:PHE:H	2.09	0.50
1:E:177:LEU:HD23	1:E:187:LEU:HD21	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:184:ALA:HA	2:D:194:LEU:HB3	1.95	0.49
3:B:111:ARG:HG2	3:B:112:THR:N	2.28	0.49
2:A:135:PRO:HB3	2:A:161:TYR:HB3	1.94	0.48
1:C:127:GLN:HG2	1:C:156:ARG:HH22	1.78	0.48
1:C:169:VAL:O	1:C:173:ILE:HG12	2.14	0.48
3:B:166:VAL:HG22	3:B:178:LEU:HD12	1.96	0.48
1:E:209:VAL:HG22	1:E:224:VAL:HG12	1.95	0.47
3:H:38:GLN:HB2	3:H:48:LEU:HD11	1.95	0.47
3:B:8:SER:OG	3:B:23:THR:OG1	2.31	0.47
1:C:198:TRP:CH2	1:C:202:GLU:HG3	2.50	0.47
3:B:84:PHE:HB3	3:B:109:ILE:CD1	2.43	0.47
2:A:31:ASN:HB2	2:A:33:TYR:CE1	2.50	0.47
3:B:38:GLN:HB3	3:B:48:LEU:HD21	1.96	0.47
1:E:142:LYS:HE2	2:D:114:TRP:CD1	2.50	0.47
1:E:212:PHE:HB2	2:D:108:PHE:HB2	1.96	0.46
1:E:125:MET:HA	1:E:156:ARG:NH2	2.30	0.46
3:H:111:ARG:HD3	3:H:112:THR:O	2.14	0.46
3:B:80:GLN:HG3	3:B:81:PRO:HD2	1.98	0.46
2:A:164:GLU:OE2	2:A:184:ALA:HB3	2.15	0.46
1:C:192:ARG:HG3	1:C:209:VAL:HB	1.98	0.45
3:B:25:ARG:NH1	4:B:313:HOH:O	2.48	0.45
1:C:177:LEU:HD23	1:C:187:LEU:HD21	1.99	0.45
2:D:138:PHE:HB3	3:H:124:SER:OG	2.17	0.45
1:E:183:VAL:HG22	3:H:96:TRP:CZ2	2.53	0.44
2:D:159:LYS:HE3	2:D:187:GLN:OE1	2.18	0.43
3:B:127:GLN:HG2	3:B:132:THR:O	2.18	0.43
2:A:79:LYS:O	2:A:81:THR:HG23	2.18	0.43
2:A:184:ALA:HA	2:A:194:LEU:HB3	2.00	0.43
1:C:166:PRO:HD3	1:C:198:TRP:CZ2	2.53	0.43
2:A:80:ASN:ND2	4:A:303:HOH:O	2.51	0.43
2:D:86:MET:HB3	2:D:89:LEU:HD21	2.00	0.43
3:B:26:ALA:O	3:B:70:THR:OG1	2.35	0.43
1:E:166:PRO:HD3	1:E:198:TRP:CZ2	2.54	0.42
3:B:185:SER:OG	3:B:188:ASP:OD2	2.34	0.42
3:H:150:GLN:HG2	3:H:157:LEU:HD22	2.02	0.42
3:H:60:PRO:HG2	3:H:63:PHE:CE2	2.55	0.41
3:H:123:PRO:HD3	3:H:135:VAL:HG22	2.02	0.41
1:E:183:VAL:HG22	3:H:96:TRP:HZ2	1.85	0.41
1:C:114:ALA:N	4:C:417:HOH:O	2.52	0.41
2:D:38:HIS:CE1	3:H:99:ILE:HD12	2.55	0.41
2:A:86:MET:HB3	2:A:89:LEU:HD21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:151:ARG:HA	1:E:155:ARG:HH21	1.86	0.41
3:B:70:THR:OG1	3:B:70:THR:O	2.40	0.41
3:H:129:LYS:H	3:H:129:LYS:HG3	1.41	0.40
1:E:192:ARG:NH1	4:E:407:HOH:O	2.52	0.40
1:C:173:ILE:HD12	1:C:191:ILE:HG23	2.02	0.40
3:H:108:GLU:HG2	3:H:109:ILE:N	2.36	0.40
1:C:124:LEU:HB2	1:C:161:ARG:HD2	2.03	0.40
3:B:148:LYS:HB2	3:B:148:LYS:HE3	1.83	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	Interatomic distance (Å)	Clash overlap (Å)
2:A:131:SER:OG	3:B:71:ASP:OD2[1_445]	2.15	0.05
4:E:416:HOH:O	4:D:331:HOH:O[1_565]	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	C	116/313 (37%)	113 (97%)	3 (3%)	0	100	100
1	E	108/313 (34%)	106 (98%)	2 (2%)	0	100	100
2	A	219/245 (89%)	216 (99%)	3 (1%)	0	100	100
2	D	221/245 (90%)	219 (99%)	2 (1%)	0	100	100
3	B	214/217 (99%)	204 (95%)	10 (5%)	0	100	100
3	H	213/217 (98%)	202 (95%)	11 (5%)	0	100	100
All	All	1091/1550 (70%)	1060 (97%)	31 (3%)	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	C	106/276 (38%)	102 (96%)	4 (4%)	33	31
1	E	96/276 (35%)	89 (93%)	7 (7%)	14	9
2	A	181/208 (87%)	177 (98%)	4 (2%)	52	55
2	D	186/208 (89%)	182 (98%)	4 (2%)	52	55
3	B	184/192 (96%)	181 (98%)	3 (2%)	62	67
3	H	186/192 (97%)	179 (96%)	7 (4%)	33	31
All	All	939/1352 (70%)	910 (97%)	29 (3%)	40	40

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	113	ARG
1	E	116	ARG
1	E	122	VAL
1	E	124	LEU
1	E	155	ARG
1	E	170	HIS
1	E	183	VAL
1	C	124	LEU
1	C	127	GLN
1	C	132	GLU
1	C	214	ASN
2	D	23	LEU
2	D	213	ASN
2	D	219	SER
2	D	220	ASN
2	A	80	ASN
2	A	101	ARG
2	A	213	ASN
2	A	220	ASN
3	B	19	ARG
3	B	30	VAL
3	B	68	SER

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Mol	Chain	Res	Type
3	H	3	ILE
3	H	61	SER
3	H	111	ARG
3	H	124	SER
3	H	125	ASP
3	H	126	SER
3	H	129	LYS

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](#)

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

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	C	118/313 (37%)	-0.14	4 (3%) 45 44	23, 37, 84, 136	0
1	E	112/313 (35%)	0.04	7 (6%) 20 19	26, 45, 86, 107	0
2	A	223/245 (91%)	-0.17	2 (0%) 84 83	20, 35, 66, 91	0
2	D	224/245 (91%)	-0.16	2 (0%) 84 83	20, 36, 62, 138	0
3	B	214/217 (98%)	-0.05	7 (3%) 46 45	20, 39, 74, 94	0
3	H	215/217 (99%)	-0.02	11 (5%) 28 27	20, 39, 77, 144	0
All	All	1106/1550 (71%)	-0.09	33 (2%) 50 49	20, 38, 74, 144	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	232	CYS	8.3
3	H	217	CYS	6.0
3	H	125	ASP	5.3
3	H	28	GLN	5.0
1	C	130	PRO	4.7
3	B	187	ALA	4.3
1	C	128	SER	3.9
1	E	113	ARG	3.9
1	E	122	VAL	3.5
3	B	157	LEU	3.5
2	D	149	GLY	3.3
1	E	124	LEU	3.2
2	A	33	TYR	2.9
3	H	27	SER	2.9
2	A	149	GLY	2.9
3	B	184	LEU	2.9
3	B	29	SER	2.8
3	H	131	GLY	2.8
1	E	178	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
3	H	216	GLU	2.7
3	H	128	LEU	2.7
1	E	114	ALA	2.6
1	E	227	GLY	2.6
1	C	129	LYS	2.5
3	H	157	LEU	2.5
3	B	28	GLN	2.4
3	H	187	ALA	2.3
3	B	27	SER	2.3
1	C	182	ARG	2.2
1	E	228	ASP	2.2
3	B	30	VAL	2.1
3	H	130	SER	2.0
3	H	132	THR	2.0

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.