



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 10, 2019 – 12:16 PM EDT

PDB ID : 6QWV
Title : SARM1 SAM1-2 domains
Authors : Sporny, M.; Isupov, N.M.; Opatowsky, Y.
Deposited on : 2019-03-06
Resolution : 2.47 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 : 1.8.0 (224370), CSD as540be (2019)
Xtriage (Phenix) : 1.13
EDS : 2.4
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.4

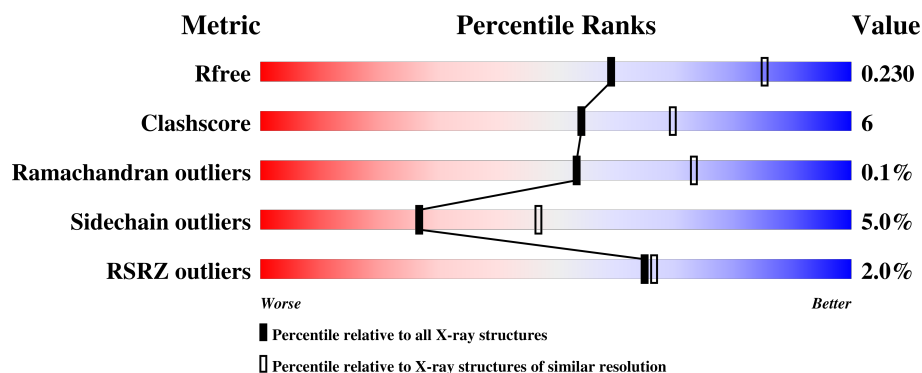
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.47 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}	111664	5140 (2.50-2.46)
Clashscore	122126	5860 (2.50-2.46)
Ramachandran outliers	120053	5763 (2.50-2.46)
Sidechain outliers	120020	5765 (2.50-2.46)
RSRZ outliers	108989	5026 (2.50-2.46)

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. 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	164	<div> <div>3%</div> <div>79% 8% • 13%</div> </div>
1	B	164	<div> <div>%</div> <div>77% 18% • •</div> </div>
1	C	164	<div> <div>2%</div> <div>79% 9% • 10%</div> </div>
1	D	164	<div> <div>%</div> <div>73% 15% • 11%</div> </div>
1	E	164	<div> <div>2%</div> <div>79% 9% • 11%</div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	164	
1	G	164	
1	H	164	
1	I	164	
1	J	164	
1	K	164	
1	L	164	
1	M	164	
1	N	164	
1	O	164	
1	P	164	

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	EDO	D	607	-	-	-	X
2	EDO	D	608	-	-	X	-
2	EDO	E	601	-	-	X	-
2	EDO	J	605	-	-	-	X
2	EDO	O	601	-	-	X	-
3	BME	D	603	-	-	X	X
3	BME	E	602	-	-	X	-
3	BME	F	602	-	-	-	X
3	BME	H	601	-	-	X	-
3	BME	J	606	-	-	X	X
3	BME	N	601	-	-	X	-
4	PEG	D	602	-	-	X	-
5	PGE	B	605	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 20654 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.

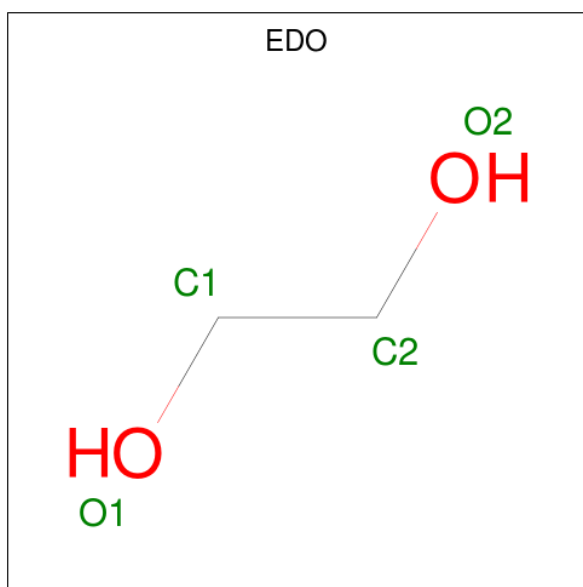
- Molecule 1 is a protein called Sterile alpha and TIR motif-containing protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	143	Total	C	N	O	S	0	7	0
			1211	763	220	221	7			
1	B	157	Total	C	N	O	S	0	8	0
			1324	832	241	244	7			
1	C	148	Total	C	N	O	S	0	5	0
			1232	775	221	229	7			
1	D	146	Total	C	N	O	S	0	3	0
			1204	756	215	226	7			
1	E	146	Total	C	N	O	S	0	3	0
			1209	761	219	222	7			
1	F	144	Total	C	N	O	S	0	7	0
			1211	762	219	223	7			
1	G	145	Total	C	N	O	S	0	5	0
			1206	758	217	224	7			
1	H	146	Total	C	N	O	S	0	4	0
			1210	761	217	225	7			
1	I	145	Total	C	N	O	S	0	9	0
			1220	768	218	227	7			
1	J	147	Total	C	N	O	S	0	4	0
			1216	764	219	226	7			
1	K	148	Total	C	N	O	S	0	5	0
			1234	776	224	227	7			
1	L	145	Total	C	N	O	S	0	5	0
			1205	758	216	224	7			
1	M	145	Total	C	N	O	S	0	6	0
			1211	763	218	223	7			
1	N	143	Total	C	N	O	S	0	4	0
			1181	744	210	220	7			
1	O	145	Total	C	N	O	S	0	6	0
			1211	763	218	223	7			
1	P	144	Total	C	N	O	S	0	6	0
			1207	759	220	221	7			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	385	GLY	-	expression tag	UNP Q6SZW1
A	386	SER	-	expression tag	UNP Q6SZW1
B	385	GLY	-	expression tag	UNP Q6SZW1
B	386	SER	-	expression tag	UNP Q6SZW1
C	385	GLY	-	expression tag	UNP Q6SZW1
C	386	SER	-	expression tag	UNP Q6SZW1
D	385	GLY	-	expression tag	UNP Q6SZW1
D	386	SER	-	expression tag	UNP Q6SZW1
E	385	GLY	-	expression tag	UNP Q6SZW1
E	386	SER	-	expression tag	UNP Q6SZW1
F	385	GLY	-	expression tag	UNP Q6SZW1
F	386	SER	-	expression tag	UNP Q6SZW1
G	385	GLY	-	expression tag	UNP Q6SZW1
G	386	SER	-	expression tag	UNP Q6SZW1
H	385	GLY	-	expression tag	UNP Q6SZW1
H	386	SER	-	expression tag	UNP Q6SZW1
I	385	GLY	-	expression tag	UNP Q6SZW1
I	386	SER	-	expression tag	UNP Q6SZW1
J	385	GLY	-	expression tag	UNP Q6SZW1
J	386	SER	-	expression tag	UNP Q6SZW1
K	385	GLY	-	expression tag	UNP Q6SZW1
K	386	SER	-	expression tag	UNP Q6SZW1
L	385	GLY	-	expression tag	UNP Q6SZW1
L	386	SER	-	expression tag	UNP Q6SZW1
M	385	GLY	-	expression tag	UNP Q6SZW1
M	386	SER	-	expression tag	UNP Q6SZW1
N	385	GLY	-	expression tag	UNP Q6SZW1
N	386	SER	-	expression tag	UNP Q6SZW1
O	385	GLY	-	expression tag	UNP Q6SZW1
O	386	SER	-	expression tag	UNP Q6SZW1
P	385	GLY	-	expression tag	UNP Q6SZW1
P	386	SER	-	expression tag	UNP Q6SZW1

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	C	1	Total	C	O	0	0
			4	2	2		
2	C	1	Total	C	O	0	0
			4	2	2		
2	C	1	Total	C	O	0	0
			4	2	2		
2	D	1	Total	C	O	0	0
			4	2	2		
2	D	1	Total	C	O	0	0
			4	2	2		
2	D	1	Total	C	O	0	0
			4	2	2		
2	D	1	Total	C	O	0	0
			4	2	2		

Continued on next page...

Continued from previous page...

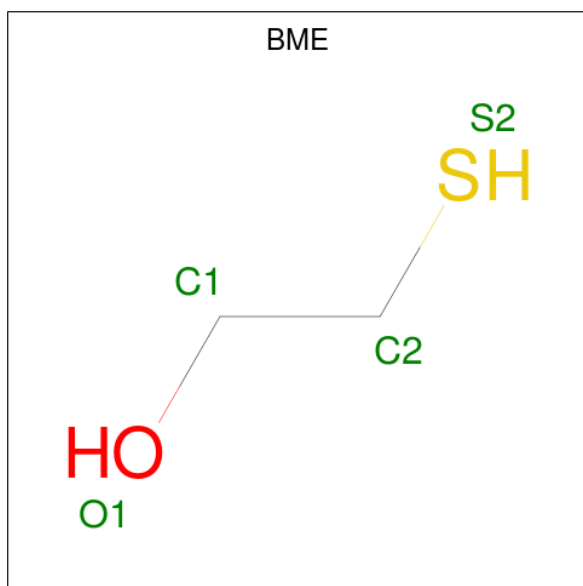
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	D	1	Total	C	O	0	0
			4	2	2		
2	E	1	Total	C	O	0	0
			4	2	2		
2	F	1	Total	C	O	0	0
			4	2	2		
2	I	1	Total	C	O	0	0
			4	2	2		
2	I	1	Total	C	O	0	0
			4	2	2		
2	J	1	Total	C	O	0	0
			4	2	2		
2	J	1	Total	C	O	0	0
			4	2	2		
2	J	1	Total	C	O	0	0
			4	2	2		
2	J	1	Total	C	O	0	0
			4	2	2		
2	J	1	Total	C	O	0	0
			4	2	2		
2	K	1	Total	C	O	0	0
			4	2	2		
2	K	1	Total	C	O	0	0
			4	2	2		
2	K	1	Total	C	O	0	0
			4	2	2		
2	K	1	Total	C	O	0	0
			4	2	2		
2	L	1	Total	C	O	0	0
			4	2	2		
2	L	1	Total	C	O	0	0
			4	2	2		
2	L	1	Total	C	O	0	0
			4	2	2		
2	M	1	Total	C	O	0	0
			4	2	2		
2	M	1	Total	C	O	0	0
			4	2	2		
2	M	1	Total	C	O	0	0
			4	2	2		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	M	1	Total	C	O	0	0
			4	2	2		
2	N	1	Total	C	O	0	0
			4	2	2		
2	O	1	Total	C	O	0	0
			4	2	2		
2	O	1	Total	C	O	0	0
			4	2	2		
2	O	1	Total	C	O	0	0
			4	2	2		
2	P	1	Total	C	O	0	0
			4	2	2		
2	P	1	Total	C	O	0	0
			4	2	2		
2	P	1	Total	C	O	0	0
			4	2	2		

- Molecule 3 is BETA-MERCAPTOETHANOL (three-letter code: BME) (formula: C₂H₆OS).



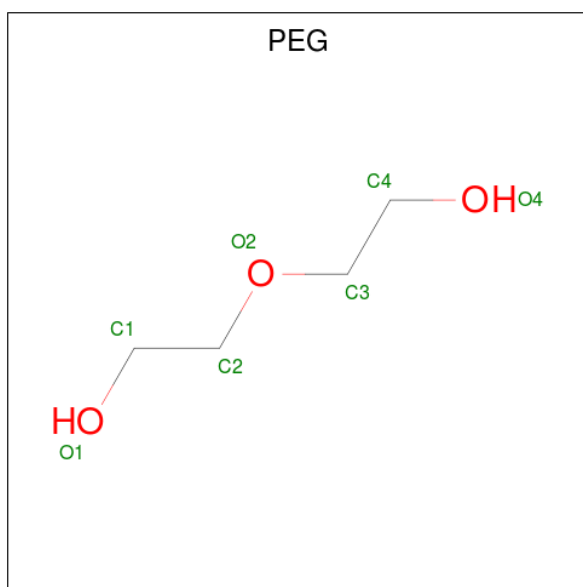
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	S	0	0
			4	2	1	1		
3	B	1	Total	C	O	S	0	0
			4	2	1	1		
3	C	1	Total	C	O	S	0	0
			4	2	1	1		

Continued on next page...

Continued from previous page...

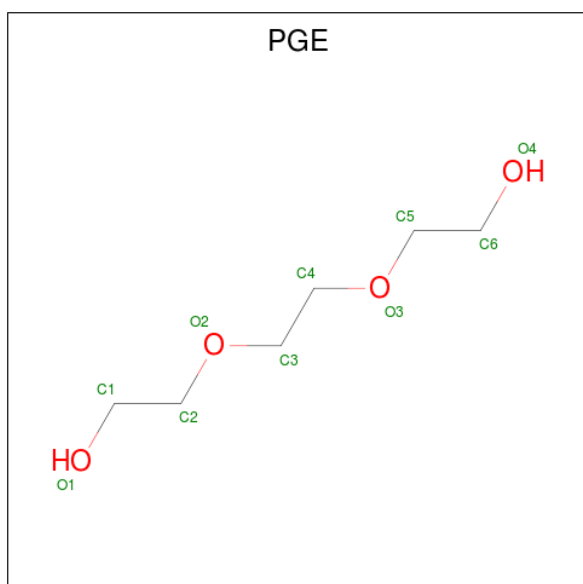
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	D	1	Total 4	C 2	O 1	S 1	0	0
3	E	1	Total 4	C 2	O 1	S 1	0	0
3	F	1	Total 4	C 2	O 1	S 1	0	0
3	G	1	Total 4	C 2	O 1	S 1	0	0
3	H	1	Total 4	C 2	O 1	S 1	0	0
3	I	1	Total 4	C 2	O 1	S 1	0	0
3	J	1	Total 4	C 2	O 1	S 1	0	0
3	K	1	Total 4	C 2	O 1	S 1	0	0
3	L	1	Total 4	C 2	O 1	S 1	0	0
3	M	1	Total 4	C 2	O 1	S 1	0	0
3	N	1	Total 4	C 2	O 1	S 1	0	0
3	O	1	Total 4	C 2	O 1	S 1	0	0
3	P	1	Total 4	C 2	O 1	S 1	0	0

- Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			7	4	3		
4	D	1	Total	C	O	0	0
			7	4	3		
4	J	1	Total	C	O	0	0
			7	4	3		
4	J	1	Total	C	O	0	0
			7	4	3		
4	K	1	Total	C	O	0	0
			7	4	3		

- Molecule 5 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			10	6	4		
5	P	1	Total	C	O	0	0
			10	6	4		

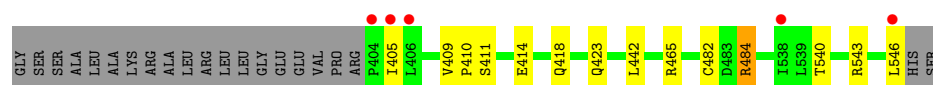
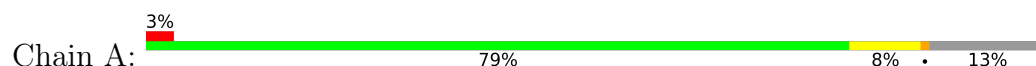
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	42	Total	O	0	0
			42	42		
6	B	62	Total	O	0	0
			62	62		
6	C	86	Total	O	0	0
			86	86		
6	D	77	Total	O	0	0
			77	77		
6	E	45	Total	O	0	0
			45	45		
6	F	37	Total	O	0	0
			37	37		
6	G	37	Total	O	0	0
			37	37		
6	H	43	Total	O	0	0
			43	43		
6	I	62	Total	O	0	0
			62	62		
6	J	84	Total	O	0	0
			84	84		
6	K	62	Total	O	0	0
			62	62		
6	L	50	Total	O	0	0
			50	50		
6	M	62	Total	O	0	0
			62	62		
6	N	25	Total	O	0	0
			25	25		
6	O	52	Total	O	0	0
			52	52		
6	P	45	Total	O	0	0
			45	45		

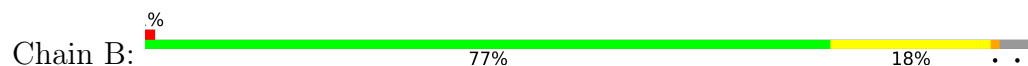
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

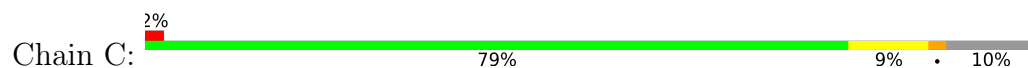
- Molecule 1: Sterile alpha and TIR motif-containing protein 1



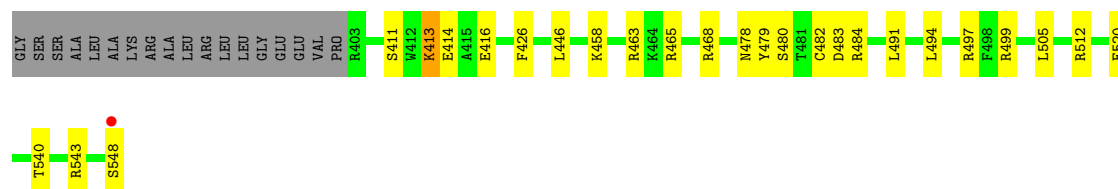
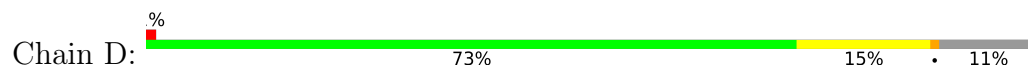
- Molecule 1: Sterile alpha and TIR motif-containing protein 1



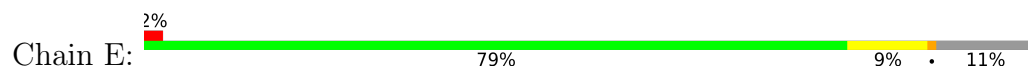
- Molecule 1: Sterile alpha and TIR motif-containing protein 1

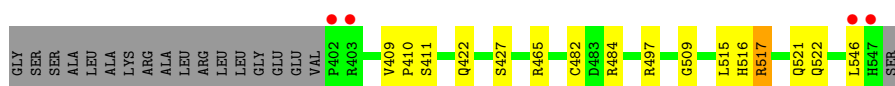


- Molecule 1: Sterile alpha and TIR motif-containing protein 1

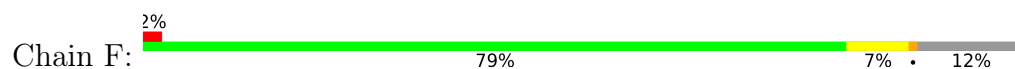


- Molecule 1: Sterile alpha and TIR motif-containing protein 1

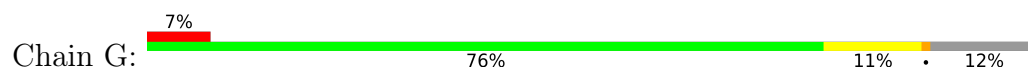




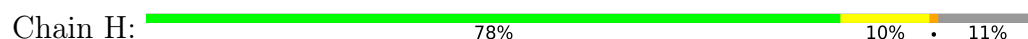
- Molecule 1: Sterile alpha and TIR motif-containing protein 1



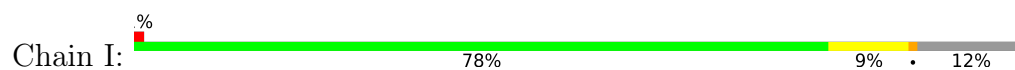
- Molecule 1: Sterile alpha and TIR motif-containing protein 1



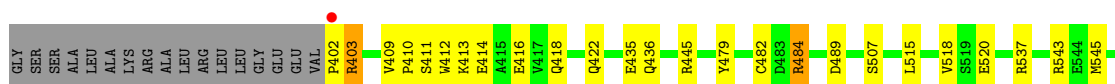
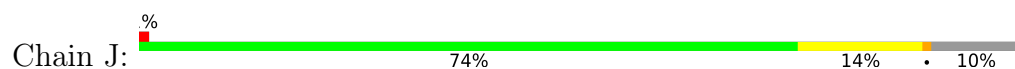
- Molecule 1: Sterile alpha and TIR motif-containing protein 1



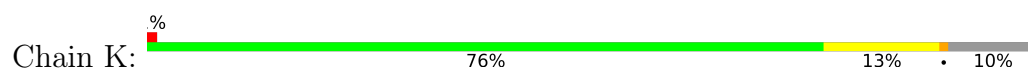
- Molecule 1: Sterile alpha and TIR motif-containing protein 1



- Molecule 1: Sterile alpha and TIR motif-containing protein 1

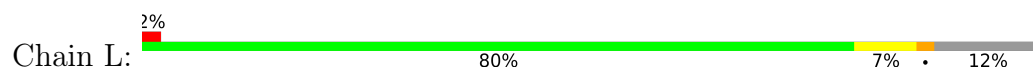


- Molecule 1: Sterile alpha and TIR motif-containing protein 1

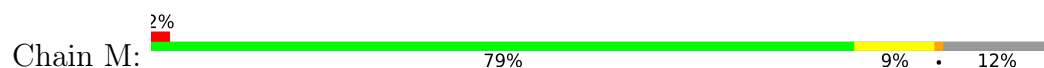




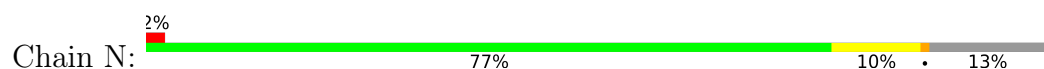
- Molecule 1: Sterile alpha and TIR motif-containing protein 1



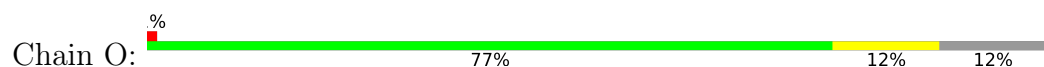
- Molecule 1: Sterile alpha and TIR motif-containing protein 1



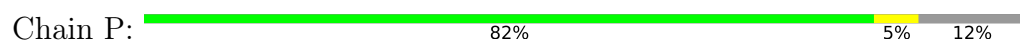
- Molecule 1: Sterile alpha and TIR motif-containing protein 1



- Molecule 1: Sterile alpha and TIR motif-containing protein 1



- Molecule 1: Sterile alpha and TIR motif-containing protein 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α , β , γ	252.25Å 252.25Å 49.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	56.40 – 2.47 56.40 – 2.47	Depositor EDS
% Data completeness (in resolution range)	99.1 (56.40-2.47) 99.2 (56.40-2.47)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.31 (at 2.48Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.189 , 0.230 0.189 , 0.230	Depositor DCC
R_{free} test set	1333 reflections (1.18%)	wwPDB-VP
Wilson B-factor (Å ²)	51.7	Xtriage
Anisotropy	0.101	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 48.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.011 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	20654	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.65% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PEG, PGE, BME, EDO

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	0.37	0/1254	0.69	0/1687
1	B	0.45	0/1372	0.80	1/1846 (0.1%)
1	C	0.46	0/1271	0.77	0/1713
1	D	0.47	0/1236	0.79	1/1665 (0.1%)
1	E	0.43	0/1242	0.72	0/1674
1	F	0.38	0/1256	0.73	1/1692 (0.1%)
1	G	0.39	0/1244	0.78	2/1674 (0.1%)
1	H	0.43	0/1245	0.72	0/1679
1	I	0.46	0/1270	0.75	1/1711 (0.1%)
1	J	0.50	0/1252	0.79	2/1686 (0.1%)
1	K	0.45	0/1273	0.75	2/1715 (0.1%)
1	L	0.43	0/1244	0.74	3/1675 (0.2%)
1	M	0.45	0/1252	0.75	2/1687 (0.1%)
1	N	0.39	0/1215	0.71	1/1637 (0.1%)
1	O	0.42	0/1252	0.74	0/1687
1	P	0.44	0/1248	0.73	0/1680
All	All	0.44	0/20126	0.75	16/27108 (0.1%)

There are no bond length outliers.

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	508	CYS	CB-CA-C	-7.05	96.29	110.40
1	M	402	PRO	CA-N-CD	-6.86	101.89	111.50
1	N	517	ARG	CG-CD-NE	-6.62	97.89	111.80
1	L	465	ARG	NE-CZ-NH2	6.18	123.39	120.30
1	D	414	GLU	CB-CG-CD	6.17	130.85	114.20

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-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 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	1211	0	1225	15	0
1	B	1324	0	1339	24	0
1	C	1232	0	1231	16	0
1	D	1204	0	1194	27	0
1	E	1209	0	1207	19	0
1	F	1211	0	1215	13	0
1	G	1206	0	1207	8	0
1	H	1210	0	1208	18	0
1	I	1220	0	1229	14	0
1	J	1216	0	1214	20	0
1	K	1234	0	1238	22	0
1	L	1205	0	1201	8	0
1	M	1211	0	1222	9	0
1	N	1181	0	1182	13	0
1	O	1211	0	1222	17	0
1	P	1207	0	1217	9	0
2	A	8	0	12	3	0
2	B	16	0	24	1	0
2	C	12	0	18	2	0
2	D	24	0	36	9	0
2	E	4	0	6	5	0
2	F	4	0	6	0	0
2	I	8	0	12	1	0
2	J	24	0	36	3	0
2	K	16	0	24	0	0
2	L	12	0	18	1	0
2	M	16	0	24	2	0
2	N	4	0	6	0	0
2	O	12	0	18	4	0
2	P	12	0	18	0	0
3	A	4	0	5	3	0
3	B	4	0	5	1	0
3	C	4	0	5	3	0
3	D	4	0	5	5	0
3	E	4	0	5	5	0
3	F	4	0	5	2	0
3	G	4	0	5	2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	H	4	0	5	4	0
3	I	4	0	5	3	0
3	J	4	0	5	7	0
3	K	4	0	5	2	0
3	L	4	0	5	2	0
3	M	4	0	5	2	0
3	N	4	0	5	6	0
3	O	4	0	5	3	0
3	P	4	0	5	2	0
4	B	7	0	10	1	0
4	D	7	0	10	8	0
4	J	14	0	20	2	0
4	K	7	0	10	2	0
5	B	10	0	14	8	0
5	P	10	0	14	1	0
6	A	42	0	0	1	0
6	B	62	0	0	3	0
6	C	86	0	0	2	0
6	D	77	0	0	0	0
6	E	45	0	0	1	0
6	F	37	0	0	0	0
6	G	37	0	0	1	0
6	H	43	0	0	0	0
6	I	62	0	0	1	0
6	J	84	0	0	1	0
6	K	62	0	0	2	0
6	L	50	0	0	2	0
6	M	62	0	0	1	0
6	N	25	0	0	1	0
6	O	52	0	0	0	0
6	P	45	0	0	0	0
All	All	20654	0	19967	228	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 6.

The worst 5 of 228 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:K:516:HIS:CE1	1:K:547:HIS:HB2	1.93	1.04
1:K:516:HIS:CE1	1:K:547:HIS:CB	2.45	0.99

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:512:ARG:HH22	2:O:601:EDO:H22	1.28	0.98
1:D:482[A]:CYS:HB3	3:D:603:BME:S2	2.05	0.96
1:O:482[A]:CYS:HB3	3:O:602:BME:S2	2.11	0.91

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	A	148/164 (90%)	146 (99%)	2 (1%)	0	100	100
1	B	163/164 (99%)	159 (98%)	4 (2%)	0	100	100
1	C	151/164 (92%)	147 (97%)	3 (2%)	1 (1%)	24	39
1	D	147/164 (90%)	145 (99%)	2 (1%)	0	100	100
1	E	147/164 (90%)	144 (98%)	3 (2%)	0	100	100
1	F	149/164 (91%)	147 (99%)	2 (1%)	0	100	100
1	G	148/164 (90%)	145 (98%)	3 (2%)	0	100	100
1	H	148/164 (90%)	144 (97%)	4 (3%)	0	100	100
1	I	152/164 (93%)	150 (99%)	2 (1%)	0	100	100
1	J	149/164 (91%)	147 (99%)	2 (1%)	0	100	100
1	K	151/164 (92%)	147 (97%)	4 (3%)	0	100	100
1	L	148/164 (90%)	146 (99%)	2 (1%)	0	100	100
1	M	149/164 (91%)	146 (98%)	3 (2%)	0	100	100
1	N	145/164 (88%)	142 (98%)	2 (1%)	1 (1%)	24	39
1	O	149/164 (91%)	147 (99%)	2 (1%)	0	100	100
1	P	148/164 (90%)	144 (97%)	4 (3%)	0	100	100
All	All	2392/2624 (91%)	2346 (98%)	44 (2%)	2 (0%)	53	73

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	402	PRO
1	N	405	ILE

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	135/144 (94%)	131 (97%)	4 (3%)	44	69
1	B	148/144 (103%)	138 (93%)	10 (7%)	17	31
1	C	138/144 (96%)	130 (94%)	8 (6%)	22	39
1	D	134/144 (93%)	126 (94%)	8 (6%)	21	37
1	E	134/144 (93%)	127 (95%)	7 (5%)	25	45
1	F	136/144 (94%)	131 (96%)	5 (4%)	37	61
1	G	135/144 (94%)	124 (92%)	11 (8%)	13	23
1	H	135/144 (94%)	127 (94%)	8 (6%)	21	38
1	I	139/144 (96%)	131 (94%)	8 (6%)	22	39
1	J	136/144 (94%)	128 (94%)	8 (6%)	21	38
1	K	138/144 (96%)	129 (94%)	9 (6%)	19	33
1	L	135/144 (94%)	130 (96%)	5 (4%)	37	61
1	M	136/144 (94%)	130 (96%)	6 (4%)	31	53
1	N	132/144 (92%)	125 (95%)	7 (5%)	25	44
1	O	136/144 (94%)	130 (96%)	6 (4%)	31	53
1	P	135/144 (94%)	130 (96%)	5 (4%)	37	61
All	All	2182/2304 (95%)	2067 (95%)	115 (5%)	27	44

5 of 115 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	545	MET
1	I	418	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	O	431	GLU
1	H	403	ARG
1	H	435	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	K	422	GLN
1	M	423	GLN
1	O	486	ASN
1	K	436	GLN
1	K	500	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

66 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	EDO	A	601	-	3,3,3	0.06	0	2,2,2	0.27	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	BME	A	602	1	3,3,3	0.25	0	1,2,2	0.90	0
2	EDO	A	603	-	3,3,3	0.17	0	2,2,2	0.24	0
2	EDO	B	601	-	3,3,3	0.51	0	2,2,2	0.72	0
2	EDO	B	602	-	3,3,3	0.22	0	2,2,2	0.27	0
4	PEG	B	603	-	6,6,6	0.17	0	5,5,5	0.12	0
3	BME	B	604	1	3,3,3	0.41	0	1,2,2	0.66	0
5	PGE	B	605	-	9,9,9	0.30	0	8,8,8	0.35	0
2	EDO	B	606	-	3,3,3	0.20	0	2,2,2	0.31	0
2	EDO	B	607	-	3,3,3	0.09	0	2,2,2	0.24	0
3	BME	C	601	1	3,3,3	0.30	0	1,2,2	0.37	0
2	EDO	C	602	-	3,3,3	0.35	0	2,2,2	0.86	0
2	EDO	C	603	-	3,3,3	0.19	0	2,2,2	0.19	0
2	EDO	C	604	-	3,3,3	0.18	0	2,2,2	0.00	0
2	EDO	D	601	-	3,3,3	0.31	0	2,2,2	0.77	0
4	PEG	D	602	-	6,6,6	0.33	0	5,5,5	0.37	0
3	BME	D	603	1	3,3,3	0.25	0	1,2,2	1.58	0
2	EDO	D	604	-	3,3,3	0.20	0	2,2,2	0.06	0
2	EDO	D	605	-	3,3,3	0.21	0	2,2,2	0.12	0
2	EDO	D	606	-	3,3,3	0.28	0	2,2,2	0.43	0
2	EDO	D	607	-	3,3,3	0.12	0	2,2,2	0.31	0
2	EDO	D	608	-	3,3,3	0.36	0	2,2,2	0.64	0
2	EDO	E	601	-	3,3,3	0.20	0	2,2,2	0.75	0
3	BME	E	602	1	3,3,3	0.33	0	1,2,2	0.94	0
2	EDO	F	601	-	3,3,3	0.06	0	2,2,2	0.04	0
3	BME	F	602	1	3,3,3	0.13	0	1,2,2	0.47	0
3	BME	G	601	1	3,3,3	0.24	0	1,2,2	0.61	0
3	BME	H	601	1	3,3,3	0.21	0	1,2,2	0.00	0
2	EDO	I	601	-	3,3,3	0.33	0	2,2,2	0.67	0
2	EDO	I	602	-	3,3,3	0.21	0	2,2,2	0.21	0
3	BME	I	603	1	3,3,3	0.14	0	1,2,2	0.45	0
4	PEG	J	601	-	6,6,6	0.52	0	5,5,5	0.32	0
4	PEG	J	602	-	6,6,6	0.55	0	5,5,5	0.27	0
2	EDO	J	603	-	3,3,3	0.22	0	2,2,2	0.46	0
2	EDO	J	604	-	3,3,3	0.19	0	2,2,2	1.10	0
2	EDO	J	605	-	3,3,3	0.19	0	2,2,2	1.02	0
3	BME	J	606	1	3,3,3	0.23	0	1,2,2	0.09	0
2	EDO	J	607	-	3,3,3	0.11	0	2,2,2	0.25	0
2	EDO	J	608	-	3,3,3	0.29	0	2,2,2	0.39	0
2	EDO	J	609	-	3,3,3	0.18	0	2,2,2	0.24	0
2	EDO	K	601	-	3,3,3	0.09	0	2,2,2	0.38	0
3	BME	K	602	1	3,3,3	0.24	0	1,2,2	0.43	0
4	PEG	K	603	-	6,6,6	0.24	0	5,5,5	0.17	0
2	EDO	K	604	-	3,3,3	0.30	0	2,2,2	0.26	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	EDO	K	605	-	3,3,3	0.50	0	2,2,2	0.63	0
2	EDO	K	606	-	3,3,3	0.10	0	2,2,2	0.10	0
2	EDO	L	601	-	3,3,3	0.09	0	2,2,2	0.50	0
3	BME	L	602	1	3,3,3	0.11	0	1,2,2	1.20	0
2	EDO	L	603	-	3,3,3	0.09	0	2,2,2	0.32	0
2	EDO	L	604	-	3,3,3	0.18	0	2,2,2	0.14	0
3	BME	M	601	1	3,3,3	0.32	0	1,2,2	1.87	0
2	EDO	M	602	-	3,3,3	0.24	0	2,2,2	0.29	0
2	EDO	M	603	-	3,3,3	0.19	0	2,2,2	0.47	0
2	EDO	M	604	-	3,3,3	0.30	0	2,2,2	0.67	0
2	EDO	M	605	-	3,3,3	0.26	0	2,2,2	0.10	0
3	BME	N	601	1	3,3,3	0.28	0	1,2,2	0.52	0
2	EDO	N	602	-	3,3,3	0.08	0	2,2,2	0.35	0
2	EDO	O	601	-	3,3,3	0.12	0	2,2,2	0.39	0
3	BME	O	602	1	3,3,3	0.14	0	1,2,2	0.44	0
2	EDO	O	603	-	3,3,3	0.19	0	2,2,2	0.48	0
2	EDO	O	604	-	3,3,3	0.16	0	2,2,2	0.31	0
2	EDO	P	601	-	3,3,3	0.12	0	2,2,2	0.31	0
2	EDO	P	602	-	3,3,3	0.24	0	2,2,2	0.41	0
3	BME	P	603	1	3,3,3	0.14	0	1,2,2	0.05	0
5	PGE	P	604	-	9,9,9	0.22	0	8,8,8	0.19	0
2	EDO	P	605	-	3,3,3	0.09	0	2,2,2	0.33	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	EDO	A	601	-	-	0/1/1/1	-
3	BME	A	602	1	-	0/1/1/1	-
2	EDO	A	603	-	-	1/1/1/1	-
2	EDO	B	601	-	-	1/1/1/1	-
2	EDO	B	602	-	-	1/1/1/1	-
4	PEG	B	603	-	-	0/4/4/4	-
3	BME	B	604	1	-	0/1/1/1	-
5	PGE	B	605	-	-	6/7/7/7	-
2	EDO	B	606	-	-	1/1/1/1	-
2	EDO	B	607	-	-	0/1/1/1	-
3	BME	C	601	1	-	1/1/1/1	-
2	EDO	C	602	-	-	0/1/1/1	-
2	EDO	C	603	-	-	0/1/1/1	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	EDO	C	604	-	-	1/1/1/1	-
2	EDO	D	601	-	-	1/1/1/1	-
4	PEG	D	602	-	-	3/4/4/4	-
3	BME	D	603	1	-	1/1/1/1	-
2	EDO	D	604	-	-	0/1/1/1	-
2	EDO	D	605	-	-	1/1/1/1	-
2	EDO	D	606	-	-	0/1/1/1	-
2	EDO	D	607	-	-	1/1/1/1	-
2	EDO	D	608	-	-	1/1/1/1	-
2	EDO	E	601	-	-	1/1/1/1	-
3	BME	E	602	1	-	0/1/1/1	-
2	EDO	F	601	-	-	0/1/1/1	-
3	BME	F	602	1	-	1/1/1/1	-
3	BME	G	601	1	-	0/1/1/1	-
3	BME	H	601	1	-	1/1/1/1	-
2	EDO	I	601	-	-	1/1/1/1	-
2	EDO	I	602	-	-	1/1/1/1	-
3	BME	I	603	1	-	0/1/1/1	-
4	PEG	J	601	-	-	3/4/4/4	-
4	PEG	J	602	-	-	2/4/4/4	-
2	EDO	J	603	-	-	0/1/1/1	-
2	EDO	J	604	-	-	1/1/1/1	-
2	EDO	J	605	-	-	1/1/1/1	-
3	BME	J	606	1	-	0/1/1/1	-
2	EDO	J	607	-	-	1/1/1/1	-
2	EDO	J	608	-	-	1/1/1/1	-
2	EDO	J	609	-	-	1/1/1/1	-
2	EDO	K	601	-	-	0/1/1/1	-
3	BME	K	602	1	-	1/1/1/1	-
4	PEG	K	603	-	-	3/4/4/4	-
2	EDO	K	604	-	-	1/1/1/1	-
2	EDO	K	605	-	-	1/1/1/1	-
2	EDO	K	606	-	-	1/1/1/1	-
2	EDO	L	601	-	-	0/1/1/1	-
3	BME	L	602	1	-	0/1/1/1	-
2	EDO	L	603	-	-	1/1/1/1	-
2	EDO	L	604	-	-	1/1/1/1	-
3	BME	M	601	1	-	0/1/1/1	-
2	EDO	M	602	-	-	0/1/1/1	-
2	EDO	M	603	-	-	0/1/1/1	-
2	EDO	M	604	-	-	0/1/1/1	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	EDO	M	605	-	-	0/1/1/1	-
3	BME	N	601	1	-	1/1/1/1	-
2	EDO	N	602	-	-	1/1/1/1	-
2	EDO	O	601	-	-	1/1/1/1	-
3	BME	O	602	1	-	0/1/1/1	-
2	EDO	O	603	-	-	1/1/1/1	-
2	EDO	O	604	-	-	0/1/1/1	-
2	EDO	P	601	-	-	1/1/1/1	-
2	EDO	P	602	-	-	1/1/1/1	-
3	BME	P	603	1	-	1/1/1/1	-
5	PGE	P	604	-	-	4/7/7/7	-
2	EDO	P	605	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 55 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	601	BME	O1-C1-C2-S2
3	N	601	BME	O1-C1-C2-S2
3	P	603	BME	O1-C1-C2-S2
5	B	605	PGE	O2-C3-C4-O3
4	J	601	PEG	O1-C1-C2-O2

There are no ring outliers.

39 monomers are involved in 105 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	602	BME	3	0
2	A	603	EDO	3	0
2	B	602	EDO	1	0
4	B	603	PEG	1	0
3	B	604	BME	1	0
5	B	605	PGE	8	0
3	C	601	BME	3	0
2	C	602	EDO	1	0
2	C	604	EDO	1	0
2	D	601	EDO	1	0
4	D	602	PEG	8	0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	603	BME	5	0
2	D	604	EDO	1	0
2	D	607	EDO	1	0
2	D	608	EDO	6	0
2	E	601	EDO	5	0
3	E	602	BME	5	0
3	F	602	BME	2	0
3	G	601	BME	2	0
3	H	601	BME	4	0
2	I	601	EDO	1	0
3	I	603	BME	3	0
4	J	601	PEG	1	0
4	J	602	PEG	1	0
2	J	604	EDO	2	0
2	J	605	EDO	1	0
3	J	606	BME	7	0
3	K	602	BME	2	0
4	K	603	PEG	2	0
3	L	602	BME	2	0
2	L	604	EDO	1	0
3	M	601	BME	2	0
2	M	602	EDO	1	0
2	M	603	EDO	1	0
3	N	601	BME	6	0
2	O	601	EDO	4	0
3	O	602	BME	3	0
3	P	603	BME	2	0
5	P	604	PGE	1	0

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	143/164 (87%)	0.06	5 (3%) 44 46	37, 62, 101, 153	0
1	B	157/164 (95%)	-0.08	2 (1%) 77 78	27, 47, 130, 161	0
1	C	148/164 (90%)	-0.07	3 (2%) 65 66	28, 45, 84, 173	0
1	D	146/164 (89%)	-0.23	1 (0%) 87 89	30, 43, 77, 127	0
1	E	146/164 (89%)	-0.08	4 (2%) 54 56	35, 52, 99, 144	0
1	F	144/164 (87%)	-0.15	3 (2%) 63 65	35, 58, 95, 151	0
1	G	145/164 (88%)	0.48	12 (8%) 11 11	38, 61, 111, 176	0
1	H	146/164 (89%)	-0.20	0 100 100	34, 54, 105, 146	0
1	I	145/164 (88%)	-0.26	1 (0%) 87 89	31, 50, 93, 154	0
1	J	147/164 (89%)	0.03	1 (0%) 87 89	28, 42, 76, 142	0
1	K	148/164 (90%)	-0.06	2 (1%) 75 76	30, 47, 103, 179	0
1	L	145/164 (88%)	0.01	4 (2%) 53 55	34, 53, 88, 151	0
1	M	145/164 (88%)	0.02	3 (2%) 63 65	34, 50, 96, 141	0
1	N	143/164 (87%)	0.11	4 (2%) 53 55	37, 62, 107, 156	0
1	O	145/164 (88%)	-0.12	2 (1%) 75 76	33, 51, 85, 145	0
1	P	144/164 (87%)	-0.04	0 100 100	34, 58, 99, 129	0
All	All	2337/2624 (89%)	-0.04	47 (2%) 65 66	27, 52, 100, 179	0

The worst 5 of 47 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	N	405	ILE	6.2
1	G	546	LEU	6.0
1	L	404	PRO	5.8
1	D	548	SER	5.5
1	G	405	ILE	5.3

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 ⓘ

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
3	BME	D	603	4/4	0.50	0.55	45,55,60,91	4
3	BME	J	606	4/4	0.54	0.74	53,53,56,80	4
2	EDO	C	603	4/4	0.55	0.15	86,92,94,120	0
2	EDO	J	608	4/4	0.68	0.36	82,88,93,118	0
3	BME	I	603	4/4	0.68	0.36	55,57,59,85	4
2	EDO	P	605	4/4	0.71	0.23	77,82,88,95	0
3	BME	F	602	4/4	0.71	0.41	48,53,78,81	4
3	BME	G	601	4/4	0.71	0.37	52,82,91,110	4
2	EDO	C	602	4/4	0.73	0.28	77,86,96,106	0
2	EDO	M	604	4/4	0.73	0.27	62,72,75,84	0
2	EDO	J	603	4/4	0.73	0.23	69,74,84,111	0
2	EDO	D	607	4/4	0.74	0.46	78,87,95,113	0
3	BME	P	603	4/4	0.74	0.36	63,66,74,93	4
2	EDO	J	605	4/4	0.75	0.45	40,47,55,59	4
2	EDO	D	604	4/4	0.76	0.25	66,84,88,107	0
2	EDO	D	606	4/4	0.78	0.24	60,73,83,95	4
2	EDO	A	601	4/4	0.80	0.14	75,92,101,102	0
2	EDO	F	601	4/4	0.80	0.46	82,88,104,105	0
4	PEG	K	603	7/7	0.81	0.24	48,76,85,91	7
2	EDO	O	603	4/4	0.81	0.29	67,73,103,112	0
2	EDO	P	602	4/4	0.81	0.26	67,92,97,117	0
3	BME	K	602	4/4	0.82	0.15	52,56,74,81	4
2	EDO	E	601	4/4	0.82	0.23	72,84,88,108	0
4	PEG	J	601	7/7	0.82	0.30	37,56,63,67	7
2	EDO	L	601	4/4	0.82	0.32	64,65,70,76	4
2	EDO	L	604	4/4	0.82	0.22	80,85,86,92	0
2	EDO	B	606	4/4	0.82	0.20	66,88,104,111	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	EDO	K	604	4/4	0.82	0.42	74,76,98,109	0
3	BME	M	601	4/4	0.83	0.32	50,56,65,81	4
3	BME	E	602	4/4	0.84	0.19	43,63,70,78	4
3	BME	O	602	4/4	0.84	0.29	47,50,53,76	4
2	EDO	N	602	4/4	0.85	0.23	49,67,68,69	4
3	BME	A	602	4/4	0.85	0.23	54,54,72,78	4
5	PGE	B	605	10/10	0.86	0.34	37,48,54,54	10
2	EDO	O	601	4/4	0.86	0.26	75,79,80,87	0
2	EDO	I	602	4/4	0.86	0.34	52,60,98,107	4
2	EDO	K	601	4/4	0.86	0.30	78,79,79,100	0
2	EDO	J	609	4/4	0.86	0.23	41,52,57,61	4
4	PEG	B	603	7/7	0.86	0.29	60,70,80,82	7
2	EDO	M	605	4/4	0.86	0.21	49,52,62,72	4
3	BME	N	601	4/4	0.86	0.21	49,49,55,76	4
3	BME	L	602	4/4	0.87	0.23	44,45,63,78	4
2	EDO	B	601	4/4	0.88	0.28	69,70,75,108	0
2	EDO	O	604	4/4	0.88	0.22	56,57,71,76	4
4	PEG	J	602	7/7	0.88	0.30	38,47,59,61	7
2	EDO	B	607	4/4	0.88	0.20	64,72,84,91	0
5	PGE	P	604	10/10	0.89	0.32	43,58,75,85	10
3	BME	H	601	4/4	0.89	0.22	52,62,75,85	4
3	BME	B	604	4/4	0.89	0.21	35,60,68,74	4
2	EDO	A	603	4/4	0.89	0.18	69,85,87,105	0
4	PEG	D	602	7/7	0.89	0.44	46,49,67,77	7
2	EDO	K	606	4/4	0.89	0.46	54,59,71,72	4
3	BME	C	601	4/4	0.90	0.25	47,47,59,79	4
2	EDO	M	602	4/4	0.90	0.18	72,74,75,79	0
2	EDO	D	605	4/4	0.90	0.21	62,70,93,103	0
2	EDO	P	601	4/4	0.91	0.38	67,82,85,92	0
2	EDO	K	605	4/4	0.91	0.23	44,45,81,101	4
2	EDO	I	601	4/4	0.91	0.32	45,51,52,70	4
2	EDO	J	607	4/4	0.91	0.20	66,71,72,98	0
2	EDO	D	608	4/4	0.91	0.19	54,66,86,90	0
2	EDO	J	604	4/4	0.92	0.29	41,44,46,49	4
2	EDO	L	603	4/4	0.93	0.27	53,77,84,86	4
2	EDO	M	603	4/4	0.93	0.24	58,61,66,68	0
2	EDO	B	602	4/4	0.95	0.34	37,40,42,45	4
2	EDO	C	604	4/4	0.95	0.34	54,60,61,118	0
2	EDO	D	601	4/4	0.95	0.19	51,54,56,56	0

6.5 Other polymers [i](#)

There are no such residues in this entry.