



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 19, 2026 – 01:18 AM UTC

PDB ID : 5SV0 / pdb_00005sv0
Title : Structure of the ExbB/ExbD complex from E. coli at pH 7.0
Authors : Celia, H.; Botos, I.; Lloubes, R.; Buchanan, S.K.; Noinaj, N.
Deposited on : 2016-08-04
Resolution : 2.60 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 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

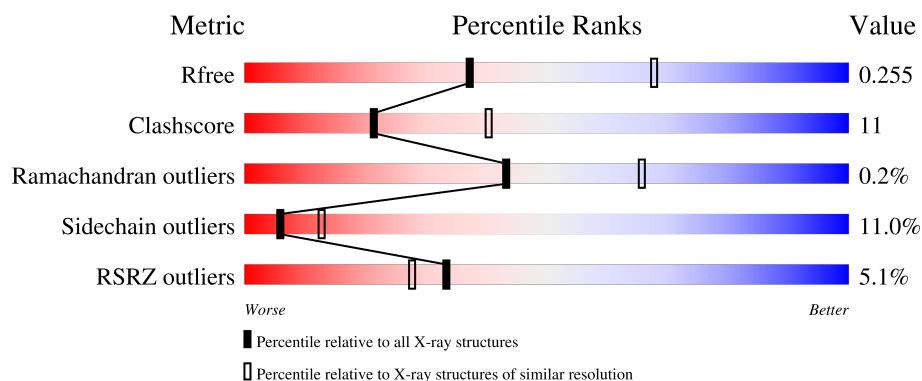
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	A	244	8% 70% 22% • 5%
1	B	244	2% 68% 20% 5% 8%
1	C	244	4% 69% 18% • 9%
1	D	244	4% 64% 20% 5% 12%
1	E	244	5% 62% 22% • • 11%

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Mol	Chain	Length	Quality of chain
1	F	244	7% 68% 20% • 9%
1	G	244	6% 70% 20% • 6%
1	H	244	3% 69% 20% • 8%
1	I	244	4% 63% 24% • 9%
1	J	244	5% 65% 20% • 12%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 16861 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 Biopolymer transport protein ExbB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	225	Total	C	N	O	S	0	0	0
			1692	1080	295	311	6			
1	C	222	Total	C	N	O	S	0	0	0
			1651	1050	289	306	6			
1	D	215	Total	C	N	O	S	0	0	0
			1615	1028	282	300	5			
1	E	216	Total	C	N	O	S	0	0	0
			1609	1025	279	300	5			
1	F	223	Total	C	N	O	S	0	0	0
			1651	1050	290	306	5			
1	G	229	Total	C	N	O	S	0	2	0
			1731	1104	301	320	6			
1	H	225	Total	C	N	O	S	0	0	0
			1700	1085	296	313	6			
1	I	223	Total	C	N	O	S	0	0	0
			1678	1068	294	310	6			
1	J	214	Total	C	N	O	S	0	0	0
			1596	1017	279	295	5			
1	A	233	Total	C	N	O	S	0	0	0
			1749	1111	308	324	6			

- Molecule 2 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: $C_8H_{18}N_2O_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	D	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
2	F	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
2	I	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	I	1	Total	Ca	0	0
			1	1		
3	A	1	Total	Ca	0	0
			1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	14	Total	O	0	0
			14	14		
4	C	11	Total	O	0	0
			11	11		
4	D	12	Total	O	0	0
			12	12		
4	E	16	Total	O	0	0
			16	16		

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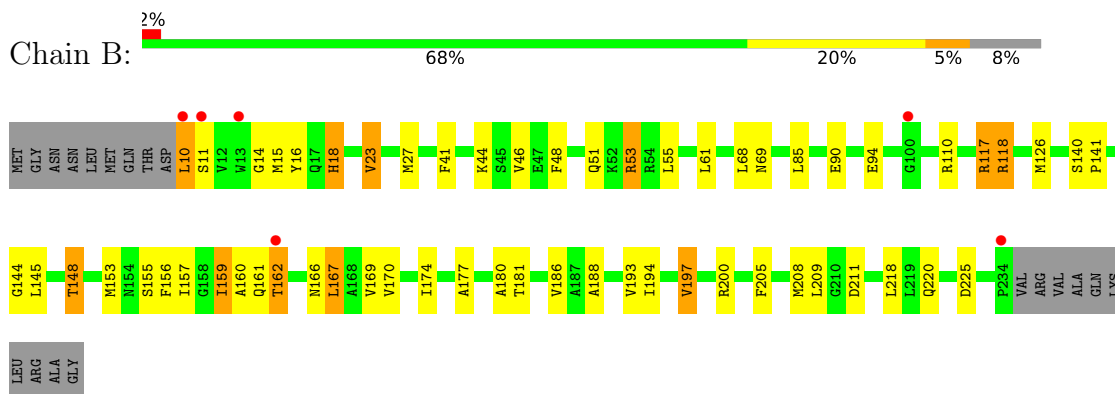
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	F	16	Total 16	O 16	0	0
4	G	15	Total 15	O 15	0	0
4	H	13	Total 13	O 13	0	0
4	I	15	Total 15	O 15	0	0
4	J	20	Total 20	O 20	0	0
4	A	10	Total 10	O 10	0	0

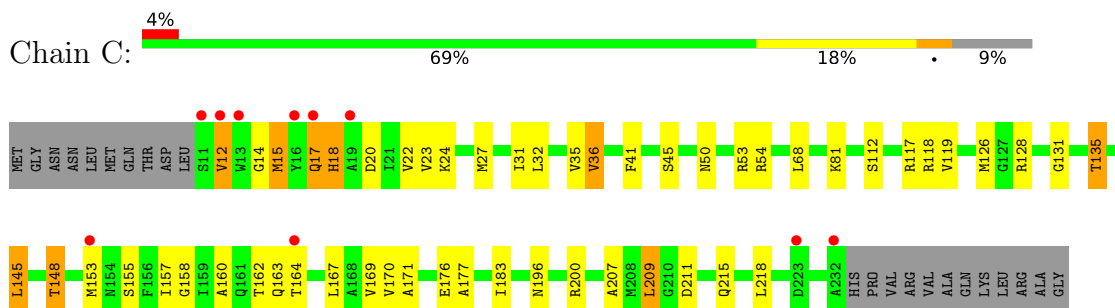
3 Residue-property plots

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

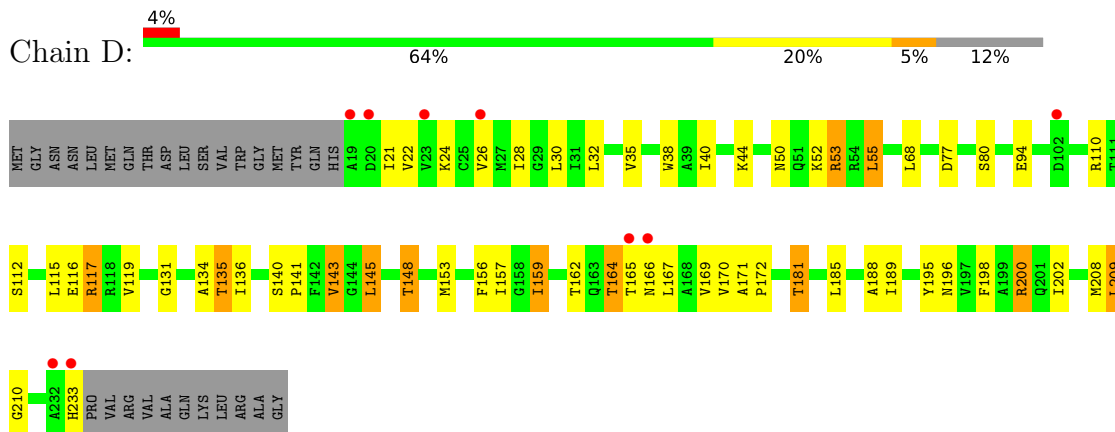
- Molecule 1: Biopolymer transport protein ExbB



- Molecule 1: Biopolymer transport protein ExbB

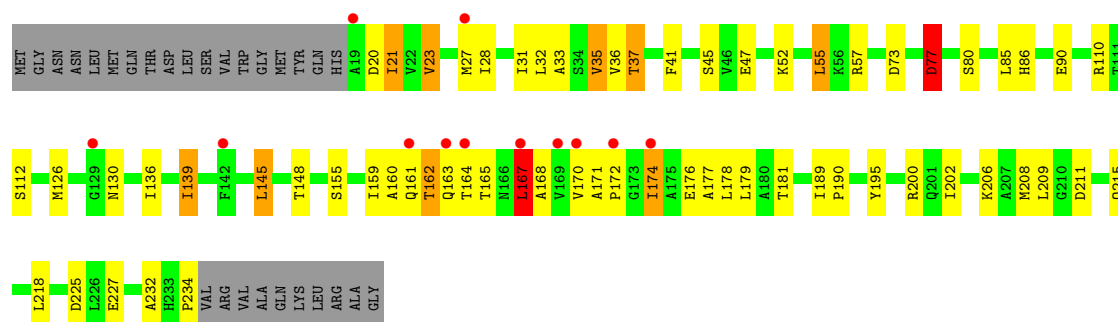


- Molecule 1: Biopolymer transport protein ExbB



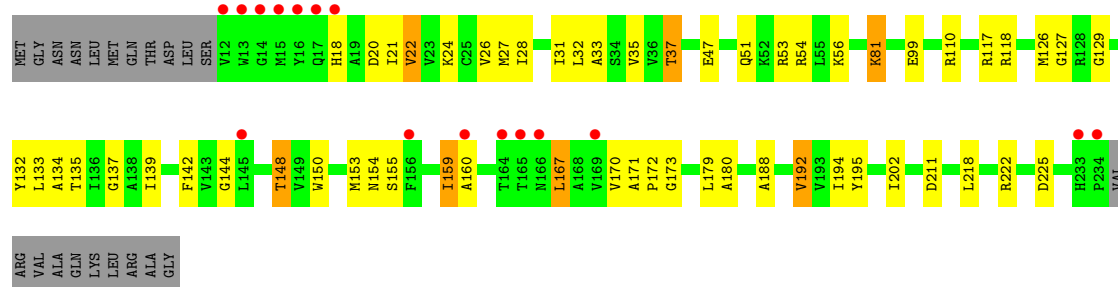
- Molecule 1: Biopolymer transport protein ExbB

Chain E: 5% 62% 22% 11%



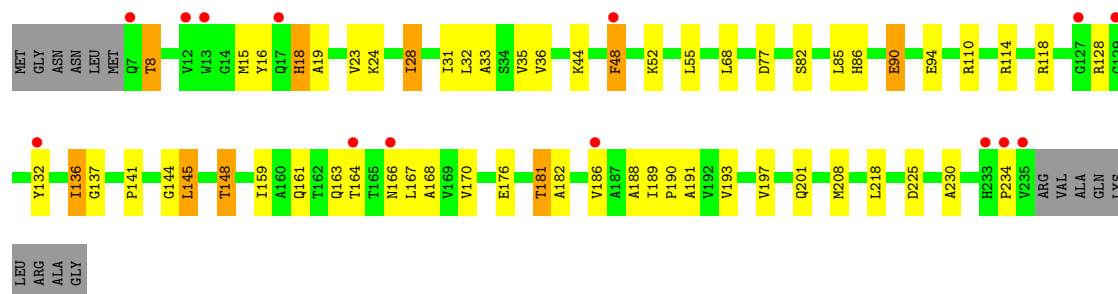
- Molecule 1: Biopolymer transport protein ExbB

Chain F: 7% 68% 20% 9%



- Molecule 1: Biopolymer transport protein ExbB

Chain G: 6% 70% 20% 6%



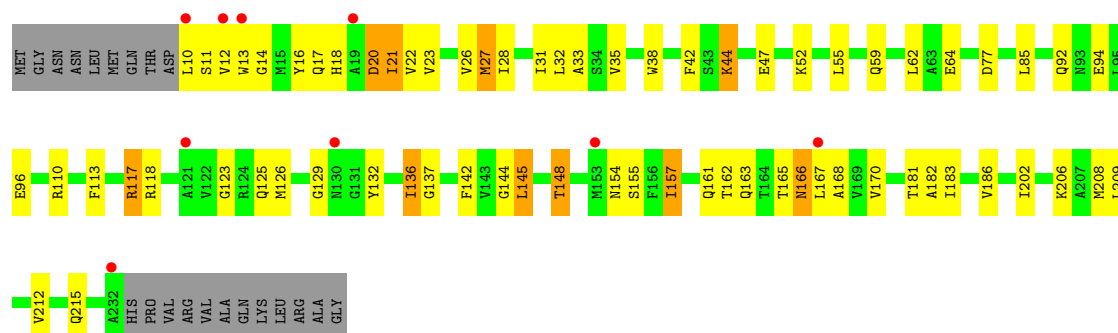
- Molecule 1: Biopolymer transport protein ExbB

Chain H: 3% 69% 20% 8%

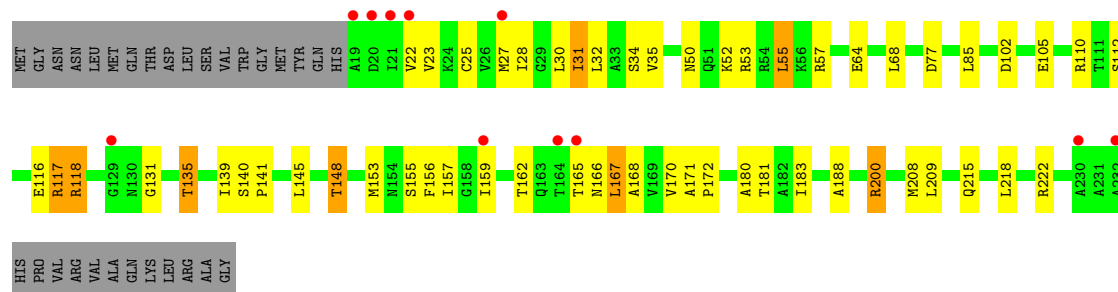




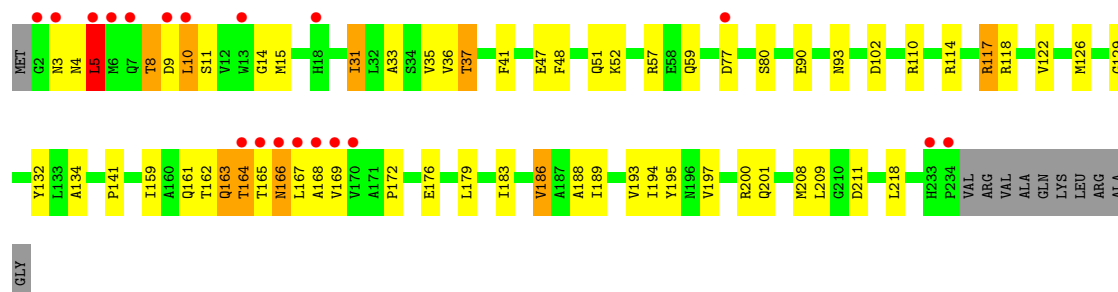
• Molecule 1: Biopolymer transport protein ExbB



• Molecule 1: Biopolymer transport protein ExbB



• Molecule 1: Biopolymer transport protein ExbB



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	137.17Å 104.78Å 149.36Å 90.00° 91.77° 90.00°	Depositor
Resolution (Å)	46.00 – 2.60 46.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	94.4 (46.00-2.60) 91.0 (46.00-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.08 (at 2.58Å)	Xtriage
Refinement program	PHENIX (1.10_2142: ???)	Depositor
R, R_{free}	0.211 , 0.258 0.212 , 0.255	Depositor DCC
R_{free} test set	2008 reflections (1.59%)	wwPDB-VP
Wilson B-factor (Å ²)	55.7	Xtriage
Anisotropy	0.185	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 71.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	16861	wwPDB-VP
Average B, all atoms (Å ²)	79.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.96% 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: MLY, CA, EPE

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	0.43	0/1764	0.65	0/2392
1	B	0.43	0/1707	0.73	3/2315 (0.1%)
1	C	0.40	0/1661	0.64	0/2249
1	D	0.45	0/1625	0.65	0/2200
1	E	0.40	0/1619	0.75	4/2195 (0.2%)
1	F	0.44	0/1662	0.65	0/2253
1	G	0.44	0/1747	0.69	0/2370
1	H	0.42	0/1715	0.66	0/2324
1	I	0.45	0/1690	0.67	0/2289
1	J	0.49	0/1605	0.69	0/2174
All	All	0.44	0/16795	0.68	7/22761 (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	A	0	1
1	C	0	2
1	D	0	1
1	E	0	1
1	G	0	3
All	All	0	8

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	167	LEU	CA-C-N	9.36	138.55	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	167	LEU	C-N-CA	9.36	138.55	121.70
1	E	77	ASP	CA-C-N	8.29	137.37	121.54
1	E	77	ASP	C-N-CA	8.29	137.37	121.54
1	B	162	THR	N-CA-C	5.60	117.06	111.07

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	17	GLN	Peptide
1	C	18	HIS	Peptide
1	D	162	THR	Peptide
1	E	167	LEU	Peptide
1	G	161	GLN	Peptide

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	1749	0	1759	46	0
1	B	1692	0	1714	41	0
1	C	1651	0	1679	31	0
1	D	1615	0	1651	38	0
1	E	1609	0	1636	41	0
1	F	1651	0	1663	45	0
1	G	1731	0	1734	42	0
1	H	1700	0	1729	31	0
1	I	1678	0	1708	55	0
1	J	1596	0	1630	45	0
2	D	15	0	17	0	0
2	F	15	0	17	1	0
2	I	15	0	17	1	0
3	A	1	0	0	0	0
3	I	1	0	0	0	0
4	A	10	0	0	0	0
4	B	14	0	0	4	0
4	C	11	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	12	0	0	1	0
4	E	16	0	0	0	0
4	F	16	0	0	1	0
4	G	15	0	0	1	0
4	H	13	0	0	1	0
4	I	15	0	0	1	0
4	J	20	0	0	0	0
All	All	16861	0	16954	366	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 11.

The worst 5 of 366 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:B:117:ARG:NH1	1:C:211:ASP:OD1	1.88	1.06
1:H:136:ILE:O	1:H:140:SER:HB3	1.68	0.93
1:B:90:GLU:HG3	1:B:118:ARG:HH22	1.33	0.92
1:C:196:ASN:HB3	1:C:200:ARG:HH11	1.39	0.87
1:A:141:PRO:HD3	1:A:188:ALA:HB2	1.54	0.87

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	230/244 (94%)	216 (94%)	12 (5%)	2 (1%)	14	30
1	B	222/244 (91%)	215 (97%)	7 (3%)	0	100	100
1	C	219/244 (90%)	217 (99%)	2 (1%)	0	100	100
1	D	212/244 (87%)	206 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	213/244 (87%)	206 (97%)	7 (3%)	0	100	100
1	F	220/244 (90%)	214 (97%)	6 (3%)	0	100	100
1	G	228/244 (93%)	222 (97%)	6 (3%)	0	100	100
1	H	222/244 (91%)	214 (96%)	7 (3%)	1 (0%)	24	46
1	I	220/244 (90%)	215 (98%)	3 (1%)	2 (1%)	14	30
1	J	211/244 (86%)	207 (98%)	4 (2%)	0	100	100
All	All	2197/2440 (90%)	2132 (97%)	60 (3%)	5 (0%)	43	66

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	I	12	VAL
1	A	168	ALA
1	H	68	LEU
1	I	21	ILE
1	A	166	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	176/189 (93%)	160 (91%)	16 (9%)	9	19
1	B	171/189 (90%)	152 (89%)	19 (11%)	6	12
1	C	166/189 (88%)	149 (90%)	17 (10%)	7	15
1	D	164/189 (87%)	143 (87%)	21 (13%)	4	8
1	E	162/189 (86%)	134 (83%)	28 (17%)	2	3
1	F	163/189 (86%)	152 (93%)	11 (7%)	15	33
1	G	173/189 (92%)	159 (92%)	14 (8%)	11	24
1	H	173/189 (92%)	152 (88%)	21 (12%)	5	10
1	I	170/189 (90%)	153 (90%)	17 (10%)	7	16

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	J	160/189 (85%)	140 (88%)	20 (12%)	4 9
All	All	1678/1890 (89%)	1494 (89%)	184 (11%)	6 13

5 of 184 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	60	GLN
1	I	145	LEU
1	H	118	ARG
1	H	209	LEU
1	J	31	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	72	ASN
1	H	154	ASN
1	I	201	GLN
1	I	92	GLN
1	I	154	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

10 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	MLY	G	108	1	9,10,11	0.83	0	6,11,13	0.77	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MLY	A	108	1	9,10,11	0.60	0	6,11,13	0.78	0
1	MLY	F	108	1	9,10,11	0.67	0	6,11,13	0.79	0
1	MLY	C	108	1	9,10,11	0.88	0	6,11,13	0.77	0
1	MLY	J	108	1	9,10,11	0.66	0	6,11,13	0.72	0
1	MLY	E	108	1	9,10,11	0.82	0	6,11,13	0.80	0
1	MLY	B	108	1	9,10,11	0.76	0	6,11,13	0.79	0
1	MLY	D	108	1	9,10,11	0.83	0	6,11,13	0.77	0
1	MLY	I	108	1	9,10,11	0.77	0	6,11,13	0.63	0
1	MLY	H	108	1	9,10,11	0.96	0	6,11,13	0.93	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
1	MLY	G	108	1	-	0/8/9/11	-
1	MLY	A	108	1	-	0/8/9/11	-
1	MLY	F	108	1	-	1/8/9/11	-
1	MLY	C	108	1	-	1/8/9/11	-
1	MLY	J	108	1	-	0/8/9/11	-
1	MLY	E	108	1	-	1/8/9/11	-
1	MLY	B	108	1	-	1/8/9/11	-
1	MLY	D	108	1	-	2/8/9/11	-
1	MLY	I	108	1	-	0/8/9/11	-
1	MLY	H	108	1	-	1/8/9/11	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	D	108	MLY	CD-CE-NZ-CH2
1	E	108	MLY	CD-CE-NZ-CH2
1	F	108	MLY	CD-CE-NZ-CH2
1	C	108	MLY	CD-CE-NZ-CH2
1	H	108	MLY	CD-CE-NZ-CH2

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 for Mogul analysis.

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	EPE	D	301	-	15,15,15	0.94	1 (6%)	19,20,20	1.76	7 (36%)
2	EPE	F	301	-	15,15,15	0.92	1 (6%)	19,20,20	2.04	5 (26%)
2	EPE	I	302	-	15,15,15	0.91	1 (6%)	19,20,20	1.91	5 (26%)

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	EPE	D	301	-	-	3/9/19/19	0/1/1/1
2	EPE	F	301	-	-	4/9/19/19	0/1/1/1
2	EPE	I	302	-	-	3/9/19/19	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	301	EPE	C10-S	3.25	1.82	1.77
2	I	302	EPE	C10-S	3.09	1.81	1.77
2	D	301	EPE	C10-S	2.87	1.81	1.77

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	301	EPE	C5-N4-C3	5.92	121.58	108.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	302	EPE	C5-N4-C3	4.26	118.01	108.84
2	I	302	EPE	C7-N4-C5	3.92	121.69	111.24
2	D	301	EPE	C5-N4-C3	3.85	117.13	108.84
2	F	301	EPE	C7-N4-C5	3.44	120.41	111.24

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	301	EPE	C9-C10-S-O2S
2	D	301	EPE	C9-C10-S-O3S
2	F	301	EPE	C9-C10-S-O2S
2	F	301	EPE	C9-C10-S-O3S
2	I	302	EPE	C8-C7-N4-C5

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	301	EPE	1	0
2	I	302	EPE	1	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	232/244 (95%)	0.35	19 (8%)	17 14	42, 74, 134, 191	0
1	B	224/244 (91%)	0.11	6 (2%)	56 50	46, 76, 121, 164	0
1	C	221/244 (90%)	0.20	10 (4%)	38 32	42, 77, 115, 160	0
1	D	214/244 (87%)	0.09	9 (4%)	40 35	41, 68, 128, 200	0
1	E	215/244 (88%)	0.18	12 (5%)	30 24	42, 76, 134, 164	0
1	F	222/244 (90%)	0.29	16 (7%)	21 17	43, 73, 147, 218	0
1	G	228/244 (93%)	0.36	14 (6%)	27 22	32, 76, 132, 214	2 (0%)
1	H	224/244 (91%)	0.14	8 (3%)	46 40	46, 75, 116, 197	0
1	I	222/244 (90%)	0.17	9 (4%)	41 36	45, 77, 123, 155	0
1	J	213/244 (87%)	0.07	11 (5%)	33 27	40, 70, 142, 181	0
All	All	2215/2440 (90%)	0.20	114 (5%)	33 28	32, 75, 132, 218	2 (0%)

The worst 5 of 114 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	165	THR	5.1
1	A	9	ASP	4.9
1	I	10	LEU	4.8
1	C	16	TYR	4.8
1	F	164	THR	4.5

6.2 Non-standard residues in protein, DNA, RNA chains [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($\text{\AA}^2$)	Q<0.9
1	MLY	G	108	11/12	0.95	0.11	32,43,52,53	0
1	MLY	F	108	11/12	0.97	0.07	44,49,62,66	0
1	MLY	C	108	11/12	0.97	0.07	38,44,60,61	0
1	MLY	H	108	11/12	0.97	0.10	35,45,57,60	0
1	MLY	I	108	11/12	0.97	0.08	33,39,65,67	0
1	MLY	J	108	11/12	0.97	0.08	31,40,59,65	0
1	MLY	E	108	11/12	0.98	0.07	52,56,68,73	0
1	MLY	B	108	11/12	0.98	0.07	38,43,50,53	0
1	MLY	D	108	11/12	0.98	0.08	36,40,49,56	0
1	MLY	A	108	11/12	0.98	0.06	33,37,55,65	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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($\text{\AA}^2$)	Q<0.9
2	EPE	D	301	15/15	0.67	0.17	95,119,159,163	0
2	EPE	I	302	15/15	0.79	0.17	85,127,167,169	0
2	EPE	F	301	15/15	0.81	0.19	88,114,157,161	0
3	CA	I	301	1/1	0.89	0.11	104,104,104,104	0
3	CA	A	301	1/1	0.93	0.08	97,97,97,97	0

6.5 Other polymers [i](#)

There are no such residues in this entry.