



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 02:16 PM GMT

PDB ID : 3WJM
Title : Crystal structure of Bombyx mori Sp2/Sp3 heterohexamer
Authors : Yuan, Y.A.; Hou, Y.
Deposited on : 2013-10-11
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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

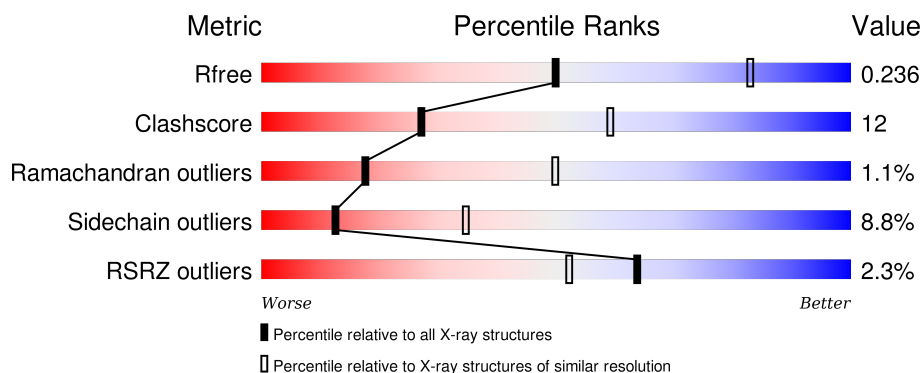
1 Overall quality at a glance ⓘ

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}	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (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. 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	703	<div> <div>3%</div> <div>71% 22% 5%</div> </div>
1	E	703	<div> <div>3%</div> <div>72% 20% 5%</div> </div>
1	F	703	<div> <div>3%</div> <div>67% 24% 5%</div> </div>
2	B	696	<div> <div>2%</div> <div>67% 24% 5%</div> </div>
2	C	696	<div> <div>2%</div> <div>68% 23% 5%</div> </div>

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Mol	Chain	Length	Quality of chain
2	D	696	<div><div><div>%</div><div><div></div></div><div>69%</div><div>24%</div><div><div></div><div></div></div></div></div>

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 34590 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 Arylphorin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	670	Total	C	N	O	S	0	0	0
			5681	3734	892	1030	25			
1	E	669	Total	C	N	O	S	0	0	0
			5669	3725	891	1028	25			
1	F	669	Total	C	N	O	S	0	0	0
			5669	3725	891	1028	25			

- Molecule 2 is a protein called Silkworm storage protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	668	Total	C	N	O	S	0	0	0
			5669	3745	877	1021	26			
2	C	668	Total	C	N	O	S	0	0	0
			5669	3745	877	1021	26			
2	D	672	Total	C	N	O	S	0	0	0
			5703	3767	881	1029	26			

- Molecule 3 is a polymer of unknown type called SUGAR (5-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	5	Total	C	N	O	0	0
			61	34	2	25		
3	F	5	Total	C	N	O	0	0
			61	34	2	25		

- Molecule 4 is a polymer of unknown type called SUGAR (5-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	5	Total	C	N	O	0	0
			61	34	2	25		

- Molecule 5 is a polymer of unknown type called SUGAR (6-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	C	6	Total	C	N	O	0	0
			72	40	2	30		

- Molecule 6 is a polymer of unknown type called SUGAR (7-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	D	7	Total	C	N	O	0	0
			83	46	2	35		

- Molecule 7 is a polymer of unknown type called SUGAR (6-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	E	6	Total	C	N	O	0	0
			72	40	2	30		

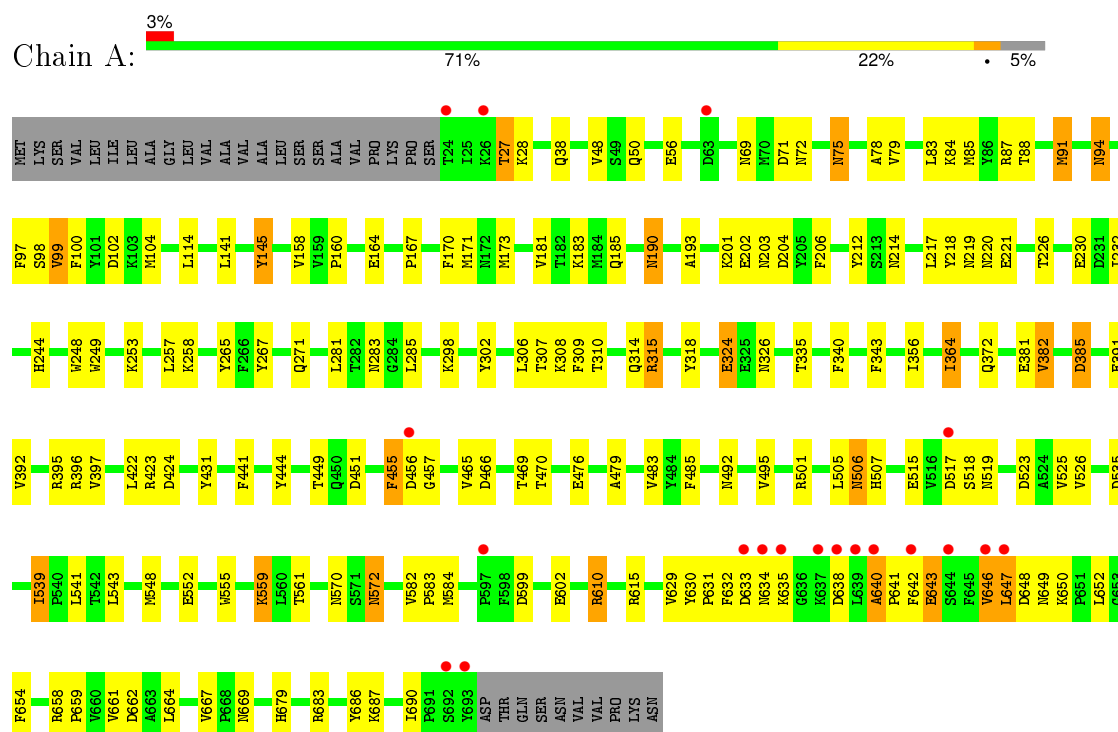
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	29	Total	O	0	0
			29	29		
8	B	14	Total	O	0	0
			14	14		
8	C	19	Total	O	0	0
			19	19		
8	D	27	Total	O	0	0
			27	27		
8	E	21	Total	O	0	0
			21	21		
8	F	10	Total	O	0	0
			10	10		

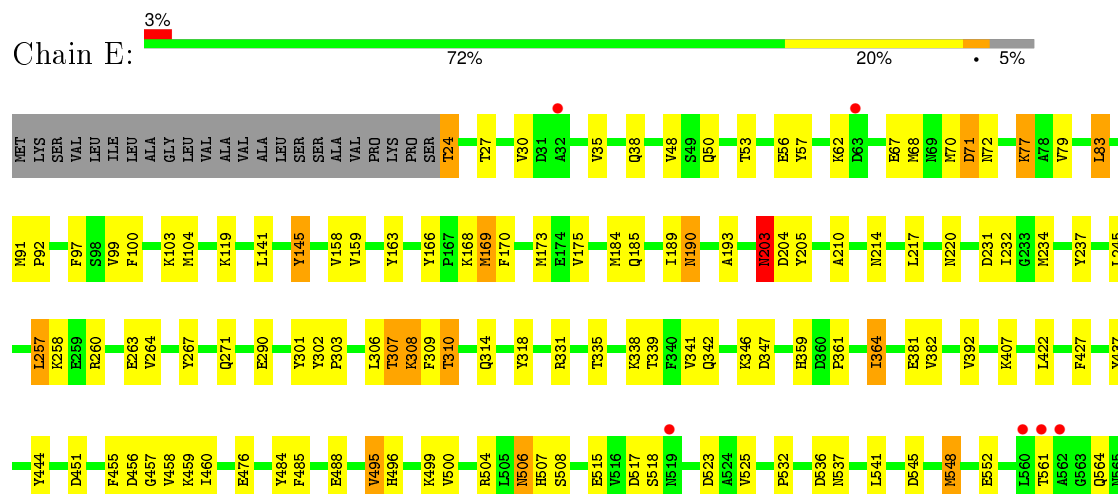
3 Residue-property plots

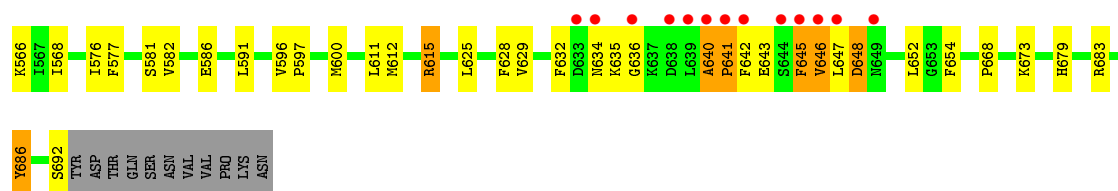
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Arylphorin

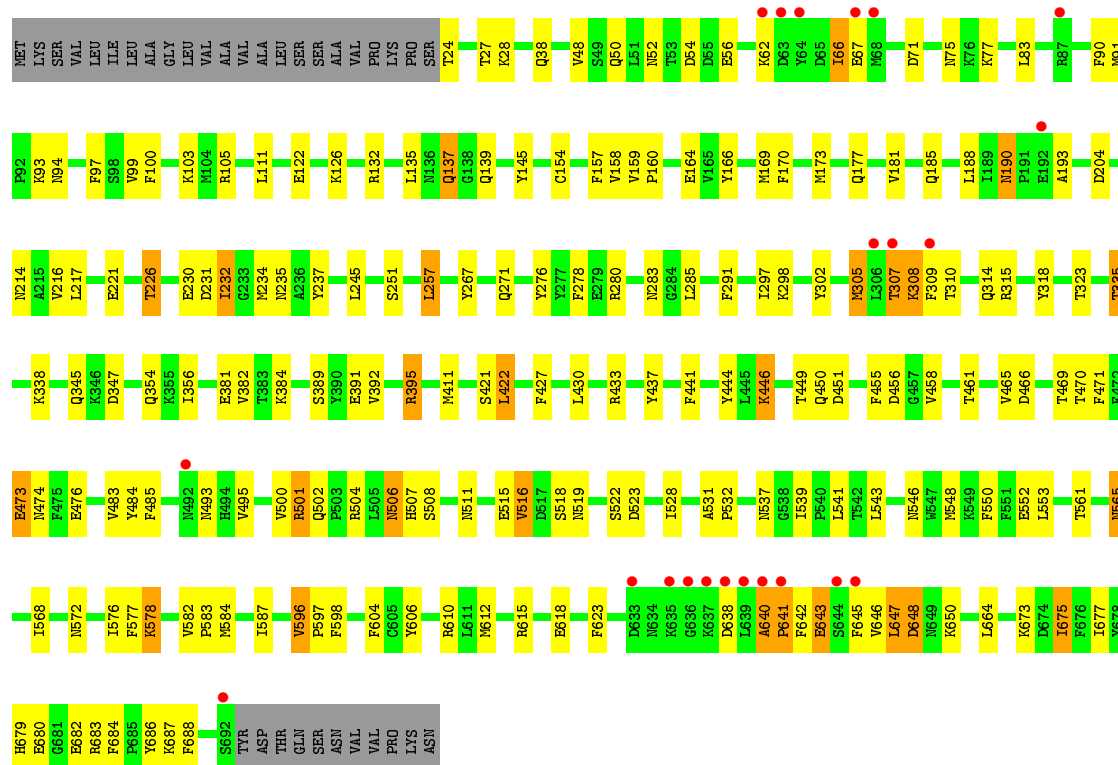


• Molecule 1: Arylphorin

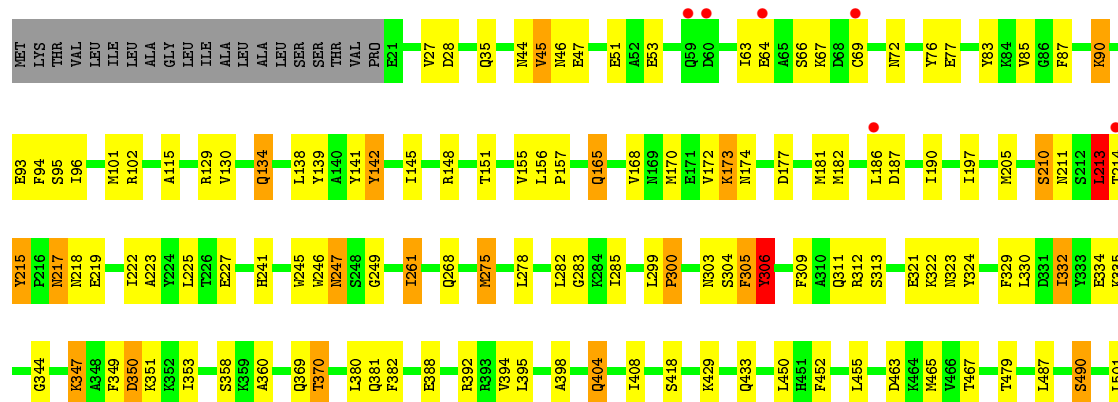


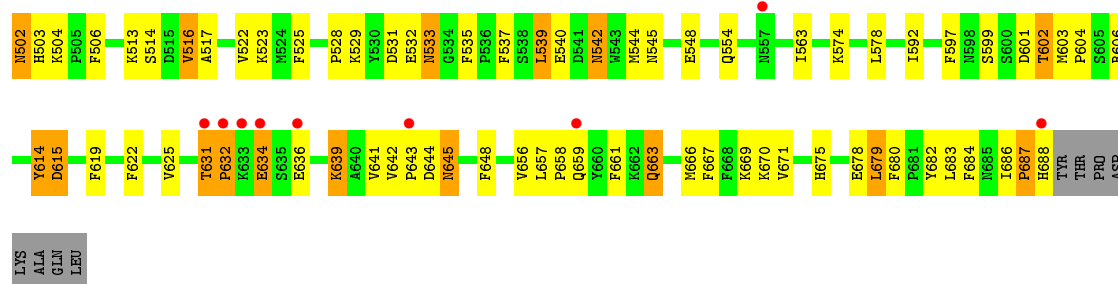


• Molecule 1: Arylphorin

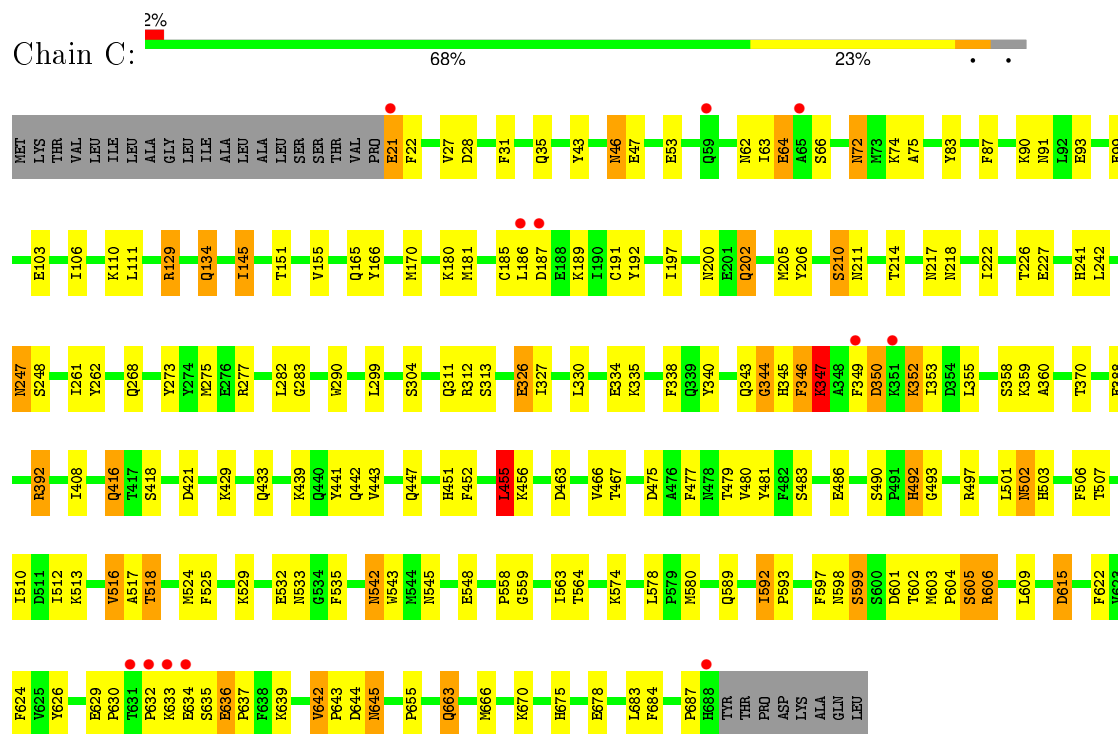


• Molecule 2: Silkworm storage protein

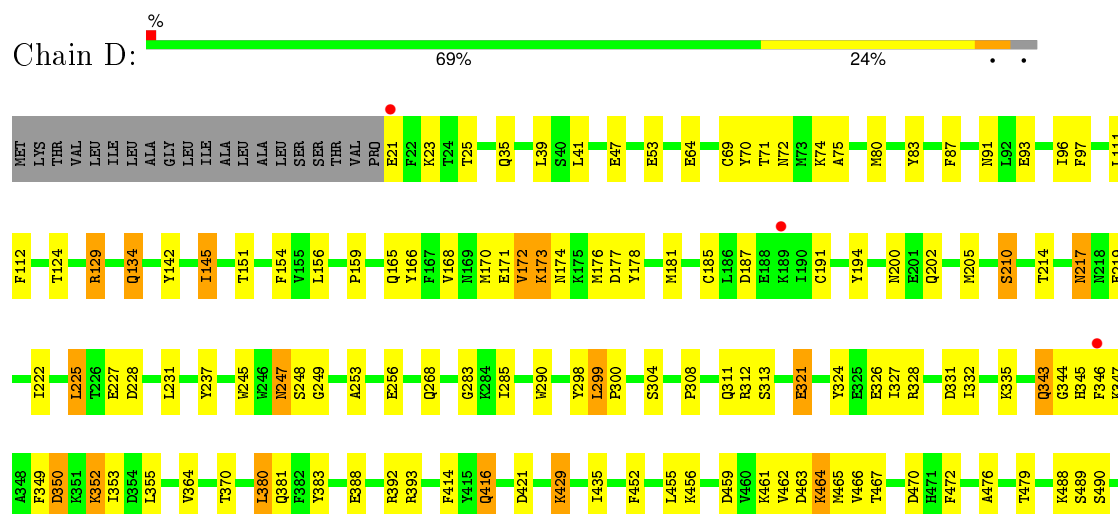


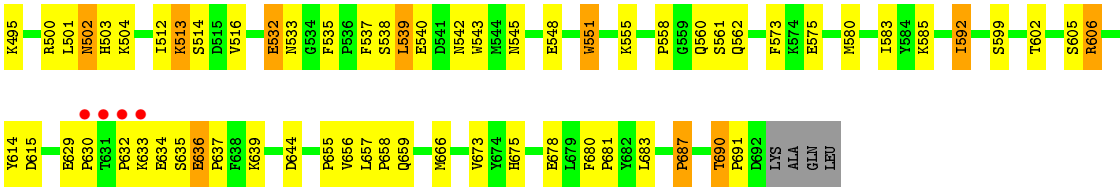


• Molecule 2: Silkworm storage protein



• Molecule 2: Silkworm storage protein





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	92.06Å 205.02Å 119.71Å 90.00° 103.00° 90.00°	Depositor
Resolution (Å)	48.37 – 2.80 48.37 – 2.80	Depositor EDS
% Data completeness (in resolution range)	96.5 (48.37-2.80) 96.5 (48.37-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.81 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.172 , 0.237 0.171 , 0.236	Depositor DCC
R_{free} test set	5121 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	50.2	Xtriage
Anisotropy	0.238	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 43.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 102314 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	34590	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.42% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: BMA, NAG, MAN

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	0.62	0/5863	0.76	3/7934 (0.0%)
1	E	0.61	0/5850	0.74	1/7916 (0.0%)
1	F	0.58	0/5850	0.74	2/7916 (0.0%)
2	B	0.61	0/5865	0.76	1/7945 (0.0%)
2	C	0.64	0/5865	0.78	5/7945 (0.1%)
2	D	0.65	1/5901 (0.0%)	0.78	2/7996 (0.0%)
All	All	0.62	1/35194 (0.0%)	0.76	14/47652 (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
2	B	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	171	GLU	CD-OE2	-5.18	1.20	1.25

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	213	LEU	CA-CB-CG	9.09	136.20	115.30
1	A	315	ARG	NE-CZ-NH2	-8.73	115.93	120.30
2	C	392	ARG	NE-CZ-NH2	-7.33	116.64	120.30
1	F	315	ARG	NE-CZ-NH2	-6.68	116.96	120.30
2	D	171	GLU	OE1-CD-OE2	-6.65	115.32	123.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	246	TRP	Peptide
2	B	614	TYR	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	5681	0	5434	125	0
1	E	5669	0	5425	117	0
1	F	5669	0	5425	150	0
2	B	5669	0	5390	193	0
2	C	5669	0	5392	145	0
2	D	5703	0	5419	140	0
3	A	61	0	52	0	0
3	F	61	0	52	0	0
4	B	61	0	52	3	0
5	C	72	0	61	0	0
6	D	83	0	70	0	0
7	E	72	0	61	1	0
8	A	29	0	0	0	0
8	B	14	0	0	0	0
8	C	19	0	0	1	0
8	D	27	0	0	0	0
8	E	21	0	0	0	0
8	F	10	0	0	1	0
All	All	34590	0	32833	809	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 12.

The worst 5 of 809 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)
2:B:631:THR:HB	2:B:632:PRO:CD	1.72	1.19

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:210:SER:HB2	2:B:214:THR:HG21	1.27	1.16
2:B:631:THR:CB	2:B:632:PRO:HD2	1.77	1.15
1:F:531:ALA:HB2	1:F:550:PHE:CD2	1.83	1.13
1:E:97:PHE:HA	1:E:104:MET:HE1	1.31	1.12

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	668/703 (95%)	629 (94%)	33 (5%)	6 (1%)	21	55
1	E	667/703 (95%)	628 (94%)	32 (5%)	7 (1%)	19	52
1	F	667/703 (95%)	630 (94%)	34 (5%)	3 (0%)	39	74
2	B	666/696 (96%)	619 (93%)	33 (5%)	14 (2%)	9	29
2	C	666/696 (96%)	633 (95%)	24 (4%)	9 (1%)	14	42
2	D	670/696 (96%)	637 (95%)	27 (4%)	6 (1%)	21	55
All	All	4004/4197 (95%)	3776 (94%)	183 (5%)	45 (1%)	17	50

5 of 45 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	308	LYS
2	B	247	ASN
2	B	632	PRO
2	B	636	GLU
2	B	687	PRO

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	610/638 (96%)	563 (92%)	47 (8%)	16	41
1	E	609/638 (96%)	563 (92%)	46 (8%)	16	42
1	F	609/638 (96%)	548 (90%)	61 (10%)	9	27
2	B	606/629 (96%)	548 (90%)	58 (10%)	10	29
2	C	606/629 (96%)	550 (91%)	56 (9%)	11	32
2	D	610/629 (97%)	556 (91%)	54 (9%)	12	34
All	All	3650/3801 (96%)	3328 (91%)	322 (9%)	12	35

5 of 322 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	535	PHE
2	D	299	LEU
1	F	493	ASN
2	C	597	PHE
2	D	71	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 103 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	471	HIS
2	D	174	ASN
1	F	493	ASN
2	C	502	ASN
2	C	663	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

34 carbohydrates 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
3	NAG	A	801	1,3	14,14,15	0.97	1 (7%)	15,19,21	2.01	4 (26%)
3	NAG	A	802	3	14,14,15	0.83	1 (7%)	15,19,21	2.01	5 (33%)
3	BMA	A	803	3	11,11,12	0.81	0	14,15,17	2.34	4 (28%)
3	MAN	A	804	3	11,11,12	0.71	0	14,15,17	1.23	1 (7%)
3	BMA	A	805	3	11,11,12	1.07	1 (9%)	14,15,17	3.50	4 (28%)
4	NAG	B	801	2,4	14,14,15	0.73	1 (7%)	15,19,21	1.68	2 (13%)
4	NAG	B	802	4	14,14,15	0.62	0	15,19,21	1.49	2 (13%)
4	BMA	B	803	4	11,11,12	1.28	1 (9%)	14,15,17	1.56	3 (21%)
4	BMA	B	804	4	11,11,12	0.62	0	14,15,17	1.27	1 (7%)
4	MAN	B	805	4	11,11,12	0.70	0	14,15,17	1.24	1 (7%)
5	NAG	C	801	2,5	14,14,15	0.59	0	15,19,21	1.80	2 (13%)
5	NAG	C	802	5	14,14,15	0.75	1 (7%)	15,19,21	1.53	1 (6%)
5	BMA	C	803	5	11,11,12	0.68	0	14,15,17	2.36	5 (35%)
5	MAN	C	804	5	11,11,12	0.77	0	14,15,17	2.03	3 (21%)
5	MAN	C	805	5	11,11,12	0.93	1 (9%)	14,15,17	2.22	4 (28%)
5	MAN	C	806	5	11,11,12	0.66	0	14,15,17	2.72	5 (35%)
6	NAG	D	801	2,6	14,14,15	0.55	0	15,19,21	1.29	1 (6%)
6	NAG	D	802	6	14,14,15	0.87	1 (7%)	15,19,21	1.53	2 (13%)
6	BMA	D	803	6	11,11,12	0.47	0	14,15,17	1.96	3 (21%)
6	MAN	D	804	6	11,11,12	0.55	0	14,15,17	1.48	1 (7%)
6	MAN	D	805	6	11,11,12	0.82	0	14,15,17	1.33	2 (14%)
6	MAN	D	807	6	11,11,12	0.65	0	14,15,17	1.20	2 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	MAN	D	808	6	11,11,12	0.66	0	14,15,17	2.74	4 (28%)
7	NAG	E	801	1,7	14,14,15	0.69	0	15,19,21	1.31	2 (13%)
7	NAG	E	802	7	14,14,15	0.53	0	15,19,21	1.10	0
7	BMA	E	803	7	11,11,12	0.62	0	14,15,17	2.31	4 (28%)
7	BMA	E	804	7	11,11,12	0.69	0	14,15,17	2.29	3 (21%)
7	BMA	E	805	7	11,11,12	0.94	1 (9%)	14,15,17	2.54	3 (21%)
7	MAN	E	806	7	11,11,12	0.82	0	14,15,17	1.78	2 (14%)
3	NAG	F	801	1,3	14,14,15	0.52	0	15,19,21	1.83	4 (26%)
3	NAG	F	802	3	14,14,15	0.54	0	15,19,21	1.27	1 (6%)
3	BMA	F	803	3	11,11,12	0.45	0	14,15,17	1.31	3 (21%)
3	MAN	F	804	3	11,11,12	0.84	1 (9%)	14,15,17	1.66	3 (21%)
3	BMA	F	805	3	11,11,12	0.71	0	14,15,17	2.64	3 (21%)

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
3	NAG	A	801	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	802	3	-	0/6/23/26	0/1/1/1
3	BMA	A	803	3	-	0/2/19/22	0/1/1/1
3	MAN	A	804	3	-	0/2/19/22	0/1/1/1
3	BMA	A	805	3	-	0/2/19/22	0/1/1/1
4	NAG	B	801	2,4	-	0/6/23/26	0/1/1/1
4	NAG	B	802	4	-	0/6/23/26	0/1/1/1
4	BMA	B	803	4	-	0/2/19/22	0/1/1/1
4	BMA	B	804	4	-	0/2/19/22	0/1/1/1
4	MAN	B	805	4	-	0/2/19/22	0/1/1/1
5	NAG	C	801	2,5	-	0/6/23/26	0/1/1/1
5	NAG	C	802	5	-	0/6/23/26	0/1/1/1
5	BMA	C	803	5	-	0/2/19/22	0/1/1/1
5	MAN	C	804	5	-	0/2/19/22	0/1/1/1
5	MAN	C	805	5	-	0/2/19/22	0/1/1/1
5	MAN	C	806	5	-	0/2/19/22	0/1/1/1
6	NAG	D	801	2,6	-	0/6/23/26	0/1/1/1
6	NAG	D	802	6	-	0/6/23/26	0/1/1/1
6	BMA	D	803	6	-	0/2/19/22	0/1/1/1
6	MAN	D	804	6	-	0/2/19/22	0/1/1/1
6	MAN	D	805	6	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	MAN	D	807	6	-	0/2/19/22	0/1/1/1
6	MAN	D	808	6	-	0/2/19/22	0/1/1/1
7	NAG	E	801	1,7	-	0/6/23/26	0/1/1/1
7	NAG	E	802	7	-	0/6/23/26	0/1/1/1
7	BMA	E	803	7	-	0/2/19/22	0/1/1/1
7	BMA	E	804	7	-	0/2/19/22	0/1/1/1
7	BMA	E	805	7	-	0/2/19/22	0/1/1/1
7	MAN	E	806	7	-	0/2/19/22	0/1/1/1
3	NAG	F	801	1,3	-	0/6/23/26	0/1/1/1
3	NAG	F	802	3	-	0/6/23/26	0/1/1/1
3	BMA	F	803	3	-	0/2/19/22	0/1/1/1
3	MAN	F	804	3	-	0/2/19/22	0/1/1/1
3	BMA	F	805	3	-	0/2/19/22	0/1/1/1

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	803	BMA	O5-C1	-3.75	1.37	1.43
3	A	801	NAG	O5-C1	-2.62	1.39	1.43
6	D	802	NAG	O5-C1	-2.27	1.39	1.43
4	B	801	NAG	O5-C1	-2.23	1.40	1.43
5	C	802	NAG	O5-C1	-2.15	1.40	1.43

The worst 5 of 90 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	805	BMA	C1-O5-C5	-9.69	99.95	112.25
3	A	801	NAG	C2-N2-C7	-5.62	115.82	123.04
3	A	802	NAG	C3-C4-C5	-4.78	101.87	110.20
3	A	805	BMA	C3-C4-C5	-4.57	102.24	110.20
6	D	802	NAG	C2-N2-C7	-4.38	117.41	123.04

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	801	NAG	1	0
4	B	802	NAG	2	0
4	B	803	BMA	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	E	804	BMA	1	0
7	E	805	BMA	1	0

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	A	670/703 (95%)	-0.51	19 (2%) 56 44	20, 43, 85, 213	0
1	E	669/703 (95%)	-0.37	19 (2%) 56 44	24, 50, 91, 234	0
1	F	669/703 (95%)	-0.22	22 (3%) 50 38	27, 59, 102, 206	0
2	B	668/696 (95%)	-0.34	15 (2%) 65 54	25, 54, 92, 167	0
2	C	668/696 (95%)	-0.46	12 (1%) 71 61	24, 46, 86, 142	0
2	D	672/696 (96%)	-0.51	7 (1%) 84 77	20, 42, 82, 159	0
All	All	4016/4197 (95%)	-0.40	94 (2%) 64 52	20, 49, 92, 234	0

The worst 5 of 94 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	21	GLU	7.2
1	E	641	PRO	7.2
1	A	638	ASP	6.7
1	F	640	ALA	6.7
1	A	644	SER	6.3

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 ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
3	NAG	A	801	14/15	0.98	0.11	-0.53	27,30,32,36	0
3	NAG	F	802	14/15	0.96	0.15	-0.59	55,60,65,68	0
4	NAG	B	801	14/15	0.96	0.14	-0.61	48,51,58,59	0
5	NAG	C	802	14/15	0.94	0.15	-0.79	51,57,63,70	0
7	NAG	E	801	14/15	0.98	0.10	-0.86	36,38,42,43	0
3	NAG	A	802	14/15	0.97	0.12	-0.90	37,42,49,49	0
6	NAG	D	802	14/15	0.96	0.13	-0.93	44,47,53,60	0
5	NAG	C	801	14/15	0.97	0.11	-0.95	40,43,46,49	0
3	NAG	F	801	14/15	0.96	0.11	-1.02	47,51,56,56	0
6	NAG	D	801	14/15	0.97	0.10	-1.09	36,37,39,43	0
7	NAG	E	802	14/15	0.96	0.11	-1.20	45,48,55,56	0
4	NAG	B	802	14/15	0.94	0.13	-1.48	58,66,76,83	0
5	MAN	C	805	11/12	0.83	0.18	-	92,96,101,105	0
6	BMA	D	803	11/12	0.90	0.18	-	66,77,88,89	0
6	MAN	D	808	11/12	0.76	0.35	-	98,111,114,115	0
3	MAN	A	804	11/12	0.85	0.17	-	66,67,72,74	0
4	BMA	B	803	11/12	0.90	0.16	-	89,95,100,101	0
7	BMA	E	803	11/12	0.92	0.13	-	57,65,73,74	0
5	MAN	C	806	11/12	0.66	0.34	-	102,112,115,115	0
5	BMA	C	803	11/12	0.89	0.16	-	72,82,88,93	0
3	BMA	F	805	11/12	0.69	0.32	-	110,121,124,125	0
3	BMA	A	805	11/12	0.80	0.20	-	82,89,96,102	0
7	BMA	E	805	11/12	0.70	0.25	-	103,108,112,114	0
5	MAN	C	804	11/12	0.69	0.28	-	88,94,97,98	0
3	BMA	F	803	11/12	0.89	0.14	-	71,74,79,87	0
4	BMA	B	804	11/12	0.88	0.21	-	104,108,110,110	0
6	MAN	D	807	11/12	0.75	0.20	-	98,100,105,111	0
7	BMA	E	804	11/12	0.85	0.17	-	78,88,92,99	0
4	MAN	B	805	11/12	0.77	0.17	-	91,97,100,100	0
6	MAN	D	804	11/12	0.92	0.22	-	89,94,100,106	0
3	MAN	F	804	11/12	0.86	0.18	-	95,97,104,108	0
3	BMA	A	803	11/12	0.93	0.14	-	50,59,65,72	0
6	MAN	D	805	11/12	0.72	0.30	-	95,110,118,122	0
7	MAN	E	806	11/12	0.85	0.16	-	69,73,76,77	0

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.