



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:19 PM GMT

PDB ID : 4OFY
Title : Crystal Structure of the Complex of SYG-1 D1-D2 and SYG-2 D1-D4
Authors : Ozkan, E.; Garcia, K.C.
Deposited on : 2014-01-15
Resolution : 3.30 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
<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

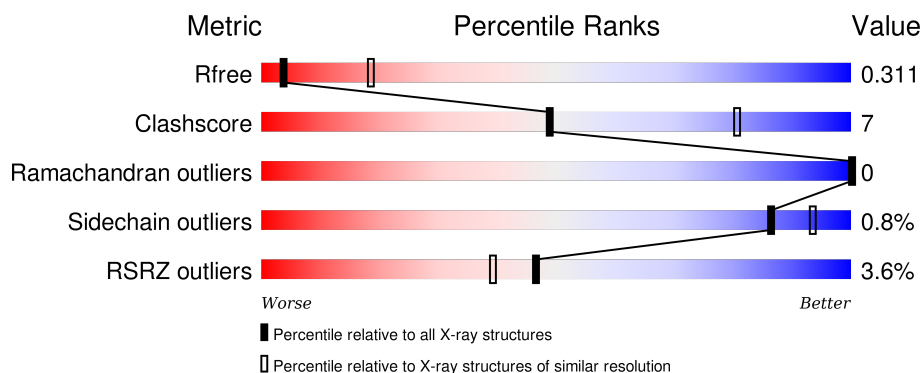
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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	2060 (3.40-3.20)
Clashscore	102246	1058 (3.38-3.22)
Ramachandran outliers	100387	1038 (3.38-3.22)
Sidechain outliers	100360	1037 (3.38-3.22)
RSRZ outliers	91569	2070 (3.40-3.20)

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	262	<div> <div>6%</div> <div> <div></div> <div>76%</div> <div>12%</div> <div>12%</div> </div> </div>
1	B	262	<div> <div>2%</div> <div> <div></div> <div>75%</div> <div>11%</div> <div>13%</div> </div> </div>
1	C	262	<div> <div>4%</div> <div> <div></div> <div>76%</div> <div>10%</div> <div>13%</div> </div> </div>
2	D	420	<div> <div>2%</div> <div> <div></div> <div>78%</div> <div>19%</div> <div>.</div> </div> </div>
2	E	420	<div> <div>3%</div> <div> <div></div> <div>76%</div> <div>20%</div> <div>.</div> </div> </div>

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Mol	Chain	Length	Quality of chain
2	F	420	

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
4	NAG	E	1502	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 14816 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 SYG-1, isoform b.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	230	Total	C	N	O	S	0	0	0
			1767	1109	310	340	8			
1	B	227	Total	C	N	O	S	0	0	0
			1752	1100	307	337	8			
1	C	227	Total	C	N	O	S	0	0	0
			1752	1100	307	337	8			

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	16	ALA	-	EXPRESSION TAG	UNP B1Q236
A	17	ASP	-	EXPRESSION TAG	UNP B1Q236
A	18	PRO	-	EXPRESSION TAG	UNP B1Q236
A	272	HIS	-	EXPRESSION TAG	UNP B1Q236
A	273	HIS	-	EXPRESSION TAG	UNP B1Q236
A	274	HIS	-	EXPRESSION TAG	UNP B1Q236
A	275	HIS	-	EXPRESSION TAG	UNP B1Q236
A	276	HIS	-	EXPRESSION TAG	UNP B1Q236
A	277	HIS	-	EXPRESSION TAG	UNP B1Q236
B	16	ALA	-	EXPRESSION TAG	UNP B1Q236
B	17	ASP	-	EXPRESSION TAG	UNP B1Q236
B	18	PRO	-	EXPRESSION TAG	UNP B1Q236
B	272	HIS	-	EXPRESSION TAG	UNP B1Q236
B	273	HIS	-	EXPRESSION TAG	UNP B1Q236
B	274	HIS	-	EXPRESSION TAG	UNP B1Q236
B	275	HIS	-	EXPRESSION TAG	UNP B1Q236
B	276	HIS	-	EXPRESSION TAG	UNP B1Q236
B	277	HIS	-	EXPRESSION TAG	UNP B1Q236
C	16	ALA	-	EXPRESSION TAG	UNP B1Q236
C	17	ASP	-	EXPRESSION TAG	UNP B1Q236
C	18	PRO	-	EXPRESSION TAG	UNP B1Q236
C	272	HIS	-	EXPRESSION TAG	UNP B1Q236
C	273	HIS	-	EXPRESSION TAG	UNP B1Q236

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Chain	Residue	Modelled	Actual	Comment	Reference
C	274	HIS	-	EXPRESSION TAG	UNP B1Q236
C	275	HIS	-	EXPRESSION TAG	UNP B1Q236
C	276	HIS	-	EXPRESSION TAG	UNP B1Q236
C	277	HIS	-	EXPRESSION TAG	UNP B1Q236

- Molecule 2 is a protein called Protein SYG-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	407	Total	C	N	O	S	0	0	0
			3045	1912	520	598	15			
2	E	407	Total	C	N	O	S	0	0	0
			3042	1910	519	598	15			
2	F	407	Total	C	N	O	S	0	0	0
			3057	1921	522	599	15			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	17	ALA	-	EXPRESSION TAG	UNP Q9U3P2
D	18	ASP	-	EXPRESSION TAG	UNP Q9U3P2
D	19	PRO	-	EXPRESSION TAG	UNP Q9U3P2
D	391	CYS	ASN	ENGINEERED MUTATION	UNP Q9U3P2
D	431	HIS	-	EXPRESSION TAG	UNP Q9U3P2
D	432	HIS	-	EXPRESSION TAG	UNP Q9U3P2
D	433	HIS	-	EXPRESSION TAG	UNP Q9U3P2
D	434	HIS	-	EXPRESSION TAG	UNP Q9U3P2
D	435	HIS	-	EXPRESSION TAG	UNP Q9U3P2
D	436	HIS	-	EXPRESSION TAG	UNP Q9U3P2
E	17	ALA	-	EXPRESSION TAG	UNP Q9U3P2
E	18	ASP	-	EXPRESSION TAG	UNP Q9U3P2
E	19	PRO	-	EXPRESSION TAG	UNP Q9U3P2
E	391	CYS	ASN	ENGINEERED MUTATION	UNP Q9U3P2
E	431	HIS	-	EXPRESSION TAG	UNP Q9U3P2
E	432	HIS	-	EXPRESSION TAG	UNP Q9U3P2
E	433	HIS	-	EXPRESSION TAG	UNP Q9U3P2
E	434	HIS	-	EXPRESSION TAG	UNP Q9U3P2
E	435	HIS	-	EXPRESSION TAG	UNP Q9U3P2
E	436	HIS	-	EXPRESSION TAG	UNP Q9U3P2
F	17	ALA	-	EXPRESSION TAG	UNP Q9U3P2
F	18	ASP	-	EXPRESSION TAG	UNP Q9U3P2
F	19	PRO	-	EXPRESSION TAG	UNP Q9U3P2
F	391	CYS	ASN	ENGINEERED MUTATION	UNP Q9U3P2

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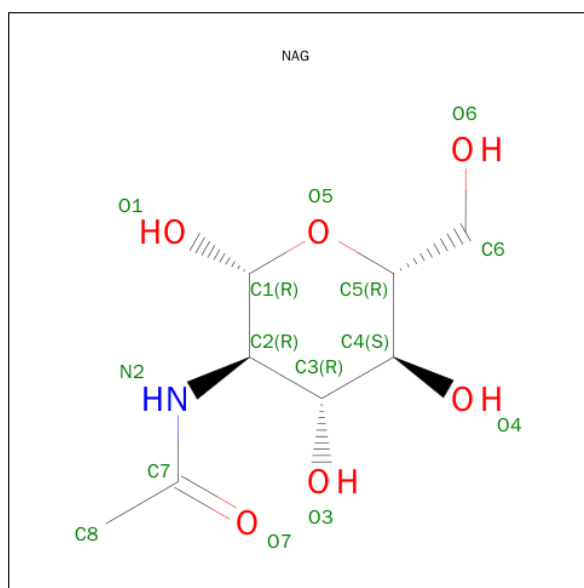
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Chain	Residue	Modelled	Actual	Comment	Reference
F	431	HIS	-	EXPRESSION TAG	UNP Q9U3P2
F	432	HIS	-	EXPRESSION TAG	UNP Q9U3P2
F	433	HIS	-	EXPRESSION TAG	UNP Q9U3P2
F	434	HIS	-	EXPRESSION TAG	UNP Q9U3P2
F	435	HIS	-	EXPRESSION TAG	UNP Q9U3P2
F	436	HIS	-	EXPRESSION TAG	UNP Q9U3P2

- Molecule 3 is a polymer of unknown type called SUGAR (2-MER).

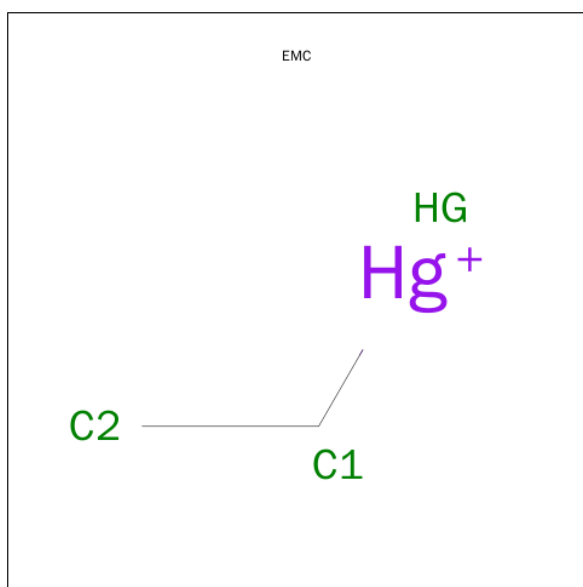
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	2	Total	C	N	O	0	0
			28	16	2	10		
3	B	2	Total	C	N	O	0	0
			28	16	2	10		
3	C	2	Total	C	N	O	0	0
			28	16	2	10		
3	D	2	Total	C	N	O	0	0
			28	16	2	10		
3	E	2	Total	C	N	O	0	0
			28	16	2	10		
3	F	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 4 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	1	Total C N O 14 8 1 5	0	0
4	D	1	Total C N O 14 8 1 5	0	0
4	D	1	Total C N O 14 8 1 5	0	0
4	D	1	Total C N O 14 8 1 5	0	0
4	D	1	Total C N O 14 8 1 5	0	0
4	D	1	Total C N O 14 8 1 5	0	0
4	E	1	Total C N O 14 8 1 5	0	0
4	E	1	Total C N O 14 8 1 5	0	0
4	E	1	Total C N O 14 8 1 5	0	0
4	E	1	Total C N O 14 8 1 5	0	0
4	E	1	Total C N O 14 8 1 5	0	0
4	F	1	Total C N O 14 8 1 5	0	0
4	F	1	Total C N O 14 8 1 5	0	0
4	F	1	Total C N O 14 8 1 5	0	0
4	F	1	Total C N O 14 8 1 5	0	0
4	F	1	Total C N O 14 8 1 5	0	0

- Molecule 5 is ETHYL MERCURY ION (three-letter code: EMC) (formula: C₂H₅Hg).

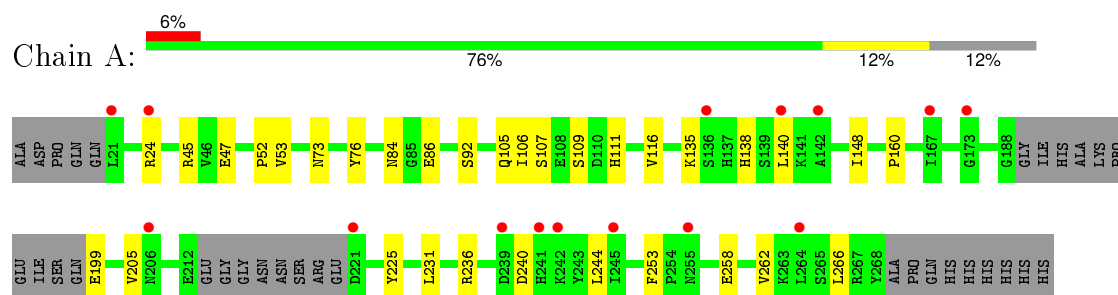


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	D	1	Total	C	Hg	0	0
			3	2	1		
5	E	1	Total	C	Hg	0	0
			3	2	1		
5	F	1	Total	C	Hg	0	0
			3	2	1		

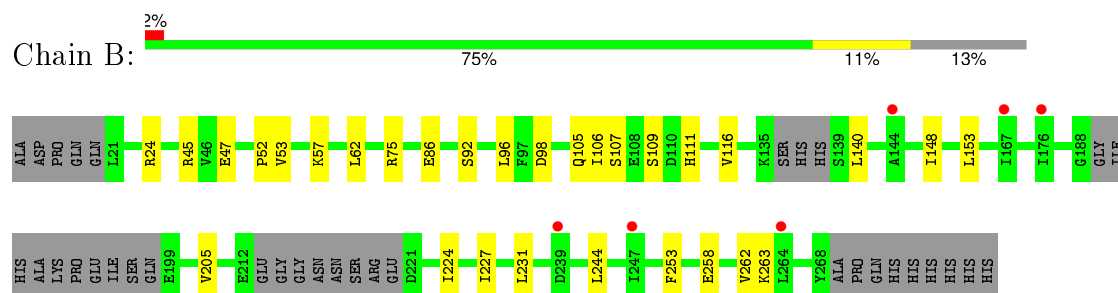
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

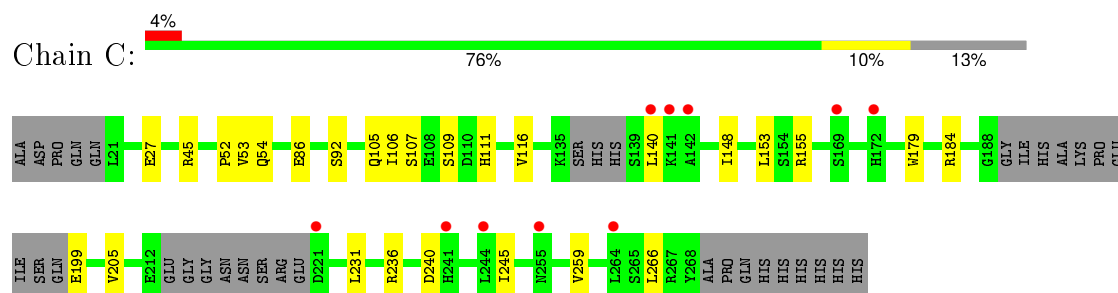
- Molecule 1: Protein SYG-1, isoform b



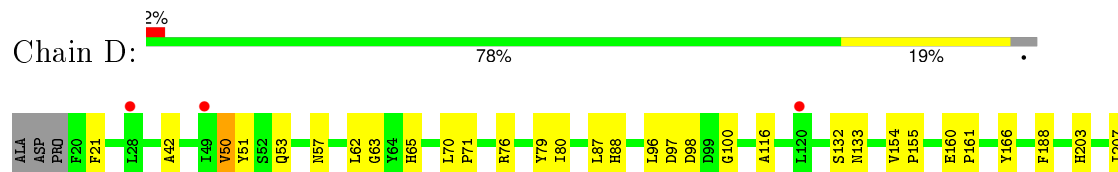
- Molecule 1: Protein SYG-1, isoform b

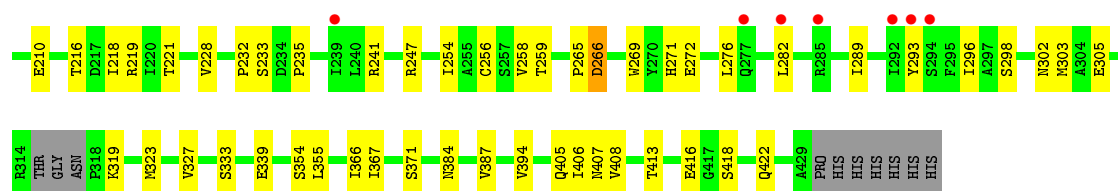


- Molecule 1: Protein SYG-1, isoform b

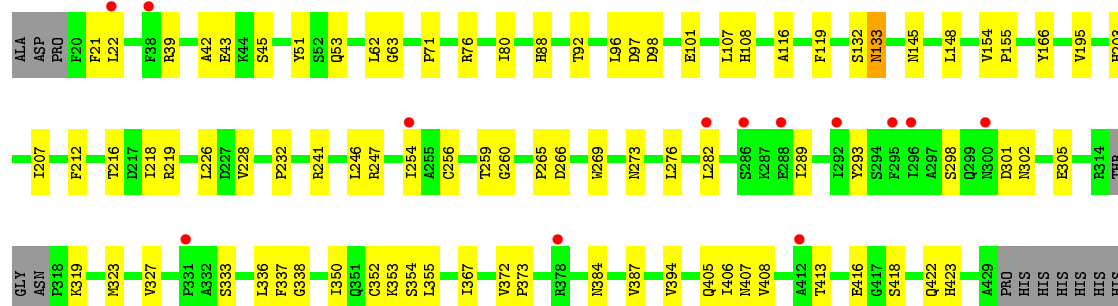
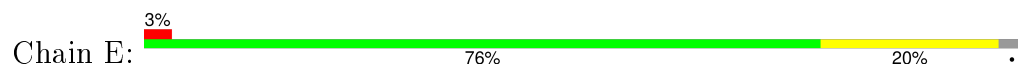


- Molecule 2: Protein SYG-2

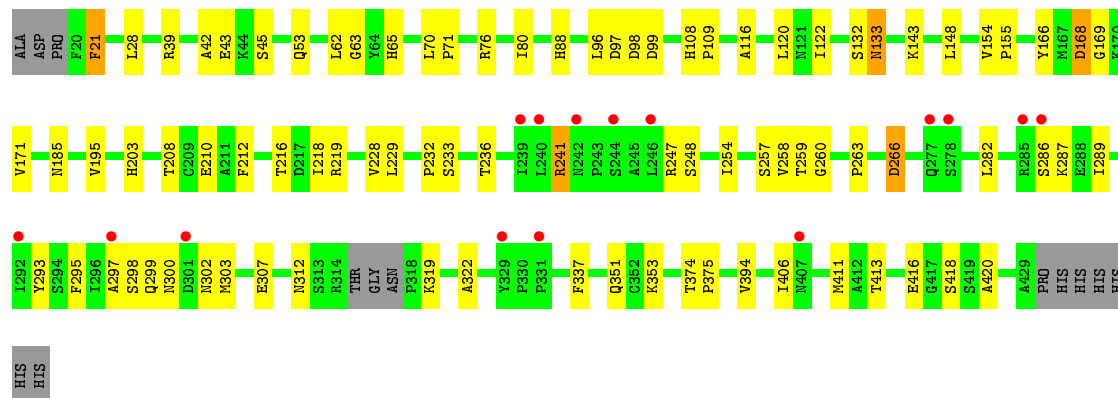
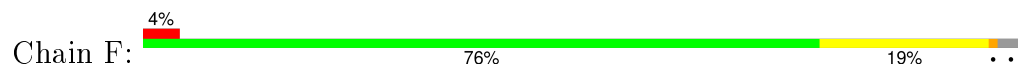




• Molecule 2: Protein SYG-2



• Molecule 2: Protein SYG-2



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	286.79Å 116.14Å 98.03Å 90.00° 107.62° 90.00°	Depositor
Resolution (Å)	41.06 – 3.30 41.06 – 3.29	Depositor EDS
% Data completeness (in resolution range)	95.3 (41.06-3.30) 95.6 (41.06-3.29)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.55 (at 3.32Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1593)	Depositor
R, R_{free}	0.259 , 0.306 0.269 , 0.311	Depositor DCC
R_{free} test set	2251 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	90.9	Xtriage
Anisotropy	0.450	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 53.2	EDS
Estimated twinning fraction	0.000 for -h-2*l,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	3 of 44718 reflections (0.007%)	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	14816	wwPDB-VP
Average B, all atoms (Å ²)	95.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 52.25 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 4.9989e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: NAG, EMC

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	0.21	0/1801	0.41	0/2439
1	B	0.21	0/1785	0.41	0/2415
1	C	0.21	0/1785	0.41	0/2415
2	D	0.25	0/3116	0.49	0/4266
2	E	0.26	0/3113	0.50	0/4263
2	F	0.25	0/3128	0.50	0/4280
All	All	0.24	0/14728	0.47	0/20078

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	A	1767	0	1751	19	0
1	B	1752	0	1744	17	0
1	C	1752	0	1743	16	0
2	D	3045	0	2835	48	2
2	E	3042	0	2820	50	3
2	F	3057	0	2857	59	0
3	A	28	0	25	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	28	0	25	1	0
3	C	28	0	25	1	0
3	D	28	0	25	0	0
3	E	28	0	25	0	0
3	F	28	0	25	0	0
4	C	14	0	13	0	0
4	D	70	0	65	1	0
4	E	70	0	65	0	0
4	F	70	0	65	0	0
5	D	3	0	0	0	0
5	E	3	0	0	0	0
5	F	3	0	0	0	0
All	All	14816	0	14108	208	3

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 7.

All (208) 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:E:282:LEU:HD13	2:E:289:ILE:HG13	1.61	0.82
2:F:39:ARG:HA	2:F:88:HIS:HD2	1.49	0.78
2:E:276:LEU:HD13	2:E:293:TYR:CE2	2.19	0.77
2:F:233:SER:HG	2:F:259:THR:HG1	1.25	0.76
2:F:53:GLN:HG3	2:F:63:GLY:HA3	1.68	0.76
1:A:140:LEU:HD21	1:A:148:ILE:HG21	1.67	0.75
2:F:21:PHE:HA	2:F:43:GLU:HG3	1.67	0.74
1:A:53:VAL:HG22	1:A:106:ILE:HG12	1.71	0.72
2:F:96:LEU:HA	2:F:122:ILE:HD13	1.72	0.72
2:F:21:PHE:HZ	2:F:116:ALA:HB2	1.54	0.71
2:D:53:GLN:HG3	2:D:63:GLY:HA3	1.74	0.70
2:D:216:THR:HB	2:D:218:ILE:HG22	1.73	0.70
2:D:233:SER:HG	2:D:259:THR:HG1	1.35	0.70
1:B:53:VAL:HG22	1:B:106:ILE:HG12	1.73	0.69
2:D:282:LEU:HD13	2:D:289:ILE:HG13	1.74	0.68
2:F:282:LEU:HD13	2:F:289:ILE:HG13	1.74	0.68
2:D:62:LEU:HG	2:D:70:LEU:HD23	1.76	0.68
2:F:216:THR:HB	2:F:218:ILE:HG22	1.75	0.67
2:E:216:THR:HB	2:E:218:ILE:HG22	1.75	0.67
1:B:140:LEU:HD21	1:B:148:ILE:HG21	1.76	0.66
2:D:21:PHE:HB2	2:D:42:ALA:HA	1.75	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:21:PHE:HB2	2:F:42:ALA:HA	1.77	0.66
2:E:21:PHE:HZ	2:E:116:ALA:HB2	1.61	0.66
2:E:21:PHE:HB2	2:E:42:ALA:HA	1.77	0.66
2:D:62:LEU:HD21	2:D:71:PRO:HD2	1.78	0.65
2:E:53:GLN:HG3	2:E:63:GLY:HA3	1.78	0.65
1:C:52:PRO:HD2	1:C:107:SER:HB2	1.80	0.64
2:D:276:LEU:HD13	2:D:293:TYR:CE2	2.34	0.62
2:D:247:ARG:NH1	2:D:416:GLU:OE2	2.32	0.62
2:E:51:TYR:HB2	2:E:107:LEU:HD13	1.81	0.62
2:D:413:THR:HG23	2:D:418:SER:HB3	1.82	0.62
1:A:52:PRO:HD2	1:A:107:SER:HB2	1.81	0.62
2:F:108:HIS:HD2	2:F:109:PRO:HD2	1.62	0.62
2:F:96:LEU:HD23	2:F:97:ASP:H	1.65	0.62
2:D:298:SER:N	2:D:302:ASN:OD1	2.25	0.61
1:A:24:ARG:NH1	1:A:47:GLU:OE2	2.34	0.61
2:E:39:ARG:HA	2:E:88:HIS:HD2	1.66	0.60
2:E:413:THR:HG23	2:E:418:SER:HB3	1.84	0.60
2:D:21:PHE:HZ	2:D:116:ALA:HB2	1.67	0.59
2:F:413:THR:HG23	2:F:418:SER:HB3	1.85	0.59
1:B:205:VAL:HG22	1:B:231:LEU:HA	1.85	0.59
2:F:80:ILE:HB	2:F:88:HIS:HB2	1.84	0.59
1:C:53:VAL:HG22	1:C:106:ILE:HG12	1.84	0.58
2:E:407:ASN:HB3	2:E:422:GLN:NE2	2.18	0.58
1:B:45:ARG:HG2	1:B:86:GLU:HG2	1.84	0.58
2:F:21:PHE:CZ	2:F:116:ALA:HB2	2.37	0.58
2:E:247:ARG:NH1	2:E:416:GLU:OE2	2.37	0.57
1:B:109:SER:O	1:B:111:HIS:N	2.36	0.57
1:C:140:LEU:HD21	1:C:148:ILE:HG21	1.87	0.57
2:E:96:LEU:HD23	2:E:97:ASP:H	1.69	0.57
2:D:266:ASP:N	2:D:266:ASP:OD1	2.30	0.56
2:F:62:LEU:HD21	2:F:71:PRO:HD2	1.87	0.56
2:D:210:GLU:HG3	2:D:221:THR:HG22	1.88	0.55
1:C:199:GLU:O	1:C:236:ARG:NH1	2.39	0.55
1:B:140:LEU:N	1:B:263:LYS:O	2.36	0.55
2:D:256:CYS:HB2	2:D:269:TRP:CZ2	2.42	0.55
2:D:394:VAL:HG11	2:D:406:ILE:HG21	1.89	0.54
1:C:109:SER:O	1:C:111:HIS:N	2.41	0.54
2:D:210:GLU:CD	2:D:219:ARG:HD2	2.28	0.54
2:E:336:LEU:HD13	2:E:423:HIS:HB2	1.90	0.54
1:A:199:GLU:O	1:A:236:ARG:NH1	2.40	0.53
1:A:45:ARG:HG2	1:A:86:GLU:HG2	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:271:HIS:CD2	2:D:272:GLU:HG3	2.44	0.53
2:F:247:ARG:NH1	2:F:416:GLU:OE2	2.41	0.53
2:D:63:GLY:O	2:D:65:HIS:ND1	2.38	0.53
1:C:45:ARG:HG2	1:C:86:GLU:HG2	1.91	0.52
2:D:232:PRO:O	2:D:319:LYS:HD2	2.09	0.52
2:D:367:ILE:HD12	2:D:408:VAL:HG22	1.90	0.52
2:E:232:PRO:O	2:E:319:LYS:HD2	2.10	0.52
2:E:232:PRO:HG3	2:E:265:PRO:HG3	1.91	0.52
2:D:296:ILE:HD11	4:D:1506:NAG:H82	1.92	0.51
2:F:337:PHE:HE2	2:F:353:LYS:HG2	1.76	0.51
2:E:80:ILE:HB	2:E:88:HIS:HB2	1.93	0.51
1:A:109:SER:O	1:A:111:HIS:N	2.40	0.51
2:F:166:TYR:CE2	2:F:171:VAL:HG12	2.46	0.51
1:C:105:GLN:HG3	1:C:116:VAL:HG22	1.93	0.51
2:D:235:PRO:HB3	2:D:258:VAL:HG22	1.92	0.51
2:F:39:ARG:HA	2:F:88:HIS:CD2	2.39	0.51
2:F:229:LEU:HD22	2:F:263:PRO:HD3	1.92	0.51
2:E:212:PHE:CD1	2:E:219:ARG:HD3	2.46	0.51
2:E:62:LEU:HD21	2:E:71:PRO:HD2	1.93	0.51
2:F:286:SER:O	2:F:287:LYS:HG2	2.11	0.51
2:F:411:MET:HG3	2:F:420:ALA:HB2	1.93	0.50
1:C:92:SER:HB2	3:C:801:NAG:H82	1.94	0.50
2:E:407:ASN:HB3	2:E:422:GLN:HE21	1.75	0.50
2:F:21:PHE:N	2:F:21:PHE:CD1	2.79	0.50
2:E:203:HIS:HB2	2:E:228:VAL:HG22	1.93	0.50
1:A:205:VAL:HG22	1:A:231:LEU:HA	1.93	0.49
2:E:305:GLU:HA	2:E:323:MET:O	2.11	0.49
2:F:298:SER:O	2:F:302:ASN:HB2	2.13	0.49
2:D:203:HIS:HB2	2:D:228:VAL:HG22	1.94	0.49
1:B:92:SER:HB2	3:B:801:NAG:H82	1.94	0.48
2:F:233:SER:OG	2:F:259:THR:OG1	2.08	0.48
2:F:232:PRO:O	2:F:319:LYS:HD2	2.14	0.48
1:B:52:PRO:HD2	1:B:107:SER:HB2	1.96	0.48
2:E:39:ARG:HA	2:E:88:HIS:CD2	2.48	0.48
2:F:210:GLU:CD	2:F:219:ARG:HD2	2.34	0.48
2:F:210:GLU:OE2	2:F:219:ARG:HD2	2.13	0.48
2:F:394:VAL:HG11	2:F:406:ILE:HG21	1.96	0.48
2:F:236:THR:OG1	2:F:257:SER:HB3	2.13	0.48
1:C:27:GLU:OE1	1:C:45:ARG:NE	2.36	0.47
2:E:22:LEU:H	2:E:43:GLU:N	2.11	0.47
2:F:45:SER:HB3	2:F:108:HIS:NE2	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:333:SER:H	2:D:355:LEU:HD12	1.80	0.47
2:D:50:VAL:HG23	2:D:51:TYR:CD2	2.49	0.47
1:C:205:VAL:HG22	1:C:231:LEU:HA	1.97	0.47
1:C:54:GLN:NE2	2:F:53:GLN:OE1	2.44	0.47
2:F:76:ARG:NH1	2:F:98:ASP:OD2	2.48	0.47
2:F:299:GLN:HG3	2:F:300:ASN:H	1.80	0.47
2:D:305:GLU:HA	2:D:323:MET:O	2.15	0.47
1:B:24:ARG:NH1	1:B:47:GLU:OE2	2.46	0.47
1:A:73:ASN:HB3	1:A:76:TYR:CG	2.50	0.46
2:D:302:ASN:HB3	2:D:327:VAL:HG21	1.97	0.46
2:F:203:HIS:HB2	2:F:228:VAL:HG22	1.97	0.46
2:E:337:PHE:HE2	2:E:353:LYS:HG2	1.80	0.46
1:C:240:ASP:HB2	1:C:266:LEU:HD22	1.97	0.46
2:F:307:GLU:HA	2:F:322:ALA:HA	1.97	0.46
2:E:354:SER:O	2:E:387:VAL:HG13	2.16	0.46
2:E:298:SER:O	2:E:302:ASN:HB2	2.15	0.46
2:F:99:ASP:HB2	2:F:122:ILE:HD12	1.97	0.46
2:E:132:SER:HA	2:E:133:ASN:HA	1.49	0.46
2:E:259:THR:OG1	2:E:260:GLY:N	2.48	0.46
2:D:354:SER:O	2:D:387:VAL:HG13	2.16	0.46
2:E:101:GLU:HB3	2:E:119:PHE:CE2	2.50	0.46
2:F:298:SER:N	2:F:302:ASN:OD1	2.39	0.45
2:F:63:GLY:O	2:F:65:HIS:ND1	2.45	0.45
2:E:246:LEU:HB2	2:E:327:VAL:HG22	1.98	0.45
2:E:154:VAL:HA	2:E:155:PRO:HD3	1.75	0.45
2:F:185:ASN:OD1	2:F:185:ASN:N	2.49	0.45
1:C:153:LEU:HD21	1:C:155:ARG:HD2	1.99	0.45
2:D:232:PRO:HG3	2:D:265:PRO:HG3	1.99	0.45
1:A:240:ASP:HB2	1:A:266:LEU:HD22	1.99	0.45
2:E:254:ILE:HG13	2:E:293:TYR:HB3	1.99	0.45
1:A:253:PHE:CE2	1:A:258:GLU:HG3	2.52	0.45
2:D:166:TYR:O	2:D:207:ILE:HA	2.17	0.45
1:A:240:ASP:HA	1:A:266:LEU:HD13	1.99	0.44
1:B:153:LEU:HD12	1:B:227:ILE:O	2.17	0.44
2:F:374:THR:HA	2:F:375:PRO:HD3	1.81	0.44
1:B:253:PHE:CE2	1:B:258:GLU:HG3	2.52	0.44
2:F:299:GLN:HG3	2:F:300:ASN:N	2.32	0.44
2:F:154:VAL:HA	2:F:155:PRO:HD3	1.83	0.44
1:B:96:LEU:HD11	1:B:224:ILE:HG23	1.99	0.44
2:D:303:MET:HG3	2:D:384:ASN:HA	1.99	0.44
2:D:160:GLU:HB3	2:D:188:PHE:CG	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:80:ILE:HB	2:D:88:HIS:HB2	1.99	0.44
2:F:248:SER:O	2:F:297:ALA:HB3	2.17	0.44
1:A:84:ASN:HB3	1:A:86:GLU:HG3	1.99	0.44
1:C:245:ILE:HG23	1:C:259:VAL:HG13	1.99	0.43
2:D:96:LEU:HD23	2:D:97:ASP:H	1.83	0.43
2:E:336:LEU:HD23	2:E:352:CYS:HB2	1.99	0.43
2:D:366:ILE:HG12	2:D:371:SER:HA	2.00	0.43
2:F:28:LEU:O	2:F:120:LEU:HA	2.18	0.43
2:E:333:SER:H	2:E:355:LEU:HD12	1.82	0.43
2:F:254:ILE:HG13	2:F:293:TYR:HB3	2.00	0.43
2:F:132:SER:HA	2:F:133:ASN:HA	1.53	0.43
2:F:241:ARG:HB2	2:F:241:ARG:HE	1.38	0.43
2:E:21:PHE:CZ	2:E:116:ALA:HB2	2.49	0.43
2:E:76:ARG:HB3	2:E:92:THR:O	2.19	0.43
2:D:160:GLU:HA	2:D:161:PRO:HD3	1.86	0.43
2:E:256:CYS:HB2	2:E:269:TRP:CZ2	2.54	0.43
2:F:258:VAL:HG12	2:F:260:GLY:H	1.83	0.43
2:D:333:SER:N	2:D:355:LEU:HD12	2.34	0.43
2:E:301:ASP:H	2:E:384:ASN:ND2	2.17	0.43
2:D:339:GLU:HG3	2:D:339:GLU:H	1.64	0.42
1:A:105:GLN:HG3	1:A:116:VAL:HG22	2.02	0.42
2:F:293:TYR:HE1	2:F:295:PHE:HB3	1.84	0.42
2:D:154:VAL:HA	2:D:155:PRO:HD3	1.78	0.42
2:F:143:LYS:HA	2:F:229:LEU:HB2	2.01	0.42
1:A:105:GLN:HG2	1:A:106:ILE:N	2.34	0.42
2:E:45:SER:HB3	2:E:108:HIS:NE2	2.35	0.42
2:D:210:GLU:OE2	2:D:219:ARG:HD2	2.20	0.42
2:E:96:LEU:C	2:E:98:ASP:H	2.23	0.42
2:F:62:LEU:HG	2:F:70:LEU:HD23	2.01	0.42
2:F:166:TYR:HB2	2:F:208:THR:HB	2.02	0.42
2:F:232:PRO:HD3	2:F:312:ASN:ND2	2.34	0.42
2:E:372:VAL:HB	2:E:373:PRO:HD2	2.01	0.42
2:F:266:ASP:N	2:F:266:ASP:OD1	2.43	0.41
2:F:148:LEU:O	2:F:195:VAL:HA	2.19	0.41
2:E:21:PHE:N	2:E:21:PHE:CD1	2.89	0.41
2:E:96:LEU:HD23	2:E:97:ASP:N	2.34	0.41
2:E:333:SER:N	2:E:355:LEU:HD12	2.35	0.41
2:E:338:GLY:HA3	2:E:350:ILE:HD13	2.03	0.41
1:A:92:SER:HB2	3:A:801:NAG:H82	2.02	0.41
2:F:96:LEU:HD23	2:F:97:ASP:N	2.32	0.41
1:B:57:LYS:HB3	1:B:62:LEU:HD21	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:244:LEU:HB3	1:B:262:VAL:HG12	2.02	0.41
2:E:394:VAL:HG11	2:E:406:ILE:HG21	2.03	0.41
1:B:105:GLN:HG2	1:B:106:ILE:N	2.35	0.41
2:D:407:ASN:HB3	2:D:422:GLN:NE2	2.35	0.41
1:C:179:TRP:CD1	1:C:184:ARG:HB2	2.55	0.41
1:C:105:GLN:HG2	1:C:106:ILE:N	2.36	0.41
2:D:254:ILE:HG21	2:D:323:MET:HE1	2.02	0.41
1:A:244:LEU:HB3	1:A:262:VAL:HG12	2.03	0.41
1:B:75:ARG:HH22	1:B:98:ASP:CG	2.24	0.41
2:D:76:ARG:NH1	2:D:98:ASP:OD2	2.52	0.41
1:B:105:GLN:HG3	1:B:116:VAL:HG22	2.03	0.40
2:D:21:PHE:CZ	2:D:116:ALA:HB2	2.51	0.40
2:F:337:PHE:HB2	2:F:351:GLN:HB3	2.03	0.40
1:A:160:PRO:HG3	1:A:225:TYR:CD1	2.56	0.40
2:E:148:LEU:O	2:E:195:VAL:HA	2.21	0.40
2:F:168:ASP:HB3	2:F:169:GLY:H	1.62	0.40
2:D:57:ASN:HB2	2:D:100:GLY:HA3	2.03	0.40
2:E:166:TYR:O	2:E:207:ILE:HA	2.20	0.40
2:E:226:LEU:HD12	2:E:226:LEU:HA	1.85	0.40
2:D:79:TYR:CD2	2:D:87:LEU:HD11	2.56	0.40
2:D:132:SER:HA	2:D:133:ASN:HA	1.47	0.40
2:E:367:ILE:HD12	2:E:408:VAL:HG22	2.03	0.40
1:A:135:LYS:HD2	1:A:138:HIS:HA	2.03	0.40

All (3) 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:D:405:GLN:NE2	2:E:422:GLN:OE1[1_452]	2.09	0.11
2:D:422:GLN:OE1	2:E:405:GLN:NE2[1_452]	2.09	0.11
2:E:145:ASN:O	2:E:273:ASN:ND2[2_658]	2.10	0.10

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	A	224/262 (86%)	212 (95%)	12 (5%)	0	100	100
1	B	219/262 (84%)	208 (95%)	11 (5%)	0	100	100
1	C	219/262 (84%)	208 (95%)	11 (5%)	0	100	100
2	D	403/420 (96%)	382 (95%)	21 (5%)	0	100	100
2	E	403/420 (96%)	382 (95%)	21 (5%)	0	100	100
2	F	403/420 (96%)	383 (95%)	20 (5%)	0	100	100
All	All	1871/2046 (91%)	1775 (95%)	96 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	197/228 (86%)	197 (100%)	0	100	100
1	B	197/228 (86%)	197 (100%)	0	100	100
1	C	197/228 (86%)	197 (100%)	0	100	100
2	D	331/380 (87%)	328 (99%)	3 (1%)	84	92
2	E	329/380 (87%)	326 (99%)	3 (1%)	84	92
2	F	333/380 (88%)	326 (98%)	7 (2%)	61	84
All	All	1584/1824 (87%)	1571 (99%)	13 (1%)	86	93

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	50	VAL
2	D	241	ARG
2	D	266	ASP
2	E	133	ASN

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Mol	Chain	Res	Type
2	E	241	ARG
2	E	266	ASP
2	F	21	PHE
2	F	133	ASN
2	F	168	ASP
2	F	212	PHE
2	F	241	ARG
2	F	266	ASP
2	F	303	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
2	D	422	GLN
2	E	88	HIS
2	E	422	GLN
2	F	88	HIS

5.3.3 RNA ⓘ

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 ⓘ

12 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	0.40	0	15,19,21	0.52	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	A	802	3	14,14,15	0.21	0	15,19,21	0.25	0
3	NAG	B	801	1,3	14,14,15	0.42	0	15,19,21	0.44	0
3	NAG	B	802	3	14,14,15	0.22	0	15,19,21	0.23	0
3	NAG	C	801	1,3	14,14,15	0.38	0	15,19,21	0.47	0
3	NAG	C	802	3	14,14,15	0.27	0	15,19,21	0.29	0
3	NAG	D	1503	3,2	14,14,15	0.28	0	15,19,21	0.42	0
3	NAG	D	1504	3	14,14,15	0.28	0	15,19,21	0.42	0
3	NAG	E	1503	3,2	14,14,15	0.41	0	15,19,21	0.39	0
3	NAG	E	1504	3	14,14,15	0.31	0	15,19,21	0.43	0
3	NAG	F	1503	3,2	14,14,15	0.19	0	15,19,21	0.47	0
3	NAG	F	1504	3	14,14,15	0.23	0	15,19,21	0.32	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
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	NAG	B	801	1,3	-	0/6/23/26	0/1/1/1
3	NAG	B	802	3	-	0/6/23/26	0/1/1/1
3	NAG	C	801	1,3	-	0/6/23/26	0/1/1/1
3	NAG	C	802	3	-	0/6/23/26	0/1/1/1
3	NAG	D	1503	3,2	-	0/6/23/26	0/1/1/1
3	NAG	D	1504	3	-	0/6/23/26	0/1/1/1
3	NAG	E	1503	3,2	-	0/6/23/26	0/1/1/1
3	NAG	E	1504	3	-	0/6/23/26	0/1/1/1
3	NAG	F	1503	3,2	-	0/6/23/26	0/1/1/1
3	NAG	F	1504	3	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	801	NAG	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	801	NAG	1	0
3	C	801	NAG	1	0

5.6 Ligand geometry

19 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	$\# Z > 2$
4	NAG	C	803	1	14,14,15	0.36	0	15,19,21	0.30	0
4	NAG	D	1501	2	14,14,15	0.27	0	15,19,21	0.42	0
4	NAG	D	1502	2	14,14,15	0.30	0	15,19,21	0.39	0
4	NAG	D	1505	2	14,14,15	0.25	0	15,19,21	0.38	0
4	NAG	D	1506	2	14,14,15	0.31	0	15,19,21	0.44	0
4	NAG	D	1507	2	14,14,15	0.28	0	15,19,21	0.49	0
5	EMC	D	1508	2	1,2,2	0.01	0	0,1,1	0.00	-
4	NAG	E	1501	2	14,14,15	0.27	0	15,19,21	0.43	0
4	NAG	E	1502	2	14,14,15	0.32	0	15,19,21	0.48	0
4	NAG	E	1505	2	14,14,15	0.26	0	15,19,21	0.41	0
4	NAG	E	1506	2	14,14,15	0.33	0	15,19,21	0.55	0
4	NAG	E	1507	2	14,14,15	0.20	0	15,19,21	0.47	0
5	EMC	E	1508	2	1,2,2	0.01	0	0,1,1	0.00	-
4	NAG	F	1501	2	14,14,15	0.28	0	15,19,21	0.27	0
4	NAG	F	1502	2	14,14,15	0.30	0	15,19,21	0.48	0
4	NAG	F	1505	2	14,14,15	0.24	0	15,19,21	0.43	0
4	NAG	F	1506	2	14,14,15	0.23	0	15,19,21	0.52	0
4	NAG	F	1507	2	14,14,15	0.33	0	15,19,21	0.42	0
5	EMC	F	1508	2	1,2,2	0.00	0	0,1,1	0.00	-

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
4	NAG	C	803	1	-	0/6/23/26	0/1/1/1
4	NAG	D	1501	2	-	0/6/23/26	0/1/1/1
4	NAG	D	1502	2	-	0/6/23/26	0/1/1/1
4	NAG	D	1505	2	-	0/6/23/26	0/1/1/1
4	NAG	D	1506	2	-	0/6/23/26	0/1/1/1
4	NAG	D	1507	2	-	0/6/23/26	0/1/1/1
5	EMC	D	1508	2	-	0/0/0/0	0/0/0/0
4	NAG	E	1501	2	-	0/6/23/26	0/1/1/1
4	NAG	E	1502	2	-	0/6/23/26	0/1/1/1
4	NAG	E	1505	2	-	0/6/23/26	0/1/1/1
4	NAG	E	1506	2	-	0/6/23/26	0/1/1/1
4	NAG	E	1507	2	-	0/6/23/26	0/1/1/1
5	EMC	E	1508	2	-	0/0/0/0	0/0/0/0
4	NAG	F	1501	2	-	0/6/23/26	0/1/1/1
4	NAG	F	1502	2	-	0/6/23/26	0/1/1/1
4	NAG	F	1505	2	-	0/6/23/26	0/1/1/1
4	NAG	F	1506	2	-	0/6/23/26	0/1/1/1
4	NAG	F	1507	2	-	0/6/23/26	0/1/1/1
5	EMC	F	1508	2	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	1506	NAG	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

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	230/262 (87%)	0.34	15 (6%)	22 18	58, 91, 153, 173	0
1	B	227/262 (86%)	0.15	6 (2%)	59 53	56, 82, 134, 153	0
1	C	227/262 (86%)	0.27	10 (4%)	38 31	57, 93, 136, 160	0
2	D	407/420 (96%)	0.09	10 (2%)	61 54	59, 89, 123, 163	0
2	E	407/420 (96%)	0.21	13 (3%)	51 44	58, 89, 131, 168	0
2	F	407/420 (96%)	0.26	15 (3%)	45 38	56, 92, 131, 181	0
All	All	1905/2046 (93%)	0.21	69 (3%)	46 39	56, 90, 137, 181	0

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	221	ASP	5.2
1	C	141	LYS	5.0
1	A	241	HIS	3.8
2	E	38	PHE	3.7
1	A	264	LEU	3.6
1	A	136	SER	3.5
1	B	264	LEU	3.5
2	F	239	ILE	3.4
2	F	292	ILE	3.2
1	C	172	HIS	3.2
2	F	240	LEU	3.2
2	F	244	SER	3.1
2	D	28	LEU	3.0
2	E	300	ASN	3.0
1	C	142	ALA	3.0
1	A	21	LEU	3.0
1	A	245	ILE	3.0
2	F	277	GLN	2.9
1	C	264	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	242	LYS	2.9
1	C	241	HIS	2.9
2	E	254	ILE	2.8
2	E	296	ILE	2.8
2	E	292	ILE	2.8
1	A	239	ASP	2.8
2	F	297	ALA	2.8
2	F	242	ASN	2.8
2	F	278	SER	2.7
2	D	49	ILE	2.7
2	D	292	ILE	2.7
2	F	246	LEU	2.6
1	C	221	ASP	2.6
2	D	294	SER	2.6
1	A	255	ASN	2.6
1	B	239	ASP	2.6
2	F	331	PRO	2.6
1	C	255	ASN	2.5
2	E	282	LEU	2.5
1	A	24	ARG	2.5
1	A	167	ILE	2.5
1	A	206	ASN	2.5
1	A	142	ALA	2.5
2	F	286	SER	2.5
2	F	329	TYR	2.5
2	D	120	LEU	2.5
2	E	331	PRO	2.4
2	D	285	ARG	2.4
1	C	244	LEU	2.4
2	E	378	ARG	2.4
2	E	286	SER	2.3
2	F	407	ASN	2.3
2	E	22	LEU	2.3
1	B	247	ILE	2.3
2	D	282	LEU	2.2
2	F	301	ASP	2.2
2	D	239	ILE	2.2
1	A	173	GLY	2.2
2	E	295	PHE	2.2
1	B	144	ALA	2.2
2	E	288	GLU	2.1
2	D	277	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	169	SER	2.1
2	F	285	ARG	2.1
2	D	293	TYR	2.1
1	C	140	LEU	2.0
2	E	412	ALA	2.0
1	B	176	ILE	2.0
1	A	140	LEU	2.0
1	B	167	ILE	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](#)

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	F	1503	14/15	0.92	0.27	0.46	62,93,115,118	0
3	NAG	E	1503	14/15	0.92	0.24	0.03	70,109,120,129	0
3	NAG	D	1503	14/15	0.92	0.17	-0.26	76,104,113,115	0
3	NAG	A	802	14/15	0.74	0.49	-	124,148,160,162	0
3	NAG	B	801	14/15	0.85	0.36	-	87,120,134,137	0
3	NAG	E	1504	14/15	0.85	0.18	-	107,118,133,146	0
3	NAG	F	1504	14/15	0.83	0.20	-	102,111,131,135	0
3	NAG	A	801	14/15	0.78	0.40	-	102,136,142,151	0
3	NAG	C	802	14/15	0.71	0.58	-	138,160,172,174	0
3	NAG	D	1504	14/15	0.88	0.14	-	116,122,124,125	0
3	NAG	C	801	14/15	0.77	0.50	-	85,142,157,158	0
3	NAG	B	802	14/15	0.78	0.41	-	114,131,140,142	0

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. 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(Å ²)	Q<0.9
4	NAG	E	1502	14/15	0.73	0.32	2.16	101,117,135,135	0
4	NAG	E	1507	14/15	0.77	0.36	0.98	118,135,147,157	0
4	NAG	D	1502	14/15	0.72	0.25	0.63	76,117,128,128	0
4	NAG	F	1505	14/15	0.88	0.20	-0.49	74,83,95,107	0
4	NAG	F	1502	14/15	0.84	0.19	-0.91	83,104,111,115	0
4	NAG	F	1506	14/15	0.68	0.17	-1.71	98,137,147,148	0
4	NAG	D	1505	14/15	0.87	0.18	-	71,96,112,118	0
4	NAG	F	1501	14/15	0.73	0.20	-	80,103,114,127	0
5	EMC	F	1508	3/3	0.90	0.21	-	166,166,187,321	0
4	NAG	C	803	14/15	0.40	0.39	-	94,155,166,171	0
4	NAG	D	1506	14/15	0.76	0.20	-	113,135,139,141	0
4	NAG	D	1501	14/15	0.84	0.15	-	99,109,130,138	0
5	EMC	E	1508	3/3	0.81	0.14	-	108,108,117,281	3
4	NAG	E	1506	14/15	0.60	0.22	-	100,127,140,140	0
4	NAG	F	1507	14/15	0.78	0.27	-	99,130,145,152	0
4	NAG	E	1501	14/15	0.81	0.18	-	87,106,123,131	0
4	NAG	E	1505	14/15	0.84	0.23	-	95,104,119,127	0
4	NAG	D	1507	14/15	0.68	0.37	-	122,139,155,168	0
5	EMC	D	1508	3/3	0.86	0.27	-	115,115,133,307	0

6.5 Other polymers

There are no such residues in this entry.