



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:46 PM GMT

PDB ID : 4JBW  
Title : Crystal structure of E. coli maltose transporter MalFGK2 in complex with its regulatory protein EIIA<sub>glc</sub>  
Authors : Chen, S.; Oldham, M.L.; Davidson, A.L.; Chen, J.  
Deposited on : 2013-02-20  
Resolution : 3.91 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](mailto: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.

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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

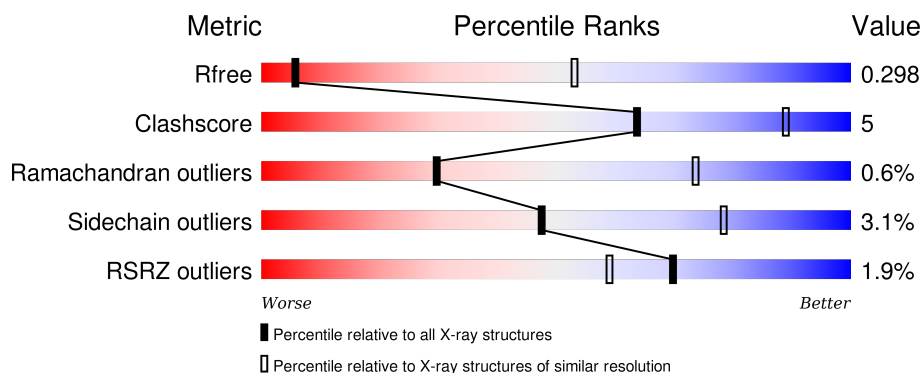
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.91 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	1047 (4.32-3.52)
Clashscore	102246	1008 (4.26-3.58)
Ramachandran outliers	100387	1044 (4.30-3.54)
Sidechain outliers	100360	1035 (4.30-3.54)
RSRZ outliers	91569	1002 (4.30-3.54)

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  $\geq 3$ , 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	F	514	<div> <div>3%</div> <div>82%</div> <div>13%</div> <div>• •</div> </div>
1	H	514	<div> <div>4%</div> <div>75%</div> <div>16%</div> <div>• 8%</div> </div>
2	G	296	<div> <div>%</div> <div>77%</div> <div>18%</div> <div>• •</div> </div>
2	I	296	<div> <div>5%</div> <div>77%</div> <div>18%</div> <div>• •</div> </div>
3	A	381	<div> <div>%</div> <div>83%</div> <div>13%</div> <div>•</div> </div>

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Mol	Chain	Length	Quality of chain
3	B	381	 81% 16% •
3	C	381	 82% 14% •
3	D	381	 79% 17% • •
4	M	172	 77% 10% 13%
4	N	172	 73% 14% 13%
4	O	172	 78% 8% • 13%
4	P	172	 74% 13% 13%

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 27958 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 Maltose transport system permease protein MalF.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	F	492	Total	C	N	O	S	0	0	0
			3805	2499	609	680	17			
1	H	472	Total	C	N	O	S	0	0	0
			3671	2416	582	656	17			

- Molecule 2 is a protein called Maltose transport system permease protein MalG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	286	Total	C	N	O	S	0	0	0
			2219	1487	354	369	9			
2	I	286	Total	C	N	O	S	0	0	0
			2219	1487	354	369	9			

- Molecule 3 is a protein called Maltose/maltodextrin import ATP-binding protein MalK.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	370	Total	C	N	O	S	0	0	0
			2871	1816	514	528	13			
3	B	370	Total	C	N	O	S	0	0	0
			2871	1816	514	528	13			
3	C	370	Total	C	N	O	S	0	0	0
			2871	1816	514	528	13			
3	D	370	Total	C	N	O	S	0	0	0
			2871	1816	514	528	13			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	372	ALA	-	EXPRESSION TAG	UNP P68187
A	373	SER	-	EXPRESSION TAG	UNP P68187
A	374	ALA	-	EXPRESSION TAG	UNP P68187
A	375	SER	-	EXPRESSION TAG	UNP P68187

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Chain	Residue	Modelled	Actual	Comment	Reference
A	376	HIS	-	EXPRESSION TAG	UNP P68187
A	377	HIS	-	EXPRESSION TAG	UNP P68187
A	378	HIS	-	EXPRESSION TAG	UNP P68187
A	379	HIS	-	EXPRESSION TAG	UNP P68187
A	380	HIS	-	EXPRESSION TAG	UNP P68187
A	381	HIS	-	EXPRESSION TAG	UNP P68187
B	372	ALA	-	EXPRESSION TAG	UNP P68187
B	373	SER	-	EXPRESSION TAG	UNP P68187
B	374	ALA	-	EXPRESSION TAG	UNP P68187
B	375	SER	-	EXPRESSION TAG	UNP P68187
B	376	HIS	-	EXPRESSION TAG	UNP P68187
B	377	HIS	-	EXPRESSION TAG	UNP P68187
B	378	HIS	-	EXPRESSION TAG	UNP P68187
B	379	HIS	-	EXPRESSION TAG	UNP P68187
B	380	HIS	-	EXPRESSION TAG	UNP P68187
B	381	HIS	-	EXPRESSION TAG	UNP P68187
C	372	ALA	-	EXPRESSION TAG	UNP P68187
C	373	SER	-	EXPRESSION TAG	UNP P68187
C	374	ALA	-	EXPRESSION TAG	UNP P68187
C	375	SER	-	EXPRESSION TAG	UNP P68187
C	376	HIS	-	EXPRESSION TAG	UNP P68187
C	377	HIS	-	EXPRESSION TAG	UNP P68187
C	378	HIS	-	EXPRESSION TAG	UNP P68187
C	379	HIS	-	EXPRESSION TAG	UNP P68187
C	380	HIS	-	EXPRESSION TAG	UNP P68187
C	381	HIS	-	EXPRESSION TAG	UNP P68187
D	372	ALA	-	EXPRESSION TAG	UNP P68187
D	373	SER	-	EXPRESSION TAG	UNP P68187
D	374	ALA	-	EXPRESSION TAG	UNP P68187
D	375	SER	-	EXPRESSION TAG	UNP P68187
D	376	HIS	-	EXPRESSION TAG	UNP P68187
D	377	HIS	-	EXPRESSION TAG	UNP P68187
D	378	HIS	-	EXPRESSION TAG	UNP P68187
D	379	HIS	-	EXPRESSION TAG	UNP P68187
D	380	HIS	-	EXPRESSION TAG	UNP P68187
D	381	HIS	-	EXPRESSION TAG	UNP P68187

- Molecule 4 is a protein called Glucose-specific phosphotransferase enzyme IIA component.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	M	150	Total	C	N	O	S	0	0	0
			1127	722	177	226	2			

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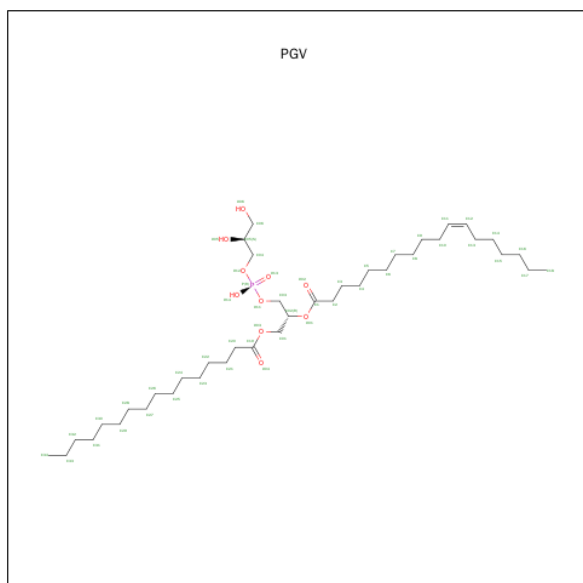
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	N	150	Total	C	N	O	S	0	0	0
			1127	722	177	226	2			
4	O	150	Total	C	N	O	S	0	0	0
			1127	722	177	226	2			
4	P	150	Total	C	N	O	S	0	0	0
			1127	722	177	226	2			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	-3	SER	-	EXPRESSION TAG	UNP P69783
M	-2	ASN	-	EXPRESSION TAG	UNP P69783
M	-1	ALA	-	EXPRESSION TAG	UNP P69783
N	-3	SER	-	EXPRESSION TAG	UNP P69783
N	-2	ASN	-	EXPRESSION TAG	UNP P69783
N	-1	ALA	-	EXPRESSION TAG	UNP P69783
O	-3	SER	-	EXPRESSION TAG	UNP P69783
O	-2	ASN	-	EXPRESSION TAG	UNP P69783
O	-1	ALA	-	EXPRESSION TAG	UNP P69783
P	-3	SER	-	EXPRESSION TAG	UNP P69783
P	-2	ASN	-	EXPRESSION TAG	UNP P69783
P	-1	ALA	-	EXPRESSION TAG	UNP P69783

- Molecule 5 is (1R)-2-{{[(2S)-2,3-DIHYDROXYPROPYL]OXY}(HYDROXY)PHOSPHORYL]OXY}-1-[(PALMITOYLOXY)METHYL]ETHYL (11E)-OCTADEC-11-ENOATE (three-letter code: PGV) (formula: C<sub>40</sub>H<sub>77</sub>O<sub>10</sub>P).

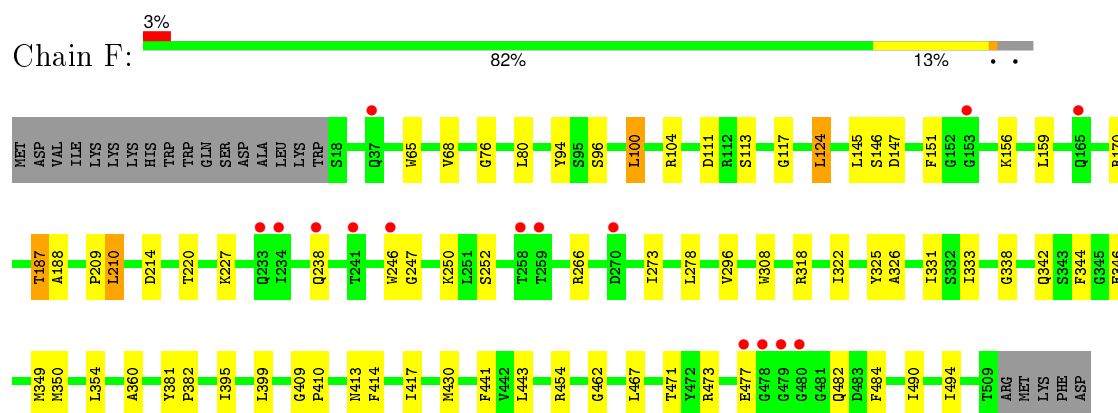


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	F	1	Total	C	O	P	0	0
			26	15	10	1		
5	H	1	Total	C	O	P	0	0
			26	15	10	1		

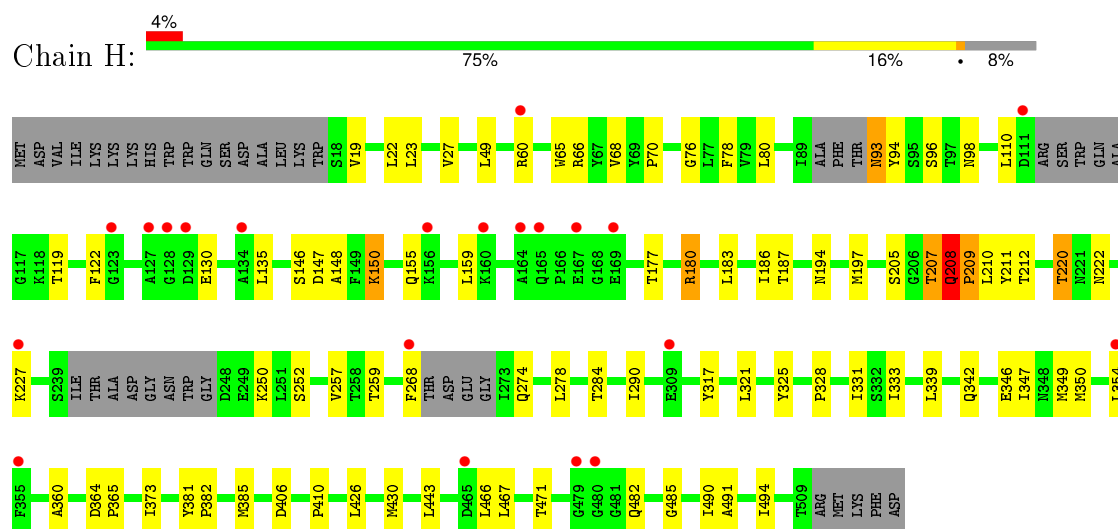
### 3 Residue-property plots

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.

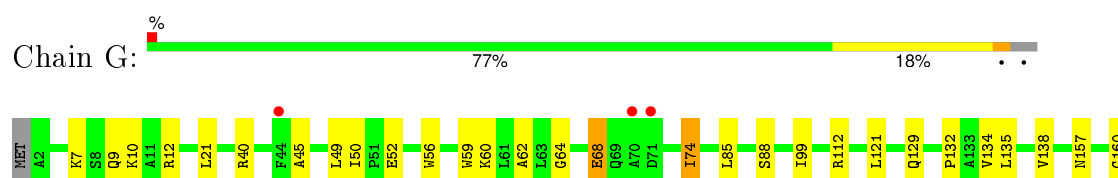
- Molecule 1: Maltose transport system permease protein MalF



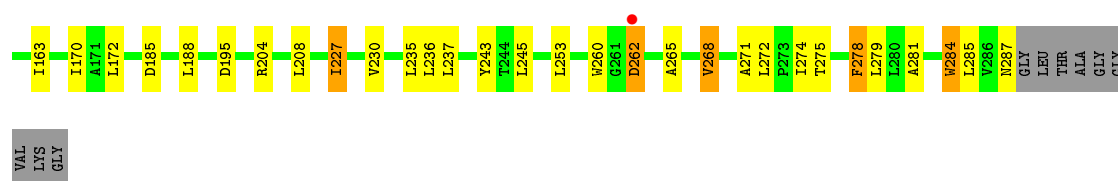
- Molecule 1: Maltose transport system permease protein MalF



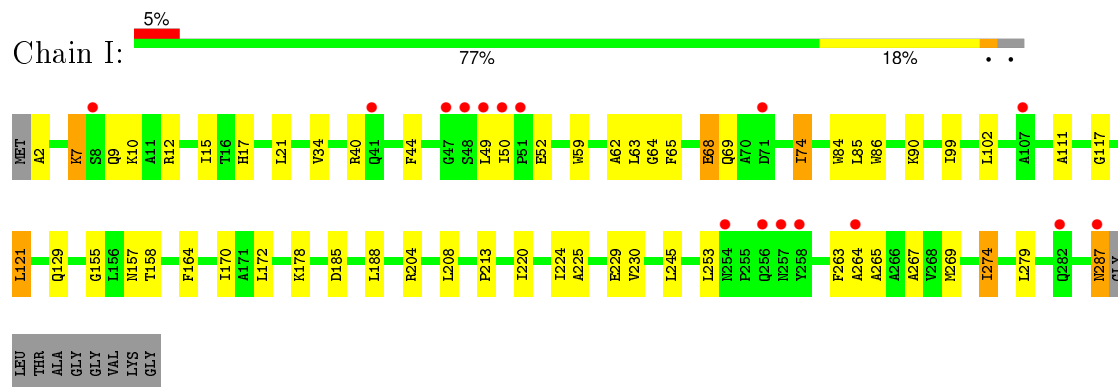
- Molecule 2: Maltose transport system permease protein MalG



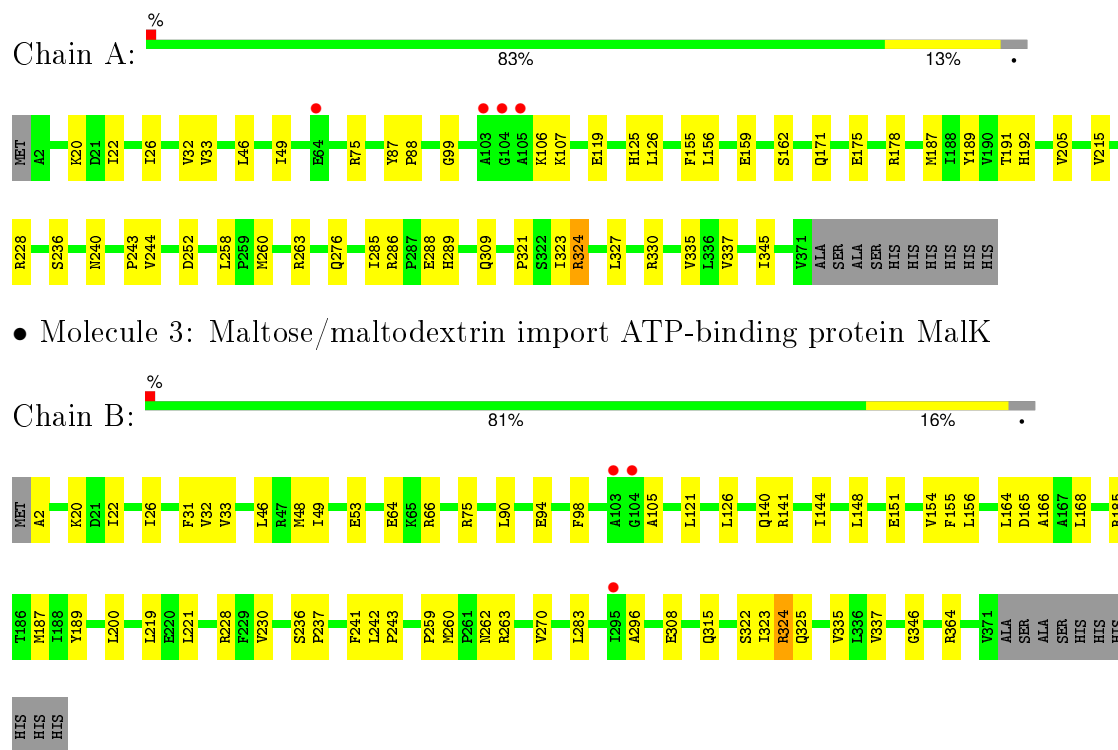




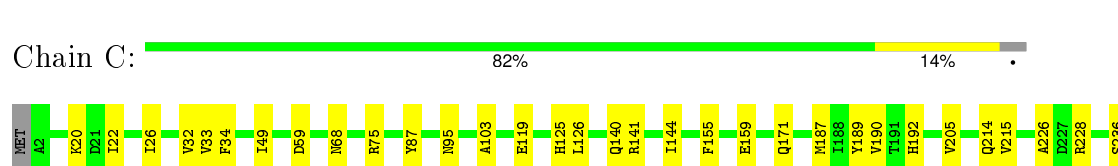
- Molecule 2: Maltose transport system permease protein MalG

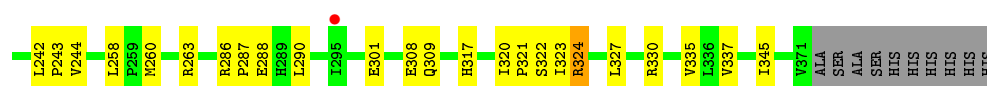


- Molecule 3: Maltose/maltodextrin import ATP-binding protein MalK



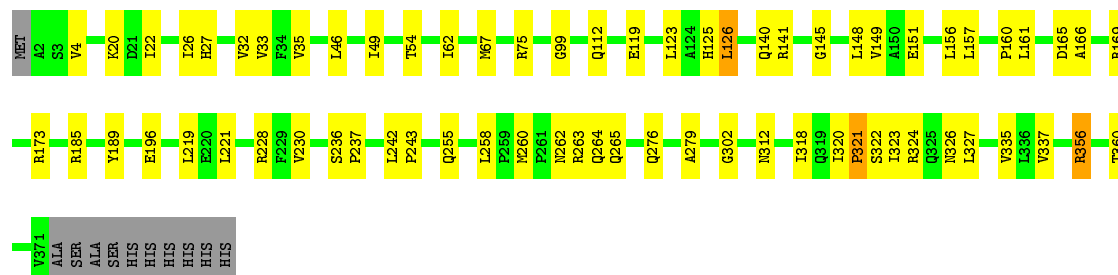
- Molecule 3: Maltose/maltodextrin import ATP-binding protein MalK





- Molecule 3: Maltose/maltodextrin import ATP-binding protein MalK

Chain D: 79% 17% . .



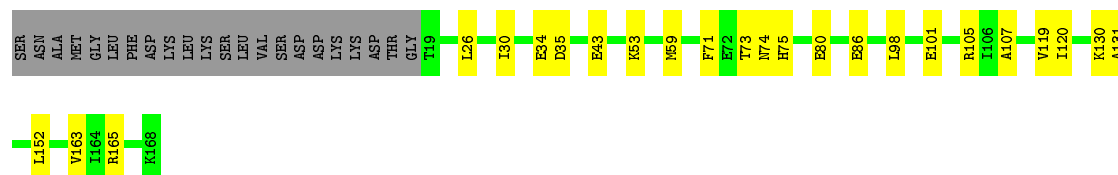
- Molecule 4: Glucose-specific phosphotransferase enzyme IIA component

Chain M: 77% 10% 13%



- Molecule 4: Glucose-specific phosphotransferase enzyme IIA component

Chain N: 73% 14% 13%



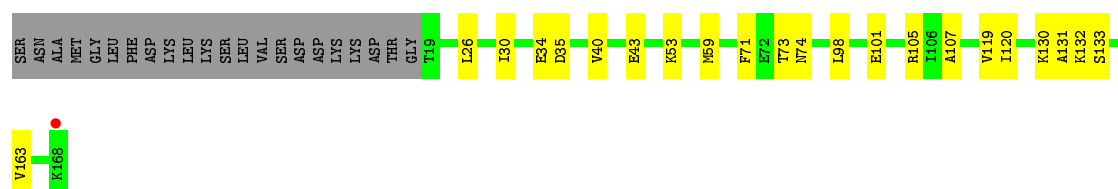
- Molecule 4: Glucose-specific phosphotransferase enzyme IIA component

Chain O: 78% 8% 13%



- Molecule 4: Glucose-specific phosphotransferase enzyme IIA component

Chain P: 74% 13% 13%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	94.53Å 208.45Å 347.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.98 – 3.91 19.98 – 3.91	Depositor EDS
% Data completeness (in resolution range)	94.9 (19.98-3.91) 94.9 (19.98-3.91)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.11	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.47 (at 3.94Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, $R_{free}$	0.226 , 0.281 0.254 , 0.298	Depositor DCC
$R_{free}$ test set	3017 reflections (5.09%)	DCC
Wilson B-factor (Å <sup>2</sup> )	162.8	Xtriage
Anisotropy	0.096	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.20 , 36.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 59252 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	27958	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	133.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.82% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PGV

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	F	0.22	0/3898	0.39	0/5308
1	H	0.22	0/3756	0.39	0/5106
2	G	0.22	0/2281	0.41	0/3120
2	I	0.22	0/2281	0.39	0/3120
3	A	0.21	0/2921	0.39	0/3961
3	B	0.21	0/2921	0.39	0/3961
3	C	0.21	0/2921	0.39	0/3961
3	D	0.21	0/2921	0.39	0/3961
4	M	0.21	0/1142	0.41	0/1545
4	N	0.21	0/1142	0.41	0/1545
4	O	0.21	0/1142	0.41	0/1545
4	P	0.21	0/1142	0.41	0/1545
All	All	0.21	0/28468	0.39	0/38678

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	H	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	H	208	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	F	3805	0	3837	43	0
1	H	3671	0	3727	46	0
2	G	2219	0	2307	32	0
2	I	2219	0	2307	28	0
3	A	2871	0	2937	29	0
3	B	2871	0	2937	33	0
3	C	2871	0	2937	33	0
3	D	2871	0	2937	43	0
4	M	1127	0	1155	9	0
4	N	1127	0	1155	13	0
4	O	1127	0	1155	10	0
4	P	1127	0	1155	16	0
5	F	26	0	22	4	0
5	H	26	0	22	2	0
All	All	27958	0	28590	296	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 5.

All (296) 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:H:93:ASN:N	1:H:259:THR:HG1	1.63	0.97
3:D:33:VAL:HG22	3:D:189:TYR:HB3	1.57	0.87
3:B:33:VAL:HG22	3:B:189:TYR:HB3	1.57	0.86
3:C:33:VAL:HG22	3:C:189:TYR:HB3	1.56	0.84
3:A:33:VAL:HG22	3:A:189:TYR:HB3	1.62	0.82
3:A:260:MET:HG2	3:A:323:ILE:HB	1.62	0.81
3:D:243:PRO:HG3	4:P:35:ASP:HB3	1.65	0.79
3:D:260:MET:HG2	3:D:323:ILE:HB	1.64	0.79
1:F:410:PRO:HB3	5:F:4001:PGV:H032	1.65	0.77
2:I:68:GLU:HG2	2:I:74:ILE:HA	1.66	0.76
3:D:324:ARG:HG2	4:P:133:SER:HB2	1.66	0.75
4:P:98:LEU:HD11	4:P:131:ALA:HB2	1.69	0.74
3:A:258:LEU:HB3	3:A:260:MET:HG3	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:96:SER:HB2	1:H:482:GLN:HB2	1.72	0.71
1:H:146:SER:HB2	1:H:159:LEU:HD23	1.72	0.70
1:F:471:THR:HG22	1:F:490:ILE:HG23	1.72	0.70
1:F:113:SER:HA	1:F:210:LEU:HB2	1.75	0.69
1:H:150:LYS:O	1:H:155:GLN:NE2	2.26	0.68
3:A:327:LEU:HD23	3:A:345:ILE:HD11	1.76	0.68
3:D:324:ARG:HE	4:P:132:LYS:HB3	1.59	0.67
1:H:209:PRO:O	1:H:222:ASN:ND2	2.26	0.66
3:C:258:LEU:HB3	3:C:260:MET:HG3	1.78	0.66
3:C:243:PRO:HG3	4:O:35:ASP:HB3	1.76	0.66
2:G:204:ARG:HA	2:G:208:LEU:HD12	1.78	0.65
2:I:185:ASP:HB3	2:I:188:LEU:HD23	1.79	0.65
1:F:325:TYR:HB2	1:F:382:PRO:HG2	1.79	0.65
3:D:151:GLU:OE1	3:D:185:ARG:NH2	2.30	0.65
3:D:140:GLN:HE22	3:D:161:LEU:HD23	1.62	0.64
1:F:350:MET:HG3	2:G:49:LEU:HD13	1.80	0.64
2:I:111:ALA:HB2	2:I:178:LYS:HG2	1.82	0.62
3:C:260:MET:HG2	3:C:323:ILE:HB	1.81	0.62
2:I:204:ARG:HA	2:I:208:LEU:HD12	1.81	0.61
3:D:302:GLY:HA2	3:D:321:PRO:HD3	1.81	0.61
2:I:287:ASN:N	2:I:287:ASN:OD1	2.33	0.61
3:C:327:LEU:HD23	3:C:345:ILE:HD11	1.82	0.60
1:H:471:THR:HG22	1:H:490:ILE:HG23	1.83	0.60
2:G:271:ALA:O	2:G:275:THR:N	2.35	0.60
4:N:98:LEU:HD11	4:N:131:ALA:HB2	1.83	0.60
3:A:155:PHE:HB2	3:A:187:MET:HG2	1.84	0.60
1:H:94:TYR:O	1:H:485:GLY:N	2.33	0.59
1:H:410:PRO:HB3	5:H:601:PGV:H032	1.85	0.58
3:B:155:PHE:HB2	3:B:187:MET:HG2	1.86	0.58
2:I:213:PRO:HB2	2:I:287:ASN:HD21	1.69	0.57
2:G:185:ASP:HB3	2:G:188:LEU:HD23	1.86	0.57
2:G:85:LEU:HD23	2:G:245:LEU:HD22	1.85	0.57
3:B:140:GLN:HE21	3:B:144:ILE:HD11	1.69	0.57
4:M:95:THR:HG22	4:M:131:ALA:HB1	1.87	0.57
3:A:159:GLU:OE2	3:A:192:HIS:ND1	2.37	0.57
4:M:83:SER:O	4:M:168:LYS:NZ	2.30	0.57
3:C:119:GLU:HG2	4:P:71:PHE:HD2	1.70	0.57
2:G:275:THR:HA	2:G:278:PHE:CZ	2.40	0.56
1:F:238:GLN:HG3	1:F:250:LYS:HG2	1.86	0.56
3:D:4:VAL:HG23	3:D:62:ILE:HG12	1.87	0.56
1:H:342:GLN:HE22	1:H:360:ALA:HA	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:141:ARG:HH12	4:P:40:VAL:HG13	1.71	0.56
1:F:326:ALA:HB1	2:G:278:PHE:CE1	2.41	0.55
4:P:119:VAL:HG12	4:P:120:ILE:HG13	1.88	0.55
4:M:22:ILE:HD13	4:M:87:LEU:HD11	1.88	0.55
4:O:119:VAL:HG12	4:O:120:ILE:HG13	1.88	0.55
3:B:260:MET:HB2	3:B:322:SER:OG	2.07	0.55
3:B:243:PRO:HG3	4:N:35:ASP:HB3	1.89	0.55
3:C:308:GLU:OE2	3:C:317:HIS:NE2	2.39	0.55
1:H:328:PRO:HD3	2:I:274:ILE:HD11	1.88	0.54
2:G:278:PHE:HD1	2:G:279:LEU:N	2.06	0.54
1:H:350:MET:HG3	2:I:49:LEU:HD13	1.90	0.54
4:O:22:ILE:HD13	4:O:87:LEU:HD11	1.89	0.54
1:H:220:THR:HB	1:H:227:LYS:HG2	1.89	0.53
3:B:241:PHE:O	3:B:325:GLN:NE2	2.41	0.53
2:I:7:LYS:HE2	2:I:12:ARG:HH22	1.73	0.53
2:I:220:ILE:HG23	2:I:224:ILE:HD13	1.89	0.53
1:H:325:TYR:HB2	1:H:382:PRO:HG2	1.91	0.53
1:H:333:ILE:HD13	1:H:443:LEU:HA	1.91	0.53
3:D:157:LEU:HD23	3:D:160:PRO:HG3	1.91	0.53
3:D:161:LEU:HB3	3:D:169:ARG:HG3	1.91	0.52
3:A:171:GLN:NE2	4:N:43:GLU:OE2	2.42	0.52
1:F:124:LEU:HD11	1:F:151:PHE:HZ	1.74	0.52
3:C:324:ARG:HB3	4:O:132:LYS:O	2.09	0.52
3:D:173:ARG:HD2	3:D:196:GLU:HG3	1.91	0.52
4:N:152:LEU:HD21	4:N:165:ARG:HH21	1.74	0.52
1:H:212:THR:HG23	1:H:222:ASN:HD21	1.74	0.52
1:F:159:LEU:HD11	1:F:188:ALA:HB1	1.91	0.51
1:F:100:LEU:HD22	1:F:104:ARG:HG2	1.93	0.51
3:C:49:ILE:O	3:C:75:ARG:NH1	2.44	0.51
2:G:262:ASP:OD2	2:G:262:ASP:N	2.43	0.51
3:C:59:ASP:HA	3:C:68:ASN:HD21	1.76	0.51
3:A:119:GLU:HG2	4:N:71:PHE:HD2	1.75	0.51
2:G:272:LEU:HA	2:G:275:THR:HG22	1.93	0.51
3:B:335:VAL:HG12	3:B:337:VAL:HG23	1.92	0.50
3:D:258:LEU:HB3	3:D:260:MET:HG3	1.91	0.50
4:P:107:ALA:HB3	4:P:119:VAL:HG13	1.93	0.50
2:G:62:ALA:HB3	2:G:265:ALA:HB3	1.94	0.50
2:G:88:SER:HB3	2:G:227:ILE:HG13	1.93	0.50
1:F:467:LEU:HB3	1:F:494:ILE:HD12	1.93	0.50
3:B:64:GLU:HG2	3:C:321:PRO:HG3	1.93	0.50
1:F:409:GLY:O	1:F:413:ASN:ND2	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:129:GLN:HG2	2:I:172:LEU:HG	1.93	0.50
2:G:237:LEU:HD23	2:G:243:TYR:HA	1.93	0.50
2:I:85:LEU:HD23	2:I:245:LEU:HD22	1.94	0.49
1:H:284:THR:HG23	1:H:466:LEU:HD22	1.94	0.49
3:B:90:LEU:HD23	3:B:94:GLU:HB3	1.95	0.49
3:D:324:ARG:CG	4:P:133:SER:HB2	2.40	0.49
3:C:244:VAL:HG12	3:C:258:LEU:HD13	1.94	0.49
4:P:26:LEU:HD23	4:P:59:MET:HG2	1.95	0.49
3:C:119:GLU:HG2	4:P:71:PHE:CD2	2.48	0.49
3:B:151:GLU:OE1	3:B:185:ARG:NH2	2.45	0.49
1:H:19:VAL:HA	1:H:22:LEU:HD13	1.94	0.49
4:N:119:VAL:HG12	4:N:120:ILE:HG13	1.95	0.49
2:G:129:GLN:HG2	2:G:172:LEU:HG	1.94	0.49
4:M:119:VAL:HG12	4:M:120:ILE:HG13	1.94	0.49
2:G:195:ASP:HB3	3:A:99:GLY:HA2	1.93	0.49
2:G:68:GLU:HG2	2:G:74:ILE:HA	1.94	0.49
2:G:99:ILE:HG23	2:G:170:ILE:HG22	1.93	0.49
2:I:225:ALA:O	2:I:229:GLU:HG2	2.12	0.49
1:H:130:GLU:HB2	1:H:148:ALA:HB1	1.95	0.49
3:B:49:ILE:O	3:B:75:ARG:NH1	2.46	0.49
4:M:150:ILE:HB	4:M:165:ARG:HG3	1.95	0.49
3:A:244:VAL:HG12	3:A:258:LEU:HD13	1.95	0.48
3:D:276:GLN:HG3	3:D:279:ALA:HB2	1.95	0.48
1:H:76:GLY:HA2	1:H:80:LEU:HB3	1.95	0.48
3:A:288:GLU:HG3	3:A:330:ARG:HD3	1.95	0.48
1:H:93:ASN:ND2	1:H:257:VAL:O	2.46	0.48
1:F:417:ILE:HD11	3:B:98:PHE:CZ	2.48	0.48
1:H:317:TYR:HH	2:I:17:HIS:HD1	1.61	0.48
1:H:467:LEU:HB3	1:H:494:ILE:HD12	1.95	0.48
4:N:74:ASN:OD1	4:N:105:ARG:NH2	2.46	0.48
3:D:335:VAL:HG12	3:D:337:VAL:HG23	1.96	0.48
3:C:26:ILE:HG12	3:C:32:VAL:HG21	1.95	0.48
3:C:171:GLN:NE2	4:P:43:GLU:OE2	2.44	0.48
3:A:46:LEU:HD11	3:A:156:LEU:HB3	1.95	0.48
1:F:454:ARG:NH1	1:F:462:GLY:O	2.47	0.47
3:C:159:GLU:OE2	3:C:192:HIS:ND1	2.47	0.47
1:H:207:THR:OG1	1:H:208:GLN:N	2.45	0.47
3:B:66:ARG:NH1	4:O:130:LYS:HE2	2.29	0.47
4:O:50:ILE:HG23	4:O:151:LYS:HD3	1.96	0.47
4:P:74:ASN:OD1	4:P:105:ARG:NH2	2.47	0.47
3:B:105:ALA:O	3:D:27:HIS:NE2	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:484:PHE:HD2	2:G:138:VAL:HG13	1.80	0.47
1:H:426:LEU:O	1:H:430:MET:N	2.47	0.47
3:A:26:ILE:HG12	3:A:32:VAL:HG21	1.95	0.47
1:F:214:ASP:OD2	1:F:214:ASP:N	2.45	0.47
1:H:110:LEU:HD23	1:H:211:TYR:HB2	1.96	0.47
1:F:220:THR:HB	1:F:227:LYS:HG2	1.95	0.47
3:D:262:ASN:O	3:D:264:GLN:N	2.48	0.47
3:C:309:GLN:HB3	3:D:219:LEU:HD11	1.95	0.47
1:H:177:THR:O	1:H:180:ARG:HD2	2.14	0.47
1:H:23:LEU:O	1:H:27:VAL:HG12	2.15	0.47
3:D:324:ARG:NE	4:P:132:LYS:HB3	2.28	0.47
2:I:86:TRP:NE1	2:I:90:LYS:HD2	2.30	0.47
1:H:93:ASN:OD1	1:H:98:ASN:ND2	2.46	0.46
3:B:31:PHE:CE2	3:B:200:LEU:HB3	2.50	0.46
3:B:242:LEU:N	3:B:283:LEU:O	2.42	0.46
1:F:410:PRO:HG2	2:G:12:ARG:NE	2.30	0.46
3:C:330:ARG:NH2	3:D:312:ASN:OD1	2.47	0.46
4:N:26:LEU:HD23	4:N:59:MET:HG2	1.97	0.46
3:B:26:ILE:HG12	3:B:32:VAL:HG21	1.97	0.46
3:C:335:VAL:HG12	3:C:337:VAL:HG23	1.98	0.46
3:A:286:ARG:HD2	3:A:289:HIS:CE1	2.51	0.46
3:C:125:HIS:CD2	3:C:126:LEU:HG	2.51	0.46
2:G:7:LYS:C	2:G:9:GLN:H	2.19	0.46
3:B:270:VAL:HG23	3:B:364:ARG:HA	1.96	0.46
3:D:46:LEU:HD11	3:D:156:LEU:HB3	1.96	0.46
1:H:321:LEU:HD13	1:H:385:MET:HE1	1.96	0.46
3:B:221:LEU:HD12	3:B:230:VAL:HG11	1.98	0.46
1:F:381:TYR:CD2	1:F:382:PRO:HD3	2.51	0.45
2:I:7:LYS:HE3	2:I:12:ARG:HH12	1.81	0.45
3:A:159:GLU:HG2	3:A:162:SER:HB3	1.97	0.45
2:G:132:PRO:HD2	2:G:135:LEU:HD12	1.98	0.45
1:H:197:MET:N	1:H:205:SER:O	2.46	0.45
3:D:20:LYS:O	3:D:22:ILE:HG23	2.17	0.45
3:A:335:VAL:HG12	3:A:337:VAL:HG23	1.98	0.45
3:A:175:GLU:OE2	3:A:178:ARG:NH2	2.49	0.45
3:A:49:ILE:O	3:A:75:ARG:NH1	2.49	0.45
1:F:76:GLY:HA2	1:F:80:LEU:HB3	1.98	0.45
3:B:324:ARG:HG2	3:B:324:ARG:H	1.46	0.45
2:G:10:LYS:HA	2:G:10:LYS:HD3	1.77	0.45
3:D:119:GLU:OE2	4:O:75:HIS:NE2	2.50	0.45
3:D:49:ILE:O	3:D:75:ARG:NH1	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:263:PHE:C	2:I:265:ALA:H	2.20	0.45
4:M:87:LEU:HD13	4:M:140:ILE:HG13	1.97	0.45
1:F:482:GLN:OE1	1:F:482:GLN:N	2.50	0.45
1:F:308:TRP:CE2	5:F:4001:PGV:H031	2.52	0.45
3:D:140:GLN:HE21	3:D:160:PRO:HB2	1.82	0.45
1:H:183:LEU:HD12	1:H:186:ILE:HD12	1.99	0.45
1:F:96:SER:HB2	1:F:482:GLN:HB2	1.98	0.45
2:G:160:GLY:HA2	2:G:163:ILE:HD12	1.98	0.45
4:N:30:ILE:HD11	4:N:163:VAL:HG12	1.98	0.45
3:A:240:ASN:HB2	3:A:285:ILE:HG23	1.99	0.45
3:A:20:LYS:O	3:A:22:ILE:HG23	2.17	0.44
1:F:296:VAL:HG21	1:F:430:MET:SD	2.57	0.44
1:F:111:ASP:OD1	1:F:156:LYS:NZ	2.36	0.44
1:H:78:PHE:CZ	2:I:164:PHE:HB3	2.53	0.44
3:A:324:ARG:HG2	3:A:324:ARG:H	1.46	0.44
3:D:165:ASP:OD1	3:D:166:ALA:N	2.45	0.44
4:P:101:GLU:OE2	4:P:130:LYS:NZ	2.48	0.44
1:H:482:GLN:OE1	1:H:482:GLN:N	2.50	0.44
2:G:56:TRP:O	2:G:60:LYS:HG2	2.17	0.44
4:O:26:LEU:HD23	4:O:59:MET:HG2	1.99	0.44
4:N:101:GLU:OE2	4:N:130:LYS:NZ	2.47	0.44
2:I:62:ALA:HB1	2:I:265:ALA:HB2	1.98	0.44
1:F:473:ARG:O	1:F:477:GLU:HB2	2.18	0.44
1:F:344:PHE:HD1	2:G:45:ALA:HB3	1.83	0.44
1:F:333:ILE:HD13	1:F:443:LEU:HA	2.00	0.44
3:A:243:PRO:HG3	4:M:35:ASP:HB3	1.98	0.44
3:C:242:LEU:HA	3:C:243:PRO:HD3	1.83	0.44
3:B:259:PRO:HG2	3:B:323:ILE:HG13	2.00	0.44
3:B:20:LYS:O	3:B:22:ILE:HG23	2.17	0.44
3:C:20:LYS:O	3:C:22:ILE:HG23	2.18	0.44
1:H:346:GLU:OE2	1:H:346:GLU:N	2.51	0.44
1:H:122:PHE:HB3	1:H:135:LEU:HD23	2.00	0.44
3:C:155:PHE:HB2	3:C:187:MET:HG2	2.00	0.43
1:F:238:GLN:NE2	1:F:247:GLY:H	2.16	0.43
3:B:236:SER:HB2	3:B:237:PRO:HD3	2.00	0.43
1:H:146:SER:OG	1:H:147:ASP:N	2.50	0.43
2:I:84:TRP:HB3	2:I:245:LEU:HA	1.99	0.43
2:I:99:ILE:HG23	2:I:170:ILE:HG22	2.01	0.43
3:D:123:LEU:HG	3:D:126:LEU:HD11	2.00	0.43
1:F:395:ILE:HG23	1:F:399:LEU:HD12	2.00	0.43
1:F:65:TRP:HA	1:F:68:VAL:HG22	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:346:GLU:N	1:F:346:GLU:OE2	2.51	0.43
1:H:70:PRO:HB2	2:I:102:LEU:HD22	2.00	0.43
2:I:63:LEU:HD22	2:I:65:PHE:HE1	1.82	0.43
4:N:107:ALA:HB3	4:N:119:VAL:HG13	2.00	0.43
4:O:91:PHE:HA	4:O:136:THR:HG23	2.00	0.43
3:A:205:VAL:HG13	3:A:215:VAL:HG22	2.00	0.43
1:H:491:ALA:HA	1:H:494:ILE:HG22	2.01	0.43
4:N:80:GLU:HB3	4:N:86:GLU:HG2	2.01	0.43
1:F:318:ARG:HG2	1:F:322:ILE:HD11	2.00	0.43
4:M:26:LEU:HD23	4:M:59:MET:HG2	2.01	0.43
3:B:296:ALA:HB3	3:B:346:GLY:HA3	2.01	0.43
3:B:164:LEU:HD13	3:B:168:LEU:HG	2.01	0.43
3:D:255:GLN:OE1	3:D:265:GLN:NE2	2.51	0.42
3:D:236:SER:HB2	3:D:237:PRO:HD3	2.02	0.42
3:C:286:ARG:HA	3:C:287:PRO:HD3	1.92	0.42
1:H:60:ARG:HD3	1:H:66:ARG:HH22	1.85	0.42
3:C:290:LEU:HD13	3:C:345:ILE:HD12	2.02	0.42
4:M:30:ILE:HD11	4:M:163:VAL:HG12	2.01	0.42
1:F:113:SER:HB3	1:F:209:PRO:HA	2.01	0.42
3:C:320:ILE:HG22	3:C:322:SER:H	1.85	0.42
2:G:281:ALA:HA	2:G:284:TRP:HE3	1.84	0.42
1:H:381:TYR:CD2	1:H:382:PRO:HD3	2.55	0.42
3:C:321:PRO:O	3:C:324:ARG:NH2	2.49	0.42
3:B:48:MET:HG2	3:B:53:GLU:HB3	2.02	0.42
3:B:260:MET:HG3	3:B:263:ARG:N	2.35	0.41
1:F:441:PHE:HB3	2:G:134:VAL:HG11	2.02	0.41
2:I:155:GLY:O	2:I:158:THR:OG1	2.38	0.41
3:D:221:LEU:HD12	3:D:230:VAL:HG11	2.02	0.41
2:I:34:VAL:HG12	2:I:267:ALA:HB2	2.01	0.41
1:F:338:GLY:HA3	2:G:260:TRP:CZ3	2.55	0.41
2:I:117:GLY:O	2:I:121:LEU:HB2	2.19	0.41
3:C:140:GLN:HE21	3:C:144:ILE:HD11	1.86	0.41
3:D:318:ILE:O	3:D:326:ASN:HA	2.20	0.41
2:G:275:THR:HA	2:G:278:PHE:CE2	2.55	0.41
3:C:34:PHE:HB2	3:C:190:VAL:HG22	2.02	0.41
3:C:205:VAL:HG13	3:C:215:VAL:HG22	2.03	0.41
3:D:320:ILE:HG22	3:D:322:SER:H	1.85	0.41
1:F:342:GLN:HG2	1:F:360:ALA:HA	2.02	0.41
1:H:406:ASP:HB3	3:D:99:GLY:HA2	2.01	0.41
3:D:320:ILE:HA	3:D:321:PRO:HD3	1.85	0.41
3:D:125:HIS:CE1	4:O:46:VAL:HG23	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:26:ILE:HG12	3:D:32:VAL:HG21	2.01	0.41
1:F:146:SER:HB3	1:F:159:LEU:HG	2.03	0.41
1:H:364:ASP:HA	1:H:365:PRO:HD3	1.93	0.41
1:H:65:TRP:HA	1:H:68:VAL:HG22	2.01	0.41
3:B:121:LEU:HD11	3:B:148:LEU:HD12	2.03	0.41
3:B:308:GLU:HB2	3:B:315:GLN:HB2	2.01	0.41
3:D:67:MET:O	3:D:75:ARG:NH2	2.53	0.41
3:B:165:ASP:OD1	3:B:166:ALA:N	2.47	0.41
3:D:242:LEU:HD11	3:D:327:LEU:HD21	2.03	0.41
4:P:30:ILE:HD11	4:P:163:VAL:HG12	2.03	0.41
3:D:356:ARG:HG2	3:D:360:THR:O	2.20	0.41
3:A:87:TYR:HA	3:A:88:PRO:HD3	1.93	0.41
3:C:87:TYR:N	3:C:95:ASN:OD1	2.51	0.41
3:A:276:GLN:OE1	3:A:276:GLN:N	2.54	0.41
1:F:266:ARG:HG2	1:F:273:ILE:HD12	2.03	0.41
3:B:46:LEU:HD11	3:B:156:LEU:HB3	2.03	0.41
3:A:309:GLN:HB3	3:B:219:LEU:HD11	2.02	0.41
1:F:94:TYR:HB3	1:F:484:PHE:HB2	2.02	0.40
1:H:93:ASN:N	1:H:259:THR:OG1	2.40	0.40
3:A:189:TYR:HE2	3:A:191:THR:HB	1.85	0.40
2:G:268:VAL:O	2:G:272:LEU:HB2	2.20	0.40
1:H:290:ILE:HG21	1:H:373:ILE:HD13	2.03	0.40
3:D:322:SER:OG	3:D:323:ILE:N	2.55	0.40
1:F:308:TRP:NE1	5:F:4001:PGV:O13	2.54	0.40
1:F:414:PHE:HB2	5:F:4001:PGV:H201	2.02	0.40
2:G:112:ARG:NH2	2:G:185:ASP:O	2.54	0.40
4:N:73:THR:OG1	4:N:75:HIS:ND1	2.39	0.40
2:I:2:ALA:O	3:D:54:THR:HG23	2.21	0.40
2:G:274:ILE:HG22	2:G:278:PHE:CD2	2.56	0.40
1:F:156:LYS:HG2	1:F:187:THR:HG23	2.04	0.40
5:H:601:PGV:O02	2:I:12:ARG:HD2	2.22	0.40
3:A:321:PRO:O	3:A:324:ARG:NH2	2.54	0.40
1:H:339:LEU:HB3	1:H:347:ILE:HG13	2.02	0.40
3:B:2:ALA:HB1	3:B:154:VAL:HG22	2.02	0.40
3:D:145:GLY:O	3:D:149:VAL:HG23	2.21	0.40
3:A:125:HIS:CD2	3:A:126:LEU:HG	2.56	0.40
3:C:214:GLN:OE1	3:C:226:ALA:N	2.55	0.40

There are no symmetry-related clashes.

## 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	F	490/514 (95%)	460 (94%)	28 (6%)	2 (0%)	39	79
1	H	462/514 (90%)	426 (92%)	29 (6%)	7 (2%)	13	57
2	G	284/296 (96%)	265 (93%)	16 (6%)	3 (1%)	17	63
2	I	284/296 (96%)	263 (93%)	17 (6%)	4 (1%)	14	58
3	A	368/381 (97%)	343 (93%)	24 (6%)	1 (0%)	46	82
3	B	368/381 (97%)	344 (94%)	24 (6%)	0	100	100
3	C	368/381 (97%)	342 (93%)	24 (6%)	2 (0%)	34	77
3	D	368/381 (97%)	341 (93%)	25 (7%)	2 (0%)	34	77
4	M	148/172 (86%)	141 (95%)	7 (5%)	0	100	100
4	N	148/172 (86%)	141 (95%)	7 (5%)	0	100	100
4	O	148/172 (86%)	141 (95%)	7 (5%)	0	100	100
4	P	148/172 (86%)	141 (95%)	7 (5%)	0	100	100
All	All	3584/3832 (94%)	3348 (93%)	215 (6%)	21 (1%)	30	73

All (21) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	117	GLY
3	A	263	ARG
1	H	208	GLN
1	H	209	PRO
3	C	263	ARG
3	D	263	ARG
3	C	103	ALA
1	H	119	THR
1	H	194	ASN
1	H	207	THR
2	I	74	ILE
2	I	264	ALA

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Mol	Chain	Res	Type
1	H	250	LYS
1	F	252	SER
2	G	64	GLY
2	G	74	ILE
1	H	252	SER
2	G	230	VAL
3	D	321	PRO
2	I	64	GLY
2	I	230	VAL

### 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	F	397/424 (94%)	385 (97%)	12 (3%)	48	79
1	H	389/424 (92%)	376 (97%)	13 (3%)	45	78
2	G	232/237 (98%)	214 (92%)	18 (8%)	16	54
2	I	232/237 (98%)	213 (92%)	19 (8%)	14	52
3	A	314/323 (97%)	308 (98%)	6 (2%)	65	86
3	B	314/323 (97%)	309 (98%)	5 (2%)	70	88
3	C	314/323 (97%)	309 (98%)	5 (2%)	70	88
3	D	314/323 (97%)	307 (98%)	7 (2%)	60	84
4	M	127/148 (86%)	126 (99%)	1 (1%)	86	94
4	N	127/148 (86%)	125 (98%)	2 (2%)	70	88
4	O	127/148 (86%)	124 (98%)	3 (2%)	57	82
4	P	127/148 (86%)	124 (98%)	3 (2%)	57	82
All	All	3014/3206 (94%)	2920 (97%)	94 (3%)	47	78

All (94) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	100	LEU

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Mol	Chain	Res	Type
1	F	124	LEU
1	F	145	LEU
1	F	147	ASP
1	F	170	ARG
1	F	187	THR
1	F	210	LEU
1	F	246	TRP
1	F	278	LEU
1	F	331	ILE
1	F	349	MET
1	F	354	LEU
2	G	21	LEU
2	G	40	ARG
2	G	50	ILE
2	G	52	GLU
2	G	59	TRP
2	G	68	GLU
2	G	121	LEU
2	G	157	ASN
2	G	227	ILE
2	G	235	LEU
2	G	236	LEU
2	G	253	LEU
2	G	262	ASP
2	G	268	VAL
2	G	278	PHE
2	G	284	TRP
2	G	285	LEU
2	G	287	ASN
3	A	106	LYS
3	A	107	LYS
3	A	228	ARG
3	A	236	SER
3	A	252	ASP
3	A	324	ARG
3	B	126	LEU
3	B	141	ARG
3	B	228	ARG
3	B	262	ASN
3	B	324	ARG
4	M	75	HIS
4	N	34	GLU

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Mol	Chain	Res	Type
4	N	53	LYS
1	H	49	LEU
1	H	93	ASN
1	H	150	LYS
1	H	180	ARG
1	H	187	THR
1	H	210	LEU
1	H	220	THR
1	H	268	PHE
1	H	274	GLN
1	H	278	LEU
1	H	331	ILE
1	H	349	MET
1	H	354	LEU
2	I	7	LYS
2	I	9	GLN
2	I	10	LYS
2	I	15	ILE
2	I	21	LEU
2	I	40	ARG
2	I	44	PHE
2	I	50	ILE
2	I	52	GLU
2	I	59	TRP
2	I	68	GLU
2	I	69	GLN
2	I	121	LEU
2	I	157	ASN
2	I	253	LEU
2	I	269	MET
2	I	274	ILE
2	I	279	LEU
2	I	287	ASN
3	C	228	ARG
3	C	236	SER
3	C	288	GLU
3	C	301	GLU
3	C	324	ARG
3	D	35	VAL
3	D	112	GLN
3	D	126	LEU
3	D	141	ARG

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Mol	Chain	Res	Type
3	D	148	LEU
3	D	228	ARG
3	D	356	ARG
4	O	75	HIS
4	O	132	LYS
4	O	145	GLU
4	P	34	GLU
4	P	53	LYS
4	P	73	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	F	231	ASN
1	F	238	GLN
1	F	445	GLN
3	B	255	GLN
3	B	265	GLN
1	H	348	ASN
3	C	125	HIS
3	C	264	GLN
3	D	140	GLN

### 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 ⓘ

There are no carbohydrates in this entry.

### 5.6 Ligand geometry ⓘ

2 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	$\# Z  > 2$
5	PGV	F	4001	-	25,25,50	1.22	2 (8%)	26,31,56	1.44	3 (11%)
5	PGV	H	601	-	25,25,50	1.21	2 (8%)	26,31,56	1.45	3 (11%)

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
5	PGV	F	4001	-	-	0/30/30/55	0/0/0/0
5	PGV	H	601	-	-	0/30/30/55	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	H	601	PGV	O01-C02	-3.41	1.37	1.46
5	F	4001	PGV	O01-C02	-3.35	1.38	1.46
5	F	4001	PGV	O03-C01	-3.03	1.38	1.45
5	H	601	PGV	O03-C01	-2.96	1.38	1.45

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	H	601	PGV	O03-C19-C20	2.71	120.15	111.90
5	F	4001	PGV	O03-C19-C20	2.72	120.19	111.90
5	F	4001	PGV	O03-C01-C02	3.47	118.04	108.69
5	H	601	PGV	O03-C01-C02	3.64	118.50	108.69
5	H	601	PGV	O01-C1-C2	4.03	120.29	111.53
5	F	4001	PGV	O01-C1-C2	4.11	120.47	111.53

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	F	4001	PGV	4	0
5	H	601	PGV	2	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	F	492/514 (95%)	-0.31	15 (3%) 54 40	81, 137, 189, 239	0
1	H	472/514 (91%)	-0.05	21 (4%) 38 27	94, 164, 203, 229	0
2	G	286/296 (96%)	-0.33	4 (1%) 78 68	87, 136, 189, 214	0
2	I	286/296 (96%)	-0.03	16 (5%) 28 20	100, 169, 217, 240	0
3	A	370/381 (97%)	-0.43	4 (1%) 82 75	71, 121, 164, 198	0
3	B	370/381 (97%)	-0.50	3 (0%) 87 82	55, 105, 152, 208	0
3	C	370/381 (97%)	-0.51	1 (0%) 94 92	65, 115, 163, 201	0
3	D	370/381 (97%)	-0.55	0 100 100	55, 105, 150, 203	0
4	M	150/172 (87%)	-0.40	0 100 100	86, 136, 174, 187	0
4	N	150/172 (87%)	-0.42	0 100 100	90, 128, 162, 186	0
4	O	150/172 (87%)	-0.42	2 (1%) 79 70	86, 141, 179, 189	0
4	P	150/172 (87%)	-0.29	1 (0%) 89 84	73, 123, 166, 194	0
All	All	3616/3832 (94%)	-0.34	67 (1%) 70 59	55, 131, 190, 240	0

All (67) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	I	51	PRO	6.4
2	I	50	ILE	6.2
1	H	134	ALA	5.9
3	A	103	ALA	5.2
1	H	128	GLY	4.9
2	G	71	ASP	4.3
1	F	241	THR	4.0
1	H	354	LEU	4.0
1	H	167	GLU	3.9
1	H	127	ALA	3.7
1	H	465	ASP	3.7

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Mol	Chain	Res	Type	RSRZ
3	A	104	GLY	3.5
3	C	295	ILE	3.3
2	I	49	LEU	3.3
1	F	478	GLY	3.2
4	P	168	LYS	3.2
2	I	48	SER	3.1
4	O	108	GLU	3.1
3	A	105	ALA	3.1
1	H	156	LYS	3.1
1	H	123	GLY	3.0
2	I	107	ALA	3.0
3	A	64	GLU	3.0
1	F	233	GLN	3.0
1	F	258	THR	3.0
2	G	70	ALA	2.9
1	F	165	GLN	2.9
1	H	355	PHE	2.8
2	I	264	ALA	2.7
1	H	165	GLN	2.7
2	I	287	ASN	2.6
1	F	238	GLN	2.6
2	I	282	GLN	2.6
2	G	44	PHE	2.6
1	F	477	GLU	2.6
2	I	8	SER	2.5
1	H	227	LYS	2.5
2	I	254	ASN	2.5
1	F	270	ASP	2.5
1	H	479	GLY	2.4
2	I	257	ASN	2.4
1	H	164	ALA	2.4
1	F	153	GLY	2.4
1	H	309	GLU	2.3
1	F	479	GLY	2.3
1	F	259	THR	2.3
1	H	160	LYS	2.3
1	H	169	GLU	2.3
2	I	71	ASP	2.3
2	I	41	GLN	2.2
2	I	256	GLN	2.2
1	F	480	GLY	2.2
1	H	480	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	H	129	ASP	2.2
3	B	103	ALA	2.1
3	B	104	GLY	2.1
2	I	47	GLY	2.1
1	F	234	ILE	2.1
2	I	258	TYR	2.1
4	O	109	GLU	2.1
3	B	295	ILE	2.1
2	G	262	ASP	2.1
1	H	60	ARG	2.0
1	H	268	PHE	2.0
1	F	37	GLN	2.0
1	F	246	TRP	2.0
1	H	111	ASP	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates 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. 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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
5	PGV	F	4001	26/51	0.86	0.33	1.02	42,107,135,141	0
5	PGV	H	601	26/51	0.86	0.36	0.76	66,147,171,182	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.