



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:03 AM GMT

PDB ID : 2P6F  
Title : Crystal structures of *Saccharomyces cerevisiae* N-myristoyltransferase with bound myristoyl-CoA and inhibitors  
Authors : Wu, J.; Ding, J.  
Deposited on : 2007-03-18  
Resolution : 3.10 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

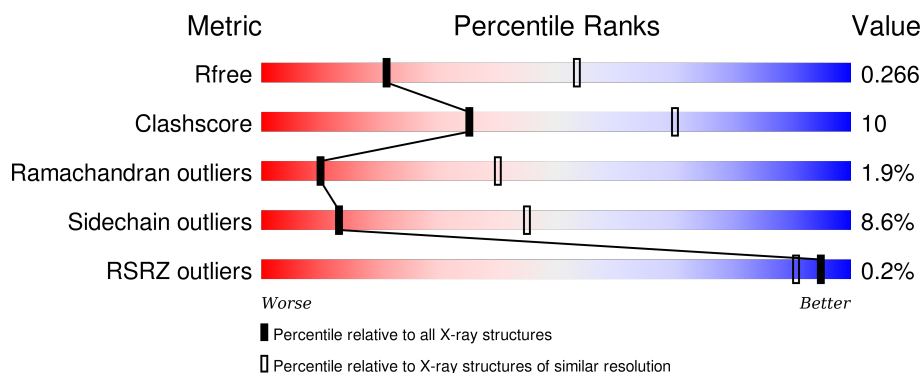
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.10 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	1114 (3.14-3.06)
Clashscore	102246	1222 (3.14-3.06)
Ramachandran outliers	100387	1174 (3.14-3.06)
Sidechain outliers	100360	1174 (3.14-3.06)
RSRZ outliers	91569	1119 (3.14-3.06)

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	A	455	
1	B	455	
1	C	455	
1	D	455	
1	E	455	

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Mol	Chain	Length	Quality of chain
1	F	455	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	MYA	A	601	X	-	-	-
2	MYA	B	602	X	-	-	-
2	MYA	C	603	X	-	-	-
2	MYA	D	604	X	-	-	-
2	MYA	E	605	X	-	-	-
2	MYA	F	606	X	-	-	-
3	GN8	A	701	-	-	-	X
3	GN8	B	702	-	-	-	X
3	GN8	C	703	-	-	-	X
3	GN8	D	704	-	-	-	X
3	GN8	E	705	-	-	-	X
3	GN8	F	706	-	-	-	X

## 2 Entry composition [i](#)

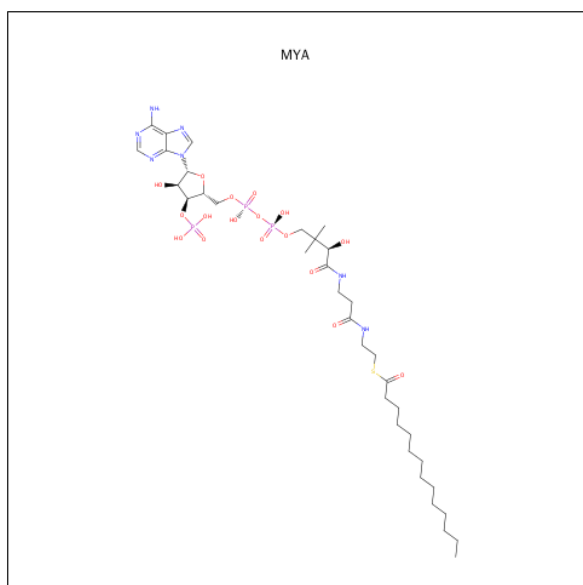
There are 3 unique types of molecules in this entry. The entry contains 21988 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Glycylpeptide N-tetradecanoyltransferase.

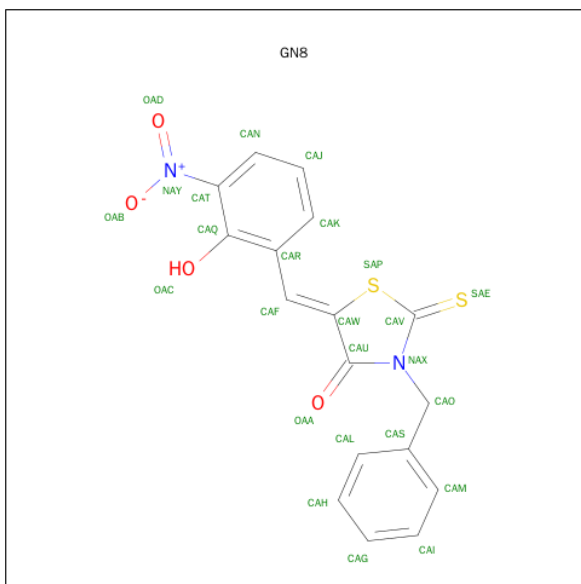
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	436	Total	C	N	O	S	0	0	0
			3578	2318	596	655	9			
1	B	436	Total	C	N	O	S	0	0	0
			3578	2318	596	655	9			
1	C	436	Total	C	N	O	S	0	0	0
			3578	2318	596	655	9			
1	D	436	Total	C	N	O	S	0	0	0
			3578	2318	596	655	9			
1	E	436	Total	C	N	O	S	0	0	0
			3578	2318	596	655	9			
1	F	435	Total	C	N	O	S	0	0	0
			3570	2314	595	652	9			

- Molecule 2 is TETRADECANOYL-COA (three-letter code: MYA) (formula:  $C_{35}H_{62}N_7O_{17}P_3S$ ).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total 63	C 35	N 7	O 17	P 3	S 1	0	0
2	B	1	Total 63	C 35	N 7	O 17	P 3	S 1	0	0
2	C	1	Total 63	C 35	N 7	O 17	P 3	S 1	0	0
2	D	1	Total 63	C 35	N 7	O 17	P 3	S 1	0	0
2	E	1	Total 63	C 35	N 7	O 17	P 3	S 1	0	0
2	F	1	Total 63	C 35	N 7	O 17	P 3	S 1	0	0

- Molecule 3 is (Z)-3-BENZYL-5-(2-HYDROXY-3-NITROBENZYLIDENE)-2-THIOXOTHIAZOLIDIN-4-ONE (three-letter code: GN8) (formula: C<sub>17</sub>H<sub>12</sub>N<sub>2</sub>O<sub>4</sub>S<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 25	C 17	N 2	O 4	S 2	0	0
3	B	1	Total 25	C 17	N 2	O 4	S 2	0	0
3	C	1	Total 25	C 17	N 2	O 4	S 2	0	0
3	D	1	Total 25	C 17	N 2	O 4	S 2	0	0
3	E	1	Total 25	C 17	N 2	O 4	S 2	0	0

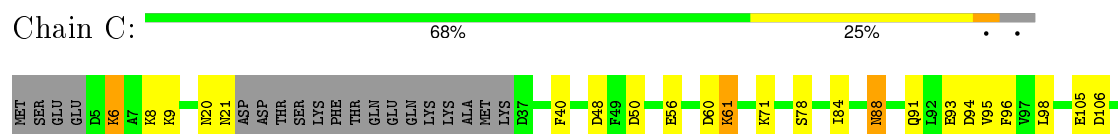
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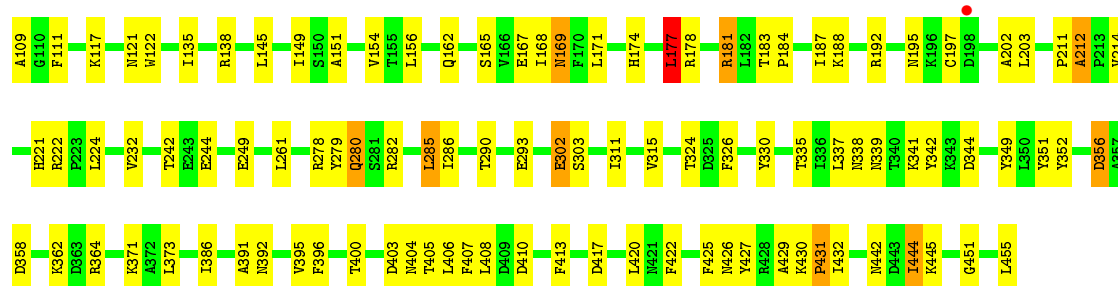
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	F	1	Total	C	N	O	S	0	0
			25	17	2	4	2		



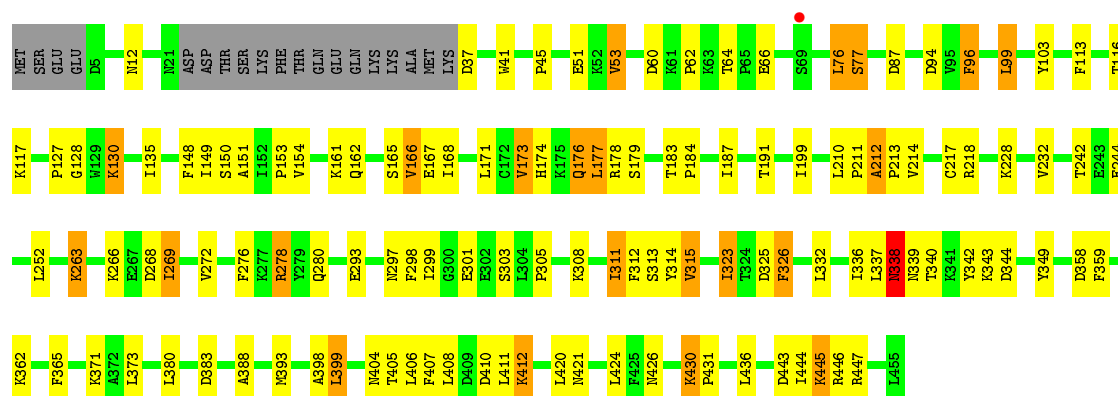
- Molecule 1: Glycylpeptide N-tetradecanoyltransferase





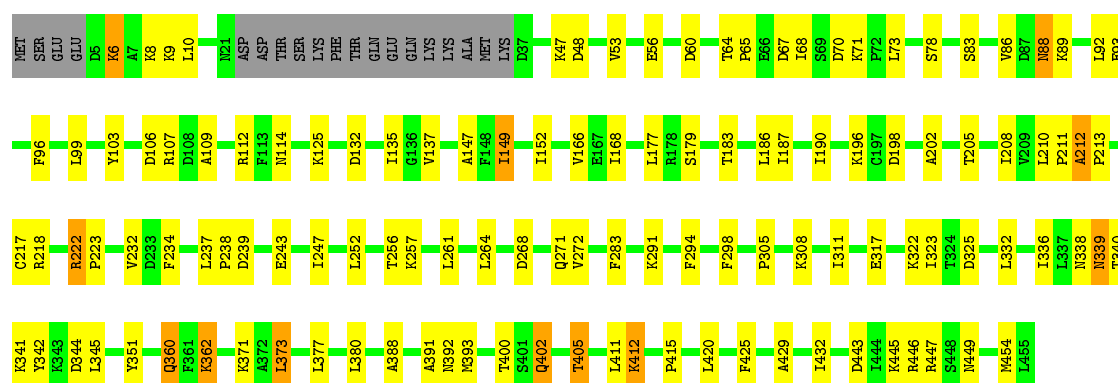
• Molecule 1: Glycylpeptide N-tetradecanoyltransferase

Chain D: 68% 23% 5%



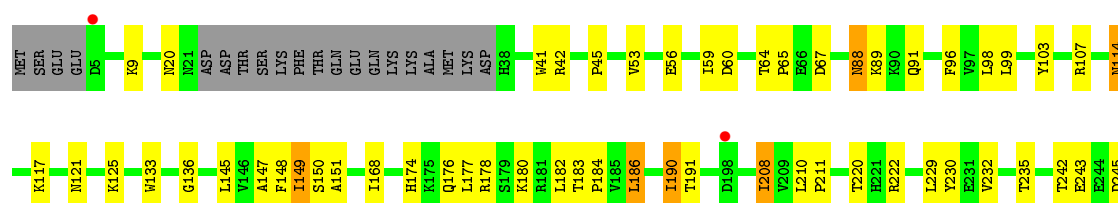
• Molecule 1: Glycylpeptide N-tetradecanoyltransferase

Chain E: 69% 24%

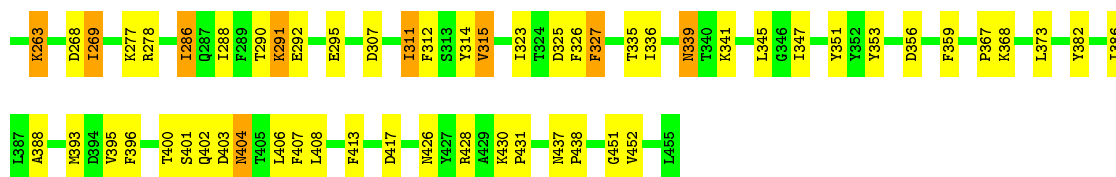


• Molecule 1: Glycylpeptide N-tetradecanoyltransferase

Chain F: 71% 22%







## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	188.76Å 151.49Å 133.94Å 90.00° 107.46° 90.00°	Depositor
Resolution (Å)	20.00 – 3.10 14.98 – 2.89	Depositor EDS
% Data completeness (in resolution range)	97.2 (20.00-3.10) 97.4 (14.98-2.89)	Depositor EDS
$R_{merge}$	0.15	Depositor
$R_{sym}$	0.15	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.42 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.270 , 0.332 0.270 , 0.266	Depositor DCC
$R_{free}$ test set	3183 reflections (5.31%)	DCC
Wilson B-factor (Å <sup>2</sup> )	34.5	Xtriage
Anisotropy	0.435	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 12.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.40$ , $\langle L^2 \rangle = 0.23$	Xtriage
Outliers	7 of 77399 reflections (0.009%)	Xtriage
$F_o, F_c$ correlation	0.87	EDS
Total number of atoms	21988	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	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 44.18 % 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 1.5840e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MYA, GN8

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	0.38	0/3666	0.51	0/4957
1	B	0.38	0/3666	0.51	0/4957
1	C	0.39	0/3666	0.53	1/4957 (0.0%)
1	D	0.38	0/3666	0.53	1/4957 (0.0%)
1	E	0.38	0/3666	0.52	0/4957
1	F	0.38	0/3658	0.52	0/4946
All	All	0.38	0/21988	0.52	2/29731 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	177	LEU	CA-CB-CG	5.51	127.98	115.30
1	C	177	LEU	CA-CB-CG	5.09	127.00	115.30

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	3578	0	3573	73	0
1	B	3578	0	3573	68	0
1	C	3578	0	3573	78	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	3578	0	3573	75	0
1	E	3578	0	3573	64	0
1	F	3570	0	3569	61	0
2	A	63	0	58	1	0
2	B	63	0	58	6	0
2	C	63	0	58	3	0
2	D	63	0	58	7	0
2	E	63	0	58	3	0
2	F	63	0	58	2	0
3	A	25	0	11	3	0
3	B	25	0	12	1	0
3	C	25	0	12	2	0
3	D	25	0	12	1	0
3	E	25	0	12	1	0
3	F	25	0	12	1	0
All	All	21988	0	21853	429	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 10.

All (429) 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)
3:C:703:GN8:HAK	3:C:703:GN8:SAP	1.92	1.09
1:A:278:ARG:HG3	1:A:278:ARG:HH11	1.16	1.05
1:A:212:ALA:H	1:A:213:PRO:HD3	1.18	1.02
3:B:702:GN8:HAK	3:B:702:GN8:SAP	2.09	0.93
3:F:706:GN8:HAK	3:F:706:GN8:SAP	2.10	0.92
3:A:701:GN8:HAK	3:A:701:GN8:SAP	2.13	0.89
1:C:192:ARG:HG2	1:C:192:ARG:HH11	1.37	0.89
1:E:336:ILE:HD11	1:E:345:LEU:HB2	1.57	0.86
3:D:704:GN8:SAP	3:D:704:GN8:HAK	2.15	0.86
1:C:60:ASP:H	1:C:426:ASN:HD21	1.25	0.84
1:C:181:ARG:HH11	1:C:181:ARG:HB3	1.44	0.83
1:D:339:ASN:HD22	1:D:342:TYR:H	1.26	0.82
1:A:278:ARG:NH1	1:A:278:ARG:HG3	1.95	0.80
1:E:149:ILE:HD11	1:E:168:ILE:HG23	1.65	0.79
1:B:60:ASP:H	1:B:426:ASN:HD21	1.32	0.78
1:E:70:ASP:HB3	1:E:196:LYS:HE3	1.66	0.77
1:A:60:ASP:H	1:A:426:ASN:HD21	1.31	0.77
1:B:297:ASN:HD21	1:B:351:TYR:HE2	1.34	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:388:ALA:O	1:A:393:MET:HG3	1.86	0.75
1:A:18:GLN:HE22	1:A:421:ASN:HD21	1.35	0.75
1:B:137:VAL:HB	1:B:147:ALA:HB3	1.66	0.75
1:D:325:ASP:HB3	1:D:380:LEU:HD11	1.67	0.74
1:B:187:ILE:HG23	2:B:602:MYA:H9MA	1.68	0.74
3:E:705:GN8:SAP	3:E:705:GN8:HAK	2.28	0.74
1:F:60:ASP:N	1:F:426:ASN:HD21	1.88	0.72
1:B:202:ALA:HB2	2:B:602:MYA:HEM	1.71	0.71
1:B:282:ARG:HH12	1:B:373:LEU:HD11	1.55	0.71
1:A:20:ASN:HD21	1:A:417:ASP:HB3	1.55	0.71
1:D:445:LYS:HD2	1:D:445:LYS:H	1.53	0.71
1:A:406:LEU:HG	1:A:447:ARG:HD3	1.73	0.71
1:A:266:LYS:HD2	1:A:269:ILE:HD12	1.73	0.70
1:A:212:ALA:H	1:A:213:PRO:CD	1.99	0.70
1:B:156:LEU:HD11	1:B:203:LEU:HB2	1.74	0.70
1:C:181:ARG:HH11	1:C:181:ARG:CB	2.05	0.69
1:F:41:TRP:HB3	1:F:211:PRO:HG3	1.74	0.69
1:B:278:ARG:HH11	1:B:278:ARG:CG	2.05	0.69
1:F:210:LEU:HB3	1:F:211:PRO:HD2	1.74	0.68
1:B:278:ARG:HH11	1:B:278:ARG:HG3	1.56	0.68
1:B:183:THR:HB	1:B:184:PRO:HD3	1.74	0.68
1:D:443:ASP:OD1	1:D:446:ARG:HG3	1.93	0.68
1:D:404:ASN:HD22	1:D:407:PHE:HZ	1.42	0.67
1:C:339:ASN:HD22	1:C:342:TYR:H	1.40	0.67
1:C:88:ASN:HB3	1:C:91:GLN:HB2	1.77	0.67
1:F:60:ASP:H	1:F:426:ASN:HD21	1.41	0.67
1:E:212:ALA:H	1:E:213:PRO:HD2	1.60	0.67
1:D:151:ALA:HB1	1:D:166:VAL:HG21	1.77	0.67
1:A:212:ALA:N	1:A:213:PRO:HD3	2.02	0.67
1:D:388:ALA:O	1:D:393:MET:HG3	1.93	0.67
1:F:408:LEU:O	1:F:413:PHE:HB2	1.96	0.66
1:C:183:THR:O	1:C:187:ILE:HG12	1.95	0.66
1:A:229:LEU:HD23	1:A:234:PHE:HB3	1.78	0.66
1:B:336:ILE:HD11	1:B:345:LEU:HB2	1.76	0.66
1:D:161:LYS:HG2	1:D:162:GLN:H	1.61	0.65
1:A:39:LYS:HG3	1:A:181:ARG:NH2	2.11	0.65
1:E:232:VAL:O	1:E:232:VAL:HG12	1.96	0.65
1:B:404:ASN:HA	1:B:407:PHE:CE2	2.30	0.65
1:D:405:THR:HG21	1:D:443:ASP:O	1.97	0.64
1:C:181:ARG:HH11	1:C:181:ARG:CG	2.11	0.64
1:E:202:ALA:HB3	1:E:425:PHE:HB3	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:60:ASP:H	1:D:426:ASN:HD21	1.46	0.64
1:E:212:ALA:H	1:E:213:PRO:CD	2.11	0.63
1:B:278:ARG:HG3	1:B:278:ARG:NH1	2.13	0.63
1:C:339:ASN:ND2	1:C:342:TYR:H	1.96	0.63
1:F:437:ASN:HB3	1:F:438:PRO:CD	2.28	0.63
1:D:165:SER:HA	1:D:199:ILE:HG23	1.80	0.63
1:E:205:THR:HG21	1:E:454:MET:HG3	1.81	0.62
1:E:325:ASP:HB3	1:E:380:LEU:HD11	1.81	0.62
1:D:53:VAL:HG13	1:D:430:LYS:HD3	1.81	0.62
1:E:210:LEU:O	1:E:213:PRO:HD3	2.00	0.62
1:E:68:ILE:HG22	1:E:196:LYS:HE2	1.81	0.62
1:D:60:ASP:N	1:D:426:ASN:HD21	1.98	0.62
1:F:263:LYS:HE3	1:F:263:LYS:H	1.65	0.62
1:C:151:ALA:HA	1:C:167:GLU:O	2.00	0.61
1:E:106:ASP:HB3	1:E:109:ALA:HB2	1.83	0.61
1:E:294:PHE:O	1:E:298:PHE:HD1	1.84	0.61
1:F:242:THR:H	1:F:245:ASP:HB2	1.66	0.60
1:D:405:THR:CG2	1:D:444:ILE:HA	2.32	0.60
1:E:211:PRO:O	1:E:212:ALA:HB2	2.01	0.60
1:C:192:ARG:NH1	1:C:192:ARG:HG2	2.13	0.60
1:A:382:TYR:O	1:A:386:ILE:HD12	2.02	0.60
1:B:68:ILE:HG13	1:B:195:ASN:HB3	1.84	0.60
1:D:305:PRO:HG2	1:D:308:LYS:HD3	1.83	0.60
1:E:137:VAL:HB	1:E:147:ALA:HB3	1.84	0.60
1:E:211:PRO:O	1:E:212:ALA:CB	2.50	0.59
1:A:14:LEU:HA	1:A:17:LEU:HD23	1.84	0.59
1:D:263:LYS:HD3	1:D:263:LYS:H	1.66	0.59
1:E:88:ASN:HD22	1:E:88:ASN:C	2.06	0.59
1:A:211:PRO:O	1:A:212:ALA:HB2	2.03	0.59
1:E:6:LYS:HD3	1:E:6:LYS:H	1.68	0.59
1:A:229:LEU:HD11	1:A:395:VAL:HB	1.85	0.59
1:D:96:PHE:HE2	1:D:117:LYS:HB3	1.68	0.59
1:E:388:ALA:O	1:E:393:MET:HG3	2.02	0.58
1:F:147:ALA:HB1	1:F:186:LEU:HD11	1.85	0.58
1:A:405:THR:CG2	1:A:444:ILE:HA	2.33	0.58
1:B:217:CYS:HB3	1:B:399:LEU:O	2.04	0.58
1:B:99:LEU:O	1:B:103:TYR:HB2	2.04	0.58
1:D:148:PHE:CZ	1:D:150:SER:HB3	2.37	0.58
1:B:117:LYS:O	1:B:121:ASN:HB2	2.03	0.58
1:F:356:ASP:HA	1:F:359:PHE:CD2	2.38	0.58
1:A:161:LYS:HG3	1:A:162:GLN:N	2.19	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:404:ASN:HA	1:F:407:PHE:CE2	2.38	0.58
1:B:324:THR:HG23	1:B:356:ASP:OD1	2.04	0.57
1:F:286:ILE:HG22	1:F:451:GLY:HA3	1.85	0.57
1:A:347:ILE:HG23	1:A:395:VAL:HG13	1.87	0.57
1:F:339:ASN:HD22	1:F:341:LYS:H	1.51	0.57
3:C:703:GN8:CAK	3:C:703:GN8:SAP	2.76	0.57
1:C:430:LYS:HG3	1:C:431:PRO:HD2	1.87	0.57
1:F:208:ILE:HD13	1:F:208:ILE:H	1.68	0.57
1:A:166:VAL:HG11	1:A:194:VAL:HG11	1.86	0.57
1:A:405:THR:HG21	1:A:443:ASP:O	2.05	0.57
1:D:232:VAL:O	1:D:232:VAL:HG12	2.05	0.57
1:E:56:GLU:HG2	1:E:429:ALA:HA	1.87	0.57
1:A:137:VAL:HB	1:A:147:ALA:HB3	1.86	0.57
1:B:159:ARG:NH2	1:B:430:LYS:HB2	2.19	0.57
1:D:212:ALA:H	1:D:213:PRO:HD3	1.70	0.57
1:C:232:VAL:HG12	1:C:232:VAL:O	2.04	0.57
1:B:444:ILE:H	1:B:444:ILE:HD13	1.69	0.57
1:E:373:LEU:HD22	1:E:377:LEU:HG	1.86	0.57
1:A:318:GLN:HG2	1:A:324:THR:OG1	2.04	0.56
1:B:229:LEU:HB3	1:B:235:THR:HG22	1.85	0.56
1:C:224:LEU:HD11	1:C:396:PHE:HB2	1.87	0.56
1:B:411:LEU:O	1:B:412:LYS:HB2	2.05	0.56
1:D:278:ARG:HD2	1:D:359:PHE:CE1	2.41	0.56
1:B:106:ASP:HB3	1:B:109:ALA:HB2	1.86	0.56
1:B:58:PRO:HB3	1:B:201:HIS:HE1	1.70	0.56
1:D:218:ARG:HB3	1:D:436:LEU:HD21	1.86	0.56
1:C:286:ILE:HG22	1:C:451:GLY:HA3	1.87	0.56
1:D:211:PRO:O	1:D:212:ALA:CB	2.53	0.56
1:C:202:ALA:HB2	2:C:603:MYA:HDMA	1.87	0.56
1:D:212:ALA:N	1:D:213:PRO:HD3	2.22	0.55
1:C:174:HIS:HB3	1:C:177:LEU:HD22	1.88	0.55
1:C:6:LYS:HE2	1:C:9:LYS:HD3	1.89	0.55
1:B:38:HIS:HA	2:B:602:MYA:P3X	2.47	0.55
1:F:403:ASP:HB3	1:F:406:LEU:HD12	1.87	0.55
1:D:242:THR:HG22	1:D:244:GLU:H	1.70	0.55
1:E:149:ILE:HD11	1:E:168:ILE:CG2	2.36	0.55
1:A:20:ASN:ND2	1:A:417:ASP:HB3	2.20	0.55
1:D:41:TRP:HH2	2:D:604:MYA:H8MA	1.72	0.55
1:D:211:PRO:O	1:D:212:ALA:HB3	2.06	0.55
1:B:202:ALA:HB3	1:B:425:PHE:HB3	1.87	0.55
1:D:365:PHE:HE2	1:D:446:ARG:HA	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:406:LEU:HG	1:D:447:ARG:HD3	1.89	0.55
1:B:102:ASN:HA	1:B:175:LYS:HE3	1.89	0.55
1:D:174:HIS:CD2	1:D:176:GLN:HB2	2.43	0.54
1:E:305:PRO:HG2	1:E:308:LYS:HG3	1.89	0.54
1:C:106:ASP:HB3	1:C:109:ALA:HB2	1.90	0.54
1:A:363:ASP:HB3	1:A:366:ASP:HB2	1.89	0.54
1:A:39:LYS:HG3	1:A:181:ARG:HH21	1.73	0.53
1:F:20:ASN:HB2	1:F:417:ASP:HB2	1.90	0.53
1:C:149:ILE:HD12	1:C:171:LEU:HD13	1.90	0.53
1:A:325:ASP:HB3	1:A:355:THR:HA	1.89	0.53
1:D:45:PRO:HB2	1:D:426:ASN:HD22	1.73	0.53
1:B:47:LYS:HB3	1:B:212:ALA:CB	2.38	0.53
1:C:60:ASP:H	1:C:426:ASN:ND2	2.01	0.53
1:D:127:PRO:HG2	1:D:293:GLU:HA	1.88	0.53
1:F:121:ASN:O	1:F:125:LYS:HB2	2.09	0.53
1:C:98:LEU:HD22	1:C:145:LEU:HG	1.91	0.53
1:D:183:THR:HB	1:D:184:PRO:HD3	1.91	0.53
1:E:205:THR:CG2	1:E:454:MET:HG3	2.39	0.53
1:F:88:ASN:HD22	1:F:89:LYS:N	2.06	0.53
1:B:269:ILE:HD11	1:B:299:ILE:HD13	1.90	0.52
1:B:175:LYS:HA	1:B:178:ARG:HG3	1.91	0.52
1:C:285:LEU:HB2	1:C:432:ILE:HD13	1.90	0.52
1:C:408:LEU:O	1:C:413:PHE:HB2	2.09	0.52
1:F:64:THR:HB	1:F:65:PRO:HD2	1.91	0.52
1:B:111:PHE:HA	1:B:335:THR:O	2.09	0.52
1:E:443:ASP:OD2	1:E:446:ARG:NH2	2.43	0.52
3:A:701:GN8:CAK	3:A:701:GN8:SAP	2.93	0.52
1:E:212:ALA:N	1:E:213:PRO:CD	2.72	0.52
1:C:202:ALA:HB3	1:C:425:PHE:HB3	1.90	0.52
1:C:156:LEU:HD11	1:C:203:LEU:HB2	1.91	0.52
1:C:242:THR:HG22	1:C:244:GLU:H	1.73	0.52
1:C:61:LYS:H	1:C:61:LYS:HD3	1.75	0.52
1:A:151:ALA:HB1	1:A:166:VAL:CG2	2.40	0.52
1:C:20:ASN:HB2	1:C:417:ASP:HB2	1.92	0.51
1:E:243:GLU:O	1:E:247:ILE:HG12	2.10	0.51
1:B:378:CYS:HA	1:B:411:LEU:HD11	1.90	0.51
1:F:315:VAL:HG13	1:F:323:ILE:HG23	1.92	0.51
1:F:336:ILE:HD13	1:F:345:LEU:HB2	1.93	0.51
1:F:290:THR:C	1:F:292:GLU:H	2.13	0.51
1:D:217:CYS:HB3	1:D:399:LEU:O	2.11	0.51
1:E:86:VAL:HG23	1:E:92:LEU:HD13	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:156:LEU:HG	1:C:165:SER:OG	2.10	0.51
1:D:336:ILE:H	1:D:344:ASP:HA	1.76	0.51
1:D:165:SER:HA	1:D:199:ILE:CG2	2.41	0.51
1:D:398:ALA:CB	1:D:408:LEU:HD21	2.41	0.50
1:C:405:THR:HG23	1:C:442:ASN:HB3	1.92	0.50
1:A:205:THR:HB	1:A:420:LEU:HD22	1.93	0.50
1:C:192:ARG:HH11	1:C:192:ARG:CG	2.17	0.50
1:A:405:THR:HG22	1:A:444:ILE:HA	1.94	0.50
1:C:403:ASP:HB3	1:C:406:LEU:HD12	1.94	0.50
1:B:186:LEU:O	1:B:190:ILE:HG22	2.12	0.50
1:F:114:ASN:HD22	1:F:114:ASN:C	2.14	0.50
1:E:360:GLN:HE21	1:E:360:GLN:HA	1.76	0.50
2:F:606:MYA:H2AA	2:F:606:MYA:H6M	1.93	0.50
1:D:263:LYS:CD	1:D:263:LYS:H	2.25	0.50
1:C:174:HIS:HB3	1:C:177:LEU:CD2	2.42	0.50
1:A:134:HIS:ND1	1:A:150:SER:HB2	2.27	0.50
1:E:298:PHE:HA	1:E:311:ILE:HG12	1.94	0.49
1:C:330:TYR:CE2	1:C:349:TYR:HB2	2.47	0.49
1:E:432:ILE:HG23	1:E:449:ASN:HB2	1.94	0.49
1:B:262:ARG:HG2	1:B:263:LYS:N	2.28	0.49
1:A:211:PRO:O	1:A:212:ALA:CB	2.61	0.49
1:E:83:SER:OG	1:E:132:ASP:OD2	2.26	0.49
1:F:59:ILE:HA	1:F:428:ARG:HH12	1.77	0.49
1:C:183:THR:HB	1:C:184:PRO:HD3	1.95	0.49
1:F:437:ASN:HB3	1:F:438:PRO:HD2	1.94	0.49
1:F:278:ARG:HD2	1:F:359:PHE:HE1	1.77	0.49
1:A:202:ALA:HB3	1:A:425:PHE:HB3	1.94	0.49
1:A:405:THR:HG21	1:A:443:ASP:C	2.33	0.49
1:A:84:ILE:HG23	1:A:91:GLN:HB3	1.94	0.49
1:B:229:LEU:HB3	1:B:235:THR:CG2	2.43	0.48
1:E:405:THR:HG21	1:E:443:ASP:O	2.12	0.48
1:D:171:LEU:HD22	2:D:604:MYA:H5MA	1.94	0.48
1:D:411:LEU:O	1:D:412:LYS:HB2	2.13	0.48
1:A:99:LEU:HB3	1:A:115:TYR:HD1	1.77	0.48
1:F:382:TYR:O	1:F:386:ILE:HD12	2.13	0.48
1:A:399:LEU:C	1:A:401:SER:H	2.17	0.48
1:B:305:PRO:HG2	1:B:308:LYS:HD2	1.96	0.48
1:D:149:ILE:HD12	1:D:171:LEU:HD13	1.96	0.48
1:B:205:THR:HB	1:B:420:LEU:HD22	1.96	0.48
1:A:154:VAL:HG21	1:A:167:GLU:HG3	1.96	0.48
1:D:405:THR:HG21	1:D:444:ILE:HA	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:187:ILE:HD12	2:C:603:MYA:H6MA	1.96	0.48
2:E:605:MYA:H6M	2:E:605:MYA:H2AA	1.95	0.48
1:C:282:ARG:HD3	1:C:364:ARG:HD2	1.95	0.48
1:B:93:GLU:HA	1:B:96:PHE:CZ	2.49	0.48
1:E:99:LEU:O	1:E:103:TYR:HB2	2.13	0.48
1:B:286:ILE:HG22	1:B:451:GLY:HA3	1.96	0.48
1:D:168:ILE:HG21	2:D:604:MYA:H7MA	1.95	0.48
1:F:149:ILE:HB	1:F:186:LEU:HD22	1.95	0.47
1:A:115:TYR:CE2	1:A:332:LEU:HD21	2.49	0.47
1:A:271:GLN:HB3	1:A:323:ILE:HD12	1.96	0.47
1:E:8:LYS:O	1:E:10:LEU:N	2.47	0.47
1:F:353:TYR:HE2	1:F:404:ASN:HD21	1.62	0.47
1:C:404:ASN:HA	1:C:407:PHE:CE2	2.49	0.47
1:B:165:SER:HB3	1:B:201:HIS:HB2	1.95	0.47
1:D:96:PHE:CD1	1:D:96:PHE:C	2.88	0.47
1:C:40:PHE:HE1	1:C:188:LYS:HE3	1.79	0.47
1:A:127:PRO:HG2	1:A:293:GLU:HA	1.96	0.47
1:D:99:LEU:HD13	1:D:103:TYR:CD1	2.49	0.47
1:C:232:VAL:CG1	1:C:232:VAL:O	2.63	0.47
1:E:187:ILE:HG23	2:E:605:MYA:H9M	1.97	0.47
1:E:65:PRO:HD3	1:E:198:ASP:OD2	2.15	0.47
1:D:191:THR:HA	2:D:604:MYA:HDMA	1.97	0.47
1:A:142:THR:O	1:A:143:GLN:HB2	2.14	0.47
1:A:258:THR:HG21	1:A:379:GLU:HB3	1.95	0.46
1:E:222:ARG:NH1	1:E:223:PRO:O	2.47	0.46
1:C:290:THR:H	1:C:293:GLU:HG2	1.79	0.46
1:C:282:ARG:HH22	1:C:358:ASP:CG	2.19	0.46
1:D:312:PHE:HB3	1:D:314:TYR:CE1	2.50	0.46
1:F:174:HIS:HD2	1:F:176:GLN:H	1.63	0.46
1:E:232:VAL:O	1:E:232:VAL:CG1	2.63	0.46
1:E:135:ILE:HG12	1:E:190:ILE:HD13	1.97	0.46
1:A:332:LEU:HB3	1:A:349:TYR:CE1	2.51	0.46
1:E:47:LYS:HG2	1:E:48:ASP:N	2.30	0.46
1:A:276:PHE:CE1	1:A:352:TYR:HB3	2.50	0.46
1:B:47:LYS:HB3	1:B:212:ALA:HB1	1.96	0.46
1:C:84:ILE:HG21	1:C:95:VAL:HG21	1.98	0.46
1:F:339:ASN:ND2	1:F:341:LYS:H	2.14	0.46
1:A:87:ASP:OD2	1:A:125:LYS:HE2	2.16	0.46
1:B:60:ASP:H	1:B:426:ASN:ND2	2.08	0.46
1:B:297:ASN:ND2	1:B:351:TYR:HE2	2.07	0.46
1:E:237:LEU:HA	1:E:238:PRO:HD3	1.84	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:339:ASN:ND2	1:E:342:TYR:H	2.13	0.46
1:B:151:ALA:HA	1:B:167:GLU:O	2.16	0.46
1:C:40:PHE:CE1	1:C:188:LYS:HE3	2.51	0.45
1:F:191:THR:HA	2:F:606:MYA:HDM	1.97	0.45
1:F:99:LEU:O	1:F:103:TYR:HB2	2.16	0.45
1:E:411:LEU:O	1:E:412:LYS:HB2	2.14	0.45
1:A:366:ASP:HB3	1:A:369:ALA:HB3	1.98	0.45
1:F:229:LEU:HB3	1:F:235:THR:HG22	1.98	0.45
1:C:122:TRP:CZ3	1:C:455:LEU:HD21	2.51	0.45
1:C:337:LEU:O	1:C:339:ASN:N	2.41	0.45
1:A:191:THR:HA	2:A:601:MYA:HDMA	1.97	0.45
1:A:159:ARG:NH2	1:A:430:LYS:O	2.49	0.45
1:D:212:ALA:H	1:D:213:PRO:CD	2.29	0.45
1:B:435:GLY:HA2	1:B:447:ARG:O	2.17	0.45
1:C:117:LYS:O	1:C:121:ASN:HB2	2.16	0.45
1:B:191:THR:HA	2:B:602:MYA:HDM	1.97	0.45
1:E:93:GLU:HA	1:E:96:PHE:CE2	2.52	0.45
1:F:232:VAL:HG12	1:F:232:VAL:O	2.16	0.45
1:D:154:VAL:HG21	1:D:167:GLU:HG3	1.99	0.45
1:D:315:VAL:HG23	1:D:326:PHE:HB2	1.99	0.45
1:E:218:ARG:HH21	1:E:415:PRO:HB2	1.82	0.45
1:B:325:ASP:HB3	1:B:380:LEU:HD11	1.98	0.45
1:B:88:ASN:HB3	1:B:91:GLN:HB2	1.99	0.45
1:F:88:ASN:HB3	1:F:91:GLN:HB2	1.98	0.45
1:F:53:VAL:HG11	1:F:428:ARG:HD3	1.99	0.45
1:A:19:LEU:HD11	1:B:177:LEU:HD22	1.98	0.45
1:D:113:PHE:HD2	1:D:332:LEU:HD21	1.81	0.45
1:B:298:PHE:HA	1:B:311:ILE:HG12	1.97	0.45
1:E:183:THR:HA	1:E:186:LEU:HD12	1.99	0.45
1:D:398:ALA:HB3	1:D:408:LEU:HD21	1.98	0.45
1:D:338:ASN:C	1:D:338:ASN:HD22	2.21	0.45
1:A:258:THR:CG2	1:A:379:GLU:HB3	2.47	0.44
1:F:178:ARG:C	1:F:180:LYS:H	2.21	0.44
1:C:122:TRP:HZ3	1:C:455:LEU:HD21	1.82	0.44
1:E:71:LYS:O	1:E:71:LYS:HG2	2.17	0.44
1:C:40:PHE:CD1	1:C:184:PRO:HB3	2.52	0.44
1:E:283:PHE:CE2	1:E:402:GLN:HA	2.52	0.44
1:F:388:ALA:O	1:F:393:MET:HG3	2.17	0.44
1:A:183:THR:HB	1:A:184:PRO:HD3	1.99	0.44
1:C:105:GLU:HG3	1:C:178:ARG:HH12	1.82	0.44
1:D:173:VAL:HB	2:D:604:MYA:H14B	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:405:THR:HG21	1:B:447:ARG:HA	2.00	0.44
1:E:362:LYS:H	1:E:362:LYS:HD2	1.81	0.44
1:E:264:LEU:HD12	1:E:268:ASP:HB2	2.00	0.44
1:F:430:LYS:HB3	1:F:431:PRO:HD2	1.99	0.44
1:E:272:VAL:HG22	1:E:323:ILE:HG21	1.99	0.44
1:B:399:LEU:O	1:B:400:THR:OG1	2.34	0.44
1:F:174:HIS:CD2	1:F:176:GLN:H	2.35	0.44
1:F:174:HIS:HB3	1:F:177:LEU:HD23	1.99	0.44
1:E:107:ARG:O	1:E:112:ARG:NH2	2.47	0.44
1:C:181:ARG:HH11	1:C:181:ARG:HG3	1.81	0.44
1:E:88:ASN:HD22	1:E:89:LYS:N	2.14	0.44
1:D:187:ILE:HG23	2:D:604:MYA:HAMA	1.98	0.44
1:D:339:ASN:ND2	1:D:342:TYR:H	2.05	0.43
1:C:154:VAL:HG21	1:C:167:GLU:HG3	1.99	0.43
1:D:228:LYS:O	1:D:232:VAL:HG23	2.18	0.43
1:A:232:VAL:O	1:A:232:VAL:CG1	2.65	0.43
1:B:159:ARG:HG3	1:B:284:GLU:HB3	1.99	0.43
1:D:191:THR:HA	2:D:604:MYA:CDM	2.48	0.43
1:D:272:VAL:HG22	1:D:323:ILE:HG21	1.99	0.43
1:E:179:SER:HA	2:E:605:MYA:O2A	2.18	0.43
1:C:93:GLU:HA	1:C:96:PHE:CZ	2.54	0.43
1:C:195:ASN:C	1:C:197:CYS:H	2.22	0.43
1:C:211:PRO:O	1:C:212:ALA:HB3	2.18	0.43
1:F:60:ASP:HB2	1:F:426:ASN:ND2	2.34	0.43
1:E:405:THR:HG21	1:E:447:ARG:HA	1.99	0.43
1:B:20:ASN:ND2	1:B:417:ASP:HB2	2.34	0.43
1:B:107:ARG:HD2	1:B:175:LYS:HZ3	1.84	0.43
1:C:138:ARG:HG2	1:C:145:LEU:HA	2.00	0.43
1:F:314:TYR:HB2	1:F:327:PHE:CE2	2.53	0.43
1:F:133:TRP:HB3	1:F:151:ALA:HB3	2.01	0.43
1:D:358:ASP:HB3	1:D:373:LEU:HB2	2.00	0.43
1:B:401:SER:O	1:B:404:ASN:HB2	2.19	0.43
1:C:169:ASN:HA	1:C:169:ASN:HD22	1.56	0.43
1:D:212:ALA:N	1:D:213:PRO:CD	2.81	0.43
1:D:128:GLY:O	1:D:153:PRO:HG3	2.19	0.43
1:D:64:THR:C	1:D:66:GLU:H	2.21	0.43
1:A:99:LEU:O	1:A:103:TYR:HB2	2.19	0.42
1:F:277:LYS:HZ1	1:F:288:ILE:HA	1.84	0.42
1:E:391:ALA:O	1:E:392:ASN:HB2	2.19	0.42
1:D:266:LYS:HA	1:D:269:ILE:HD12	2.00	0.42
1:B:40:PHE:CD1	1:B:184:PRO:HB3	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:64:THR:O	1:E:67:ASP:HB2	2.19	0.42
1:C:444:ILE:H	1:C:444:ILE:HD13	1.83	0.42
3:A:701:GN8:SAE	3:A:701:GN8:CAS	3.07	0.42
1:A:165:SER:HB3	1:A:201:HIS:HB2	2.01	0.42
1:D:404:ASN:HA	1:D:407:PHE:CE2	2.54	0.42
1:D:332:LEU:HB3	1:D:349:TYR:CE1	2.54	0.42
1:C:324:THR:HG23	1:C:356:ASP:OD1	2.20	0.42
1:C:391:ALA:O	1:C:392:ASN:HB2	2.19	0.42
1:B:201:HIS:ND1	1:B:426:ASN:O	2.50	0.42
1:B:99:LEU:HD13	1:B:103:TYR:CE1	2.54	0.42
1:D:214:VAL:HG21	1:D:424:LEU:HD12	2.02	0.42
1:A:252:LEU:HD21	1:A:385:CYS:HB3	2.00	0.42
1:A:278:ARG:CG	1:A:278:ARG:NH1	2.72	0.42
1:B:425:PHE:CG	2:B:602:MYA:HBMA	2.54	0.42
1:F:88:ASN:HD22	1:F:88:ASN:C	2.23	0.42
1:A:99:LEU:HD12	1:A:103:TYR:CD1	2.53	0.42
1:A:232:VAL:HG12	1:A:232:VAL:O	2.18	0.42
1:D:96:PHE:HD1	1:D:96:PHE:C	2.21	0.42
1:C:352:TYR:CE1	1:C:451:GLY:O	2.73	0.42
1:E:10:LEU:HD12	1:E:10:LEU:H	1.83	0.42
1:F:148:PHE:CE2	1:F:150:SER:HB2	2.55	0.42
1:A:311:ILE:HD13	1:A:312:PHE:N	2.35	0.42
1:B:301:GLU:HB3	1:B:304:LEU:HD11	2.01	0.42
1:D:311:ILE:HD13	1:D:312:PHE:N	2.34	0.42
1:B:445:LYS:HD2	1:B:446:ARG:H	1.85	0.42
1:F:190:ILE:HD13	1:F:190:ILE:HA	1.92	0.42
1:D:130:LYS:HA	1:D:130:LYS:HE2	2.02	0.42
1:D:178:ARG:O	1:D:179:SER:HB2	2.20	0.42
1:C:352:TYR:HE1	1:C:451:GLY:O	2.03	0.41
1:D:298:PHE:O	1:D:313:SER:HB2	2.18	0.41
1:F:59:ILE:HG23	1:F:428:ARG:NH2	2.35	0.41
1:C:93:GLU:HA	1:C:96:PHE:CE2	2.55	0.41
1:B:194:VAL:HG11	2:B:602:MYA:HEMA	2.02	0.41
1:B:256:THR:HB	1:B:383:ASP:OD1	2.20	0.41
1:F:136:GLY:HA3	1:F:145:LEU:HD11	2.00	0.41
1:C:280:GLN:HG3	1:C:286:ILE:HG21	2.00	0.41
1:C:111:PHE:HA	1:C:335:THR:O	2.19	0.41
1:E:86:VAL:HG11	1:E:125:LYS:HG2	2.00	0.41
1:C:279:TYR:O	1:C:282:ARG:HG2	2.20	0.41
1:B:406:LEU:HD11	1:B:447:ARG:NH1	2.35	0.41
1:C:214:VAL:HG12	1:C:422:PHE:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:311:ILE:HD13	1:F:312:PHE:N	2.36	0.41
1:A:96:PHE:CD1	1:A:96:PHE:C	2.94	0.41
1:E:271:GLN:OE1	1:E:322:LYS:HG2	2.21	0.41
1:A:437:ASN:HB3	1:A:438:PRO:HD2	2.02	0.41
1:F:230:TYR:HD2	1:F:235:THR:O	2.04	0.41
1:B:406:LEU:HG	1:B:447:ARG:HD3	2.03	0.41
1:C:302:GLU:HG3	1:C:303:SER:N	2.36	0.41
1:C:192:ARG:NH1	1:C:192:ARG:CG	2.79	0.41
1:F:396:PHE:HD2	1:F:413:PHE:HZ	1.66	0.41
1:C:400:THR:HA	1:C:408:LEU:HD11	2.02	0.41
1:C:356:ASP:OD1	1:C:356:ASP:C	2.58	0.41
1:C:56:GLU:HG2	1:C:429:ALA:HA	2.01	0.41
1:A:86:VAL:HG13	1:A:92:LEU:HD13	2.03	0.41
1:C:181:ARG:NH1	1:C:181:ARG:HB3	2.23	0.41
1:E:149:ILE:HD12	1:E:190:ILE:HG21	2.03	0.41
1:F:222:ARG:HB2	1:F:413:PHE:CE2	2.55	0.41
1:F:98:LEU:HD22	1:F:145:LEU:HD23	2.03	0.41
1:E:217:CYS:HB3	1:E:400:THR:OG1	2.21	0.41
1:A:60:ASP:H	1:A:426:ASN:ND2	2.09	0.41
1:F:183:THR:HB	1:F:184:PRO:HD3	2.03	0.41
1:A:174:HIS:HD2	1:A:176:GLN:HB2	1.86	0.41
1:A:256:THR:HG21	1:A:387:LEU:HG	2.02	0.41
1:F:347:ILE:HG23	1:F:395:VAL:HG13	2.03	0.41
1:A:237:LEU:HA	1:A:238:PRO:HD3	1.95	0.41
1:C:168:ILE:HG21	2:C:603:MYA:H7M	2.02	0.41
1:E:339:ASN:ND2	1:E:341:LYS:H	2.19	0.41
1:D:276:PHE:O	1:D:280:GLN:HB2	2.21	0.41
1:A:73:LEU:HD23	1:A:74:PRO:HD2	2.03	0.41
1:A:426:ASN:O	1:A:427:TYR:HB2	2.21	0.40
1:F:45:PRO:HB2	1:F:426:ASN:HD22	1.86	0.40
1:C:339:ASN:ND2	1:C:341:LYS:H	2.19	0.40
1:A:73:LEU:HA	1:A:74:PRO:HD3	1.90	0.40
1:A:180:LYS:HA	1:A:180:LYS:HD3	1.86	0.40
1:A:404:ASN:HA	1:A:407:PHE:CE2	2.56	0.40
1:B:283:PHE:CE2	1:B:402:GLN:HA	2.57	0.40
1:C:181:ARG:NH1	1:C:181:ARG:CG	2.78	0.40
1:F:404:ASN:C	1:F:406:LEU:H	2.24	0.40
1:C:91:GLN:O	1:C:95:VAL:HG23	2.20	0.40
1:D:210:LEU:HB3	1:D:211:PRO:HD2	2.04	0.40
1:F:401:SER:O	1:F:402:GLN:HB2	2.22	0.40
1:D:76:LEU:HB3	1:D:77:SER:H	1.61	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:306:LEU:HD21	1:B:391:ALA:HA	2.04	0.40

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	432/455 (95%)	391 (90%)	33 (8%)	8 (2%)	10	40
1	B	432/455 (95%)	382 (88%)	38 (9%)	12 (3%)	6	30
1	C	432/455 (95%)	376 (87%)	50 (12%)	6 (1%)	14	48
1	D	432/455 (95%)	376 (87%)	44 (10%)	12 (3%)	6	30
1	E	432/455 (95%)	391 (90%)	35 (8%)	6 (1%)	14	48
1	F	431/455 (95%)	373 (86%)	52 (12%)	6 (1%)	14	48
All	All	2591/2730 (95%)	2289 (88%)	252 (10%)	50 (2%)	10	40

All (50) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	212	ALA
1	B	78	SER
1	C	302	GLU
1	D	135	ILE
1	D	212	ALA
1	D	301	GLU
1	E	9	LYS
1	E	212	ALA
1	B	77	SER
1	B	413	PHE
1	C	78	SER

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Mol	Chain	Res	Type
1	D	51	GLU
1	D	77	SER
1	B	88	ASN
1	B	140	LYS
1	B	303	SER
1	C	338	ASN
1	C	427	TYR
1	D	76	LEU
1	D	337	LEU
1	E	78	SER
1	E	338	ASN
1	F	56	GLU
1	A	158	VAL
1	B	306	LEU
1	B	321	GLY
1	D	303	SER
1	D	338	ASN
1	D	412	LYS
1	F	42	ARG
1	F	269	ILE
1	F	291	LYS
1	A	65	PRO
1	A	78	SER
1	A	159	ARG
1	B	269	ILE
1	B	291	LYS
1	C	212	ALA
1	C	431	PRO
1	E	402	GLN
1	E	412	LYS
1	F	400	THR
1	A	400	THR
1	D	62	PRO
1	A	74	PRO
1	B	211	PRO
1	D	431	PRO
1	B	212	ALA
1	F	367	PRO
1	A	127	PRO



### 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	394/413 (95%)	361 (92%)	33 (8%)	14	46
1	B	394/413 (95%)	361 (92%)	33 (8%)	14	46
1	C	394/413 (95%)	358 (91%)	36 (9%)	12	40
1	D	394/413 (95%)	358 (91%)	36 (9%)	12	40
1	E	394/413 (95%)	362 (92%)	32 (8%)	15	47
1	F	393/413 (95%)	359 (91%)	34 (9%)	13	44
All	All	2363/2478 (95%)	2159 (91%)	204 (9%)	13	45

All (204) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	LEU
1	A	21	ASN
1	A	64	THR
1	A	70	ASP
1	A	73	LEU
1	A	96	PHE
1	A	99	LEU
1	A	108	ASP
1	A	114	ASN
1	A	116	THR
1	A	132	ASP
1	A	135	ILE
1	A	181	ARG
1	A	190	ILE
1	A	220	THR
1	A	222	ARG
1	A	229	LEU
1	A	261	LEU
1	A	278	ARG
1	A	286	ILE
1	A	311	ILE
1	A	320	ASP

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Mol	Chain	Res	Type
1	A	325	ASP
1	A	326	PHE
1	A	332	LEU
1	A	335	THR
1	A	338	ASN
1	A	339	ASN
1	A	347	ILE
1	A	351	TYR
1	A	373	LEU
1	A	410	ASP
1	A	438	PRO
1	B	19	LEU
1	B	37	ASP
1	B	71	LYS
1	B	73	LEU
1	B	88	ASN
1	B	99	LEU
1	B	103	TYR
1	B	165	SER
1	B	181	ARG
1	B	208	ILE
1	B	210	LEU
1	B	222	ARG
1	B	229	LEU
1	B	242	THR
1	B	261	LEU
1	B	268	ASP
1	B	270	ASP
1	B	278	ARG
1	B	297	ASN
1	B	320	ASP
1	B	325	ASP
1	B	332	LEU
1	B	339	ASN
1	B	351	TYR
1	B	362	LYS
1	B	371	LYS
1	B	383	ASP
1	B	399	LEU
1	B	410	ASP
1	B	420	LEU
1	B	444	ILE

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Mol	Chain	Res	Type
1	B	445	LYS
1	B	452	VAL
1	C	6	LYS
1	C	8	LYS
1	C	21	ASN
1	C	48	ASP
1	C	50	ASP
1	C	61	LYS
1	C	71	LYS
1	C	88	ASN
1	C	94	ASP
1	C	135	ILE
1	C	162	GLN
1	C	169	ASN
1	C	177	LEU
1	C	181	ARG
1	C	221	HIS
1	C	222	ARG
1	C	249	GLU
1	C	261	LEU
1	C	278	ARG
1	C	280	GLN
1	C	285	LEU
1	C	311	ILE
1	C	315	VAL
1	C	326	PHE
1	C	344	ASP
1	C	351	TYR
1	C	356	ASP
1	C	362	LYS
1	C	371	LYS
1	C	373	LEU
1	C	386	ILE
1	C	395	VAL
1	C	410	ASP
1	C	420	LEU
1	C	444	ILE
1	C	445	LYS
1	D	12	ASN
1	D	37	ASP
1	D	53	VAL
1	D	87	ASP

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Mol	Chain	Res	Type
1	D	94	ASP
1	D	96	PHE
1	D	99	LEU
1	D	116	THR
1	D	130	LYS
1	D	166	VAL
1	D	173	VAL
1	D	176	GLN
1	D	177	LEU
1	D	252	LEU
1	D	263	LYS
1	D	268	ASP
1	D	269	ILE
1	D	278	ARG
1	D	297	ASN
1	D	299	ILE
1	D	311	ILE
1	D	315	VAL
1	D	323	ILE
1	D	326	PHE
1	D	338	ASN
1	D	340	THR
1	D	343	LYS
1	D	362	LYS
1	D	371	LYS
1	D	383	ASP
1	D	399	LEU
1	D	410	ASP
1	D	420	LEU
1	D	421	ASN
1	D	430	LYS
1	D	445	LYS
1	E	6	LYS
1	E	53	VAL
1	E	60	ASP
1	E	73	LEU
1	E	88	ASN
1	E	114	ASN
1	E	149	ILE
1	E	152	ILE
1	E	166	VAL
1	E	177	LEU

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Mol	Chain	Res	Type
1	E	208	ILE
1	E	222	ARG
1	E	234	PHE
1	E	239	ASP
1	E	252	LEU
1	E	256	THR
1	E	257	LYS
1	E	261	LEU
1	E	291	LYS
1	E	317	GLU
1	E	332	LEU
1	E	339	ASN
1	E	340	THR
1	E	344	ASP
1	E	351	TYR
1	E	360	GLN
1	E	362	LYS
1	E	371	LYS
1	E	373	LEU
1	E	405	THR
1	E	420	LEU
1	E	445	LYS
1	F	9	LYS
1	F	67	ASP
1	F	88	ASN
1	F	96	PHE
1	F	107	ARG
1	F	114	ASN
1	F	117	LYS
1	F	149	ILE
1	F	168	ILE
1	F	182	LEU
1	F	186	LEU
1	F	190	ILE
1	F	208	ILE
1	F	220	THR
1	F	243	GLU
1	F	263	LYS
1	F	268	ASP
1	F	269	ILE
1	F	286	ILE
1	F	291	LYS

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Mol	Chain	Res	Type
1	F	295	GLU
1	F	307	ASP
1	F	311	ILE
1	F	315	VAL
1	F	325	ASP
1	F	326	PHE
1	F	327	PHE
1	F	335	THR
1	F	339	ASN
1	F	351	TYR
1	F	368	LYS
1	F	373	LEU
1	F	404	ASN
1	F	452	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (75) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	174	HIS
1	A	195	ASN
1	A	250	ASN
1	A	338	ASN
1	A	339	ASN
1	A	397	ASN
1	A	404	ASN
1	A	421	ASN
1	A	426	ASN
1	B	20	ASN
1	B	88	ASN
1	B	174	HIS
1	B	176	GLN
1	B	195	ASN
1	B	297	ASN
1	B	318	GLN
1	B	339	ASN
1	B	397	ASN
1	B	404	ASN
1	B	421	ASN
1	B	426	ASN
1	B	442	ASN
1	C	20	ASN
1	C	88	ASN

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Mol	Chain	Res	Type
1	C	91	GLN
1	C	114	ASN
1	C	162	GLN
1	C	169	ASN
1	C	174	HIS
1	C	339	ASN
1	C	397	ASN
1	C	404	ASN
1	C	421	ASN
1	C	426	ASN
1	C	437	ASN
1	D	18	GLN
1	D	20	ASN
1	D	21	ASN
1	D	114	ASN
1	D	176	GLN
1	D	195	ASN
1	D	221	HIS
1	D	241	HIS
1	D	338	ASN
1	D	339	ASN
1	D	397	ASN
1	D	421	ASN
1	D	426	ASN
1	D	442	ASN
1	E	88	ASN
1	E	114	ASN
1	E	121	ASN
1	E	174	HIS
1	E	195	ASN
1	E	339	ASN
1	E	360	GLN
1	E	397	ASN
1	E	404	ASN
1	E	421	ASN
1	E	426	ASN
1	E	437	ASN
1	E	449	ASN
1	F	88	ASN
1	F	91	GLN
1	F	114	ASN
1	F	174	HIS

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Mol	Chain	Res	Type
1	F	176	GLN
1	F	195	ASN
1	F	296	HIS
1	F	338	ASN
1	F	339	ASN
1	F	397	ASN
1	F	404	ASN
1	F	421	ASN
1	F	426	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

12 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	MYA	A	601	-	53,65,65	0.71	2 (3%)	65,91,91	1.86	8 (12%)
3	GN8	A	701	-	24,27,27	3.42	5 (20%)	32,38,38	3.35	11 (34%)
2	MYA	B	602	-	53,65,65	0.71	1 (1%)	65,91,91	1.96	9 (13%)
3	GN8	B	702	-	24,27,27	3.39	6 (25%)	32,38,38	3.36	11 (34%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	MYA	C	603	-	53,65,65	0.70	2 (3%)	65,91,91	1.88	9 (13%)
3	GN8	C	703	-	24,27,27	3.38	5 (20%)	32,38,38	3.48	10 (31%)
2	MYA	D	604	-	53,65,65	0.73	2 (3%)	65,91,91	1.85	9 (13%)
3	GN8	D	704	-	24,27,27	3.41	5 (20%)	32,38,38	3.41	12 (37%)
2	MYA	E	605	-	53,65,65	0.71	1 (1%)	65,91,91	1.90	8 (12%)
3	GN8	E	705	-	24,27,27	3.63	10 (41%)	32,38,38	3.30	12 (37%)
2	MYA	F	606	-	53,65,65	0.70	1 (1%)	65,91,91	1.88	9 (13%)
3	GN8	F	706	-	24,27,27	3.42	6 (25%)	32,38,38	3.32	11 (34%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MYA	A	601	-	1/1/12/14	0/59/80/80	0/3/3/3
3	GN8	A	701	-	-	0/9/28/28	0/3/3/3
2	MYA	B	602	-	1/1/12/14	0/59/80/80	0/3/3/3
3	GN8	B	702	-	-	0/9/28/28	0/3/3/3
2	MYA	C	603	-	1/1/12/14	0/59/80/80	0/3/3/3
3	GN8	C	703	-	-	0/9/28/28	0/3/3/3
2	MYA	D	604	-	1/1/12/14	0/59/80/80	0/3/3/3
3	GN8	D	704	-	-	0/9/28/28	0/3/3/3
2	MYA	E	605	-	1/1/12/14	0/59/80/80	0/3/3/3
3	GN8	E	705	-	-	0/9/28/28	0/3/3/3
2	MYA	F	606	-	1/1/12/14	0/59/80/80	0/3/3/3
3	GN8	F	706	-	-	0/9/28/28	0/3/3/3

All (46) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	705	GN8	CAU-CAW	-4.62	1.39	1.48
3	A	701	GN8	CAU-CAW	-4.55	1.39	1.48
3	F	706	GN8	CAU-CAW	-4.50	1.39	1.48
3	B	702	GN8	CAU-CAW	-4.46	1.39	1.48
3	C	703	GN8	CAU-CAW	-4.44	1.39	1.48
3	D	704	GN8	CAU-CAW	-4.42	1.39	1.48
2	E	605	MYA	C2-S1	-3.43	1.76	1.81
2	B	602	MYA	C2-S1	-3.37	1.76	1.81
2	D	604	MYA	C2-S1	-3.36	1.76	1.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	MYA	C2-S1	-3.19	1.77	1.81
2	C	603	MYA	C2-S1	-2.80	1.77	1.81
2	F	606	MYA	C2-S1	-2.67	1.77	1.81
3	E	705	GN8	CAU-NAX	-2.11	1.35	1.39
3	F	706	GN8	CAU-NAX	-2.08	1.35	1.39
3	B	702	GN8	CAU-NAX	-2.02	1.35	1.39
2	D	604	MYA	O4X-C1X	2.01	1.43	1.41
2	A	601	MYA	O4X-C1X	2.05	1.43	1.41
2	C	603	MYA	O4X-C1X	2.10	1.43	1.41
3	E	705	GN8	CAG-CAI	2.46	1.44	1.38
3	E	705	GN8	CAL-CAS	2.57	1.44	1.38
3	A	701	GN8	OAA-CAU	2.80	1.29	1.23
3	E	705	GN8	OAA-CAU	2.80	1.29	1.23
3	F	706	GN8	OAA-CAU	2.91	1.29	1.23
3	B	702	GN8	OAA-CAU	2.92	1.29	1.23
3	C	703	GN8	OAA-CAU	2.96	1.29	1.23
3	D	704	GN8	OAA-CAU	3.01	1.29	1.23
3	E	705	GN8	CAH-CAG	3.12	1.46	1.38
3	E	705	GN8	CAM-CAS	3.47	1.46	1.38
3	D	704	GN8	CAV-SAE	4.60	1.77	1.66
3	A	701	GN8	CAV-SAE	4.62	1.77	1.66
3	B	702	GN8	CAV-SAE	4.62	1.77	1.66
3	E	705	GN8	CAV-SAE	4.65	1.78	1.66
3	F	706	GN8	CAV-SAE	4.65	1.78	1.66
3	C	703	GN8	CAV-SAE	4.66	1.78	1.66
3	B	702	GN8	OAD-NAY	8.63	1.39	1.22
3	E	705	GN8	OAD-NAY	8.65	1.39	1.22
3	F	706	GN8	OAD-NAY	8.65	1.39	1.22
3	A	701	GN8	OAD-NAY	8.66	1.39	1.22
3	D	704	GN8	OAD-NAY	8.71	1.40	1.22
3	C	703	GN8	OAD-NAY	8.77	1.40	1.22
3	C	703	GN8	CAF-CAW	11.65	1.49	1.34
3	B	702	GN8	CAF-CAW	11.75	1.49	1.34
3	F	706	GN8	CAF-CAW	11.83	1.49	1.34
3	D	704	GN8	CAF-CAW	11.87	1.49	1.34
3	A	701	GN8	CAF-CAW	11.91	1.49	1.34
3	E	705	GN8	CAF-CAW	12.04	1.50	1.34

All (119) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	602	MYA	N3A-C2A-N1A	-10.63	120.75	128.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	603	MYA	N3A-C2A-N1A	-10.24	121.05	128.89
2	D	604	MYA	N3A-C2A-N1A	-10.16	121.11	128.89
2	F	606	MYA	N3A-C2A-N1A	-10.05	121.20	128.89
2	A	601	MYA	N3A-C2A-N1A	-9.97	121.26	128.89
2	E	605	MYA	N3A-C2A-N1A	-9.96	121.27	128.89
3	C	703	GN8	CAF-CAW-SAP	-8.48	119.87	129.31
3	B	702	GN8	CAF-CAW-SAP	-7.25	121.25	129.31
3	F	706	GN8	CAF-CAW-SAP	-7.21	121.29	129.31
3	A	701	GN8	CAF-CAW-SAP	-7.17	121.33	129.31
3	D	704	GN8	CAF-CAW-SAP	-7.00	121.53	129.31
3	B	702	GN8	CAV-SAP-CAW	-6.73	86.33	92.96
3	D	704	GN8	CAV-SAP-CAW	-6.67	86.39	92.96
3	A	701	GN8	CAV-SAP-CAW	-6.65	86.41	92.96
3	F	706	GN8	CAV-SAP-CAW	-6.63	86.43	92.96
3	C	703	GN8	CAV-SAP-CAW	-6.61	86.45	92.96
3	E	705	GN8	CAV-SAP-CAW	-6.54	86.51	92.96
3	D	704	GN8	CAN-CAT-CAQ	-5.72	119.11	121.77
3	E	705	GN8	OAA-CAU-CAW	-5.67	119.73	126.50
3	E	705	GN8	CAF-CAW-SAP	-5.51	123.18	129.31
3	E	705	GN8	CAN-CAT-CAQ	-5.46	119.23	121.77
3	A	701	GN8	OAA-CAU-CAW	-5.26	120.22	126.50
3	D	704	GN8	OAA-CAU-CAW	-5.21	120.28	126.50
3	C	703	GN8	OAA-CAU-CAW	-5.04	120.48	126.50
3	F	706	GN8	OAA-CAU-CAW	-5.02	120.51	126.50
3	B	702	GN8	OAA-CAU-CAW	-5.01	120.52	126.50
3	E	705	GN8	CAV-NAX-CAU	-4.93	105.77	116.87
3	A	701	GN8	CAV-NAX-CAU	-4.90	105.84	116.87
3	F	706	GN8	CAN-CAT-CAQ	-4.85	119.52	121.77
3	D	704	GN8	CAV-NAX-CAU	-4.83	106.01	116.87
3	B	702	GN8	CAV-NAX-CAU	-4.83	106.01	116.87
3	F	706	GN8	CAV-NAX-CAU	-4.68	106.33	116.87
3	C	703	GN8	CAV-NAX-CAU	-4.62	106.48	116.87
3	B	702	GN8	CAN-CAT-CAQ	-4.62	119.62	121.77
3	C	703	GN8	CAN-CAT-CAQ	-4.55	119.66	121.77
3	A	701	GN8	CAN-CAT-CAQ	-4.24	119.80	121.77
3	C	703	GN8	CAR-CAF-CAW	-4.09	123.46	130.44
2	E	605	MYA	C2-C3-N4	-4.02	104.32	112.36
2	A	601	MYA	P2A-O3A-P1A	-3.84	121.95	132.73
2	B	602	MYA	P2A-O3A-P1A	-3.65	122.47	132.73
2	E	605	MYA	P2A-O3A-P1A	-3.55	122.77	132.73
2	C	603	MYA	C2-C3-N4	-3.54	105.28	112.36
2	B	602	MYA	C2-C3-N4	-3.53	105.30	112.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	701	GN8	SAP-CAV-SAE	-3.52	116.26	123.28
3	D	704	GN8	SAP-CAV-SAE	-3.48	116.34	123.28
3	C	703	GN8	SAP-CAV-SAE	-3.44	116.42	123.28
3	F	706	GN8	SAP-CAV-SAE	-3.43	116.44	123.28
3	B	702	GN8	SAP-CAV-SAE	-3.34	116.63	123.28
2	F	606	MYA	C2-C3-N4	-3.33	105.70	112.36
2	D	604	MYA	P2A-O3A-P1A	-3.30	123.47	132.73
3	E	705	GN8	SAP-CAV-SAE	-3.29	116.73	123.28
2	B	602	MYA	C6-C7-N8	-3.27	104.69	111.88
2	A	601	MYA	C2-C3-N4	-3.27	105.81	112.36
2	F	606	MYA	P2A-O3A-P1A	-3.05	124.17	132.73
2	C	603	MYA	P2A-O3A-P1A	-3.02	124.24	132.73
2	E	605	MYA	C6-C7-N8	-3.02	105.25	111.88
3	B	702	GN8	CAR-CAF-CAW	-2.78	125.70	130.44
3	F	706	GN8	CAR-CAF-CAW	-2.70	125.83	130.44
2	D	604	MYA	C2-C3-N4	-2.61	107.13	112.36
3	A	701	GN8	CAR-CAF-CAW	-2.52	126.14	130.44
2	F	606	MYA	C6-C7-N8	-2.41	106.60	111.88
2	D	604	MYA	C6-C7-N8	-2.37	106.69	111.88
2	C	603	MYA	C6-C7-N8	-2.32	106.80	111.88
3	D	704	GN8	CAR-CAF-CAW	-2.24	126.63	130.44
2	C	603	MYA	C4A-C5A-N7A	-2.23	107.43	109.48
2	B	602	MYA	C4A-C5A-N7A	-2.20	107.45	109.48
2	E	605	MYA	C4A-C5A-N7A	-2.12	107.53	109.48
2	F	606	MYA	C4A-C5A-N7A	-2.05	107.59	109.48
2	C	603	MYA	C13-C11-C12	-2.02	105.88	108.50
2	A	601	MYA	C4A-C5A-N7A	-2.02	107.62	109.48
2	D	604	MYA	C4A-C5A-N7A	-2.00	107.64	109.48
2	F	606	MYA	C2-S1-C2M	2.02	103.32	100.40
3	E	705	GN8	CAN-CAT-NAY	2.05	119.24	116.59
2	F	606	MYA	C3-N4-C5	2.12	126.96	122.79
2	D	604	MYA	C14-C11-C10	2.20	113.37	109.34
3	D	704	GN8	CAN-CAT-NAY	2.21	119.45	116.59
2	B	602	MYA	C3-N4-C5	2.27	127.25	122.79
2	A	601	MYA	C14-C11-C10	2.28	113.51	109.34
2	A	601	MYA	C3-N4-C5	2.31	127.34	122.79
2	C	603	MYA	C3-N4-C5	2.36	127.44	122.79
2	E	605	MYA	C3-N4-C5	2.43	127.57	122.79
3	E	705	GN8	CAL-CAS-CAM	2.46	122.07	118.13
2	B	602	MYA	C14-C11-C10	2.49	113.89	109.34
2	A	601	MYA	C7-N8-C9	2.50	127.48	122.53
3	F	706	GN8	CAS-CAO-NAX	2.52	116.75	113.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	603	MYA	C7-N8-C9	2.54	127.56	122.53
2	D	604	MYA	C2-S1-C2M	2.55	104.09	100.40
2	E	605	MYA	C7-N8-C9	2.56	127.59	122.53
2	F	606	MYA	C7-N8-C9	2.69	127.86	122.53
2	D	604	MYA	C7-N8-C9	2.89	128.25	122.53
3	A	701	GN8	CAS-CAO-NAX	3.23	117.79	113.06
3	B	702	GN8	CAS-CAO-NAX	3.57	118.29	113.06
2	B	602	MYA	C7-N8-C9	3.74	129.94	122.53
3	D	704	GN8	CAS-CAO-NAX	4.14	119.11	113.06
3	E	705	GN8	CAS-CAO-NAX	4.30	119.35	113.06
3	C	703	GN8	CAW-CAU-NAX	4.79	117.56	109.99
3	F	706	GN8	CAW-CAU-NAX	5.08	118.01	109.99
3	B	702	GN8	CAW-CAU-NAX	5.16	118.13	109.99
3	D	704	GN8	CAW-CAU-NAX	5.20	118.20	109.99
2	B	602	MYA	O2M-C2M-C3M	5.35	118.83	109.05
3	A	701	GN8	CAW-CAU-NAX	5.35	118.44	109.99
2	D	604	MYA	O2M-C2M-C3M	5.43	118.98	109.05
3	E	705	GN8	CAW-CAU-NAX	5.64	118.89	109.99
2	A	601	MYA	O2M-C2M-C3M	5.80	119.65	109.05
2	F	606	MYA	O2M-C2M-C3M	5.81	119.67	109.05
2	C	603	MYA	O2M-C2M-C3M	5.90	119.83	109.05
3	E	705	GN8	CAF-CAW-CAU	5.99	126.42	120.40
2	E	605	MYA	O2M-C2M-C3M	6.02	120.06	109.05
3	D	704	GN8	CAF-CAW-CAU	7.25	127.68	120.40
3	B	702	GN8	CAF-CAW-CAU	7.47	127.89	120.40
3	F	706	GN8	CAF-CAW-CAU	7.50	127.92	120.40
3	A	701	GN8	CAF-CAW-CAU	7.53	127.96	120.40
3	E	705	GN8	SAP-CAV-NAX	8.00	118.42	109.82
3	F	706	GN8	SAP-CAV-NAX	8.02	118.44	109.82
3	C	703	GN8	SAP-CAV-NAX	8.07	118.49	109.82
3	D	704	GN8	SAP-CAV-NAX	8.17	118.60	109.82
3	A	701	GN8	SAP-CAV-NAX	8.17	118.60	109.82
3	B	702	GN8	SAP-CAV-NAX	8.23	118.67	109.82
3	C	703	GN8	CAF-CAW-CAU	8.68	129.11	120.40

All (6) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	C	603	MYA	C10
2	D	604	MYA	C10
2	E	605	MYA	C10
2	A	601	MYA	C10

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Mol	Chain	Res	Type	Atom
2	F	606	MYA	C10
2	B	602	MYA	C10

There are no torsion outliers.

There are no ring outliers.

12 monomers are involved in 31 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	MYA	1	0
3	A	701	GN8	3	0
2	B	602	MYA	6	0
3	B	702	GN8	1	0
2	C	603	MYA	3	0
3	C	703	GN8	2	0
2	D	604	MYA	7	0
3	D	704	GN8	1	0
2	E	605	MYA	3	0
3	E	705	GN8	1	0
2	F	606	MYA	2	0
3	F	706	GN8	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	A	436/455 (95%)	-0.52	0 100 100	16, 31, 54, 69	0
1	B	436/455 (95%)	-0.58	1 (0%) 95 91	15, 29, 56, 66	0
1	C	436/455 (95%)	-0.35	1 (0%) 95 91	15, 42, 65, 104	0
1	D	436/455 (95%)	-0.50	1 (0%) 95 91	17, 34, 54, 69	0
1	E	436/455 (95%)	-0.61	0 100 100	15, 26, 48, 65	0
1	F	435/455 (95%)	-0.29	2 (0%) 91 83	17, 47, 66, 106	0
All	All	2615/2730 (95%)	-0.48	5 (0%) 95 91	15, 34, 61, 106	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	5	ASP	2.6
1	D	69	SER	2.2
1	F	198	ASP	2.2
1	C	198	ASP	2.1
1	B	367	PRO	2.1

### 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

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(Å <sup>2</sup> )	Q<0.9
3	GN8	D	704	25/25	0.64	0.42	9.56	59,68,77,78	0
3	GN8	F	706	25/25	0.76	0.38	5.63	65,72,76,78	0
3	GN8	E	705	25/25	0.72	0.43	4.33	62,67,73,74	0
3	GN8	B	702	25/25	0.66	0.38	4.13	67,72,78,78	0
3	GN8	C	703	25/25	0.77	0.35	4.02	60,66,73,74	0
3	GN8	A	701	25/25	0.68	0.36	3.43	50,62,72,73	0
2	MYA	C	603	63/63	0.89	0.21	0.04	47,50,55,55	0
2	MYA	F	606	63/63	0.90	0.20	-0.15	53,60,65,66	0
2	MYA	E	605	63/63	0.95	0.14	-0.59	13,25,30,32	0
2	MYA	B	602	63/63	0.95	0.13	-0.68	16,26,29,31	0
2	MYA	D	604	63/63	0.94	0.16	-0.68	25,39,43,43	0
2	MYA	A	601	63/63	0.95	0.13	-0.91	21,31,44,46	0

## 6.5 Other polymers

There are no such residues in this entry.