



Full wwPDB X-ray Structure Validation Report

Mar 1, 2014 – 03:48 AM GMT

PDB ID : 3DMK
Title : Crystal structure of Down Syndrome Cell Adhesion Molecule (DSCAM) isoform 1.30.30, N-terminal eight Ig domains
Authors : Sawaya, M.R.; Wojtowicz, W.M.; Eisenberg, D.; Zipursky, S.L.
Deposited on : 2008-07-01
Resolution : 4.19 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

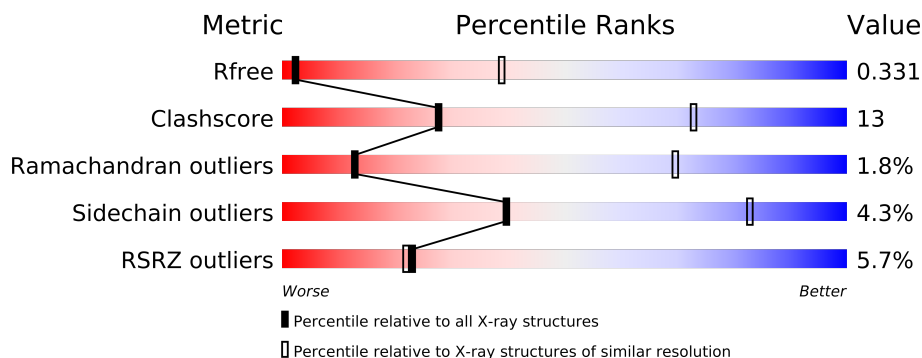
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 4.19 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}	66092	1001 (4.84-3.50)
Clashscore	79885	1259 (4.84-3.50)
Ramachandran outliers	78287	1192 (4.84-3.50)
Sidechain outliers	78261	1175 (4.84-3.50)
RSRZ outliers	66119	1001 (4.84-3.50)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	816	
1	B	816	
1	C	816	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
6	GOL	A	786	-	X
6	GOL	B	794	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 16740 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Down Syndrome Cell Adhesion Molecule (DSCAM) isoform 1.30.30, N-terminal eight Ig domains.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	775	Total	C	N	O	S	0	0	0
			5985	3778	1035	1147	25			
1	B	676	Total	C	N	O	S	0	0	0
			5223	3295	908	998	22			
1	C	676	Total	C	N	O	S	0	0	0
			5223	3295	908	998	22			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	776	HIS	-	EXPRESSION TAG	PDB 3DMK
A	777	HIS	-	EXPRESSION TAG	PDB 3DMK
A	778	HIS	-	EXPRESSION TAG	PDB 3DMK
A	779	HIS	-	EXPRESSION TAG	PDB 3DMK
A	780	HIS	-	EXPRESSION TAG	PDB 3DMK
A	781	HIS	-	EXPRESSION TAG	PDB 3DMK
B	776	HIS	-	EXPRESSION TAG	PDB 3DMK
B	777	HIS	-	EXPRESSION TAG	PDB 3DMK
B	778	HIS	-	EXPRESSION TAG	PDB 3DMK
B	779	HIS	-	EXPRESSION TAG	PDB 3DMK
B	780	HIS	-	EXPRESSION TAG	PDB 3DMK
B	781	HIS	-	EXPRESSION TAG	PDB 3DMK
C	776	HIS	-	EXPRESSION TAG	PDB 3DMK
C	777	HIS	-	EXPRESSION TAG	PDB 3DMK
C	778	HIS	-	EXPRESSION TAG	PDB 3DMK
C	779	HIS	-	EXPRESSION TAG	PDB 3DMK
C	780	HIS	-	EXPRESSION TAG	PDB 3DMK
C	781	HIS	-	EXPRESSION TAG	PDB 3DMK

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

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

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	776	HIS	-	EXPRESSION TAG	PDB 3DMK
A	777	HIS	-	EXPRESSION TAG	PDB 3DMK
A	778	HIS	-	EXPRESSION TAG	PDB 3DMK
A	779	HIS	-	EXPRESSION TAG	PDB 3DMK
A	780	HIS	-	EXPRESSION TAG	PDB 3DMK
A	781	HIS	-	EXPRESSION TAG	PDB 3DMK
A	776	HIS	-	EXPRESSION TAG	PDB 3DMK
A	777	HIS	-	EXPRESSION TAG	PDB 3DMK
A	778	HIS	-	EXPRESSION TAG	PDB 3DMK
A	779	HIS	-	EXPRESSION TAG	PDB 3DMK
A	780	HIS	-	EXPRESSION TAG	PDB 3DMK
A	781	HIS	-	EXPRESSION TAG	PDB 3DMK
B	776	HIS	-	EXPRESSION TAG	PDB 3DMK
B	777	HIS	-	EXPRESSION TAG	PDB 3DMK
B	778	HIS	-	EXPRESSION TAG	PDB 3DMK
B	779	HIS	-	EXPRESSION TAG	PDB 3DMK
B	780	HIS	-	EXPRESSION TAG	PDB 3DMK
B	781	HIS	-	EXPRESSION TAG	PDB 3DMK
B	776	HIS	-	EXPRESSION TAG	PDB 3DMK
B	777	HIS	-	EXPRESSION TAG	PDB 3DMK
B	778	HIS	-	EXPRESSION TAG	PDB 3DMK
B	779	HIS	-	EXPRESSION TAG	PDB 3DMK
B	780	HIS	-	EXPRESSION TAG	PDB 3DMK
B	781	HIS	-	EXPRESSION TAG	PDB 3DMK

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	C	3	Total	C	N	O	0	0
			42	24	3	15		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	3	Total	C	N	O	0	0
			42	24	3	15		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	776	HIS	-	EXPRESSION TAG	PDB 3DMK
C	777	HIS	-	EXPRESSION TAG	PDB 3DMK
C	778	HIS	-	EXPRESSION TAG	PDB 3DMK
C	779	HIS	-	EXPRESSION TAG	PDB 3DMK
C	780	HIS	-	EXPRESSION TAG	PDB 3DMK
C	781	HIS	-	EXPRESSION TAG	PDB 3DMK
B	776	HIS	-	EXPRESSION TAG	PDB 3DMK
B	777	HIS	-	EXPRESSION TAG	PDB 3DMK
B	778	HIS	-	EXPRESSION TAG	PDB 3DMK
B	779	HIS	-	EXPRESSION TAG	PDB 3DMK
B	780	HIS	-	EXPRESSION TAG	PDB 3DMK
B	781	HIS	-	EXPRESSION TAG	PDB 3DMK

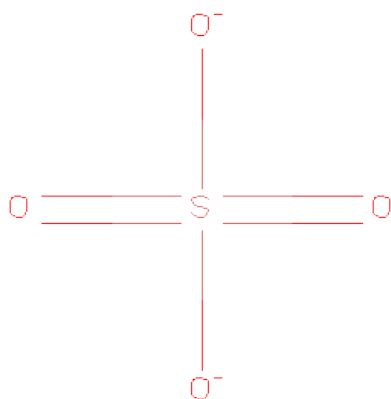
- Molecule 4 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	3	Total	C	N	O	0	0
			42	24	3	15		
4	C	3	Total	C	N	O	0	0
			42	24	3	15		

There are 12 discrepancies between the modelled and reference sequences:

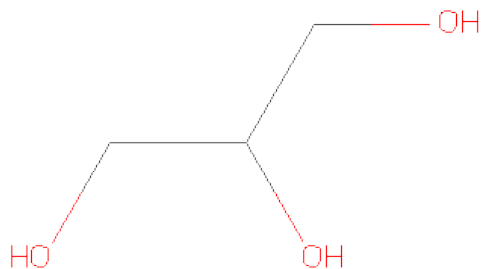
Chain	Residue	Modelled	Actual	Comment	Reference
B	776	HIS	-	EXPRESSION TAG	PDB 3DMK
B	777	HIS	-	EXPRESSION TAG	PDB 3DMK
B	778	HIS	-	EXPRESSION TAG	PDB 3DMK
B	779	HIS	-	EXPRESSION TAG	PDB 3DMK
B	780	HIS	-	EXPRESSION TAG	PDB 3DMK
B	781	HIS	-	EXPRESSION TAG	PDB 3DMK
C	776	HIS	-	EXPRESSION TAG	PDB 3DMK
C	777	HIS	-	EXPRESSION TAG	PDB 3DMK
C	778	HIS	-	EXPRESSION TAG	PDB 3DMK
C	779	HIS	-	EXPRESSION TAG	PDB 3DMK
C	780	HIS	-	EXPRESSION TAG	PDB 3DMK
C	781	HIS	-	EXPRESSION TAG	PDB 3DMK

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			6	3	3		
6	A	1	Total	C	O	0	0
			6	3	3		

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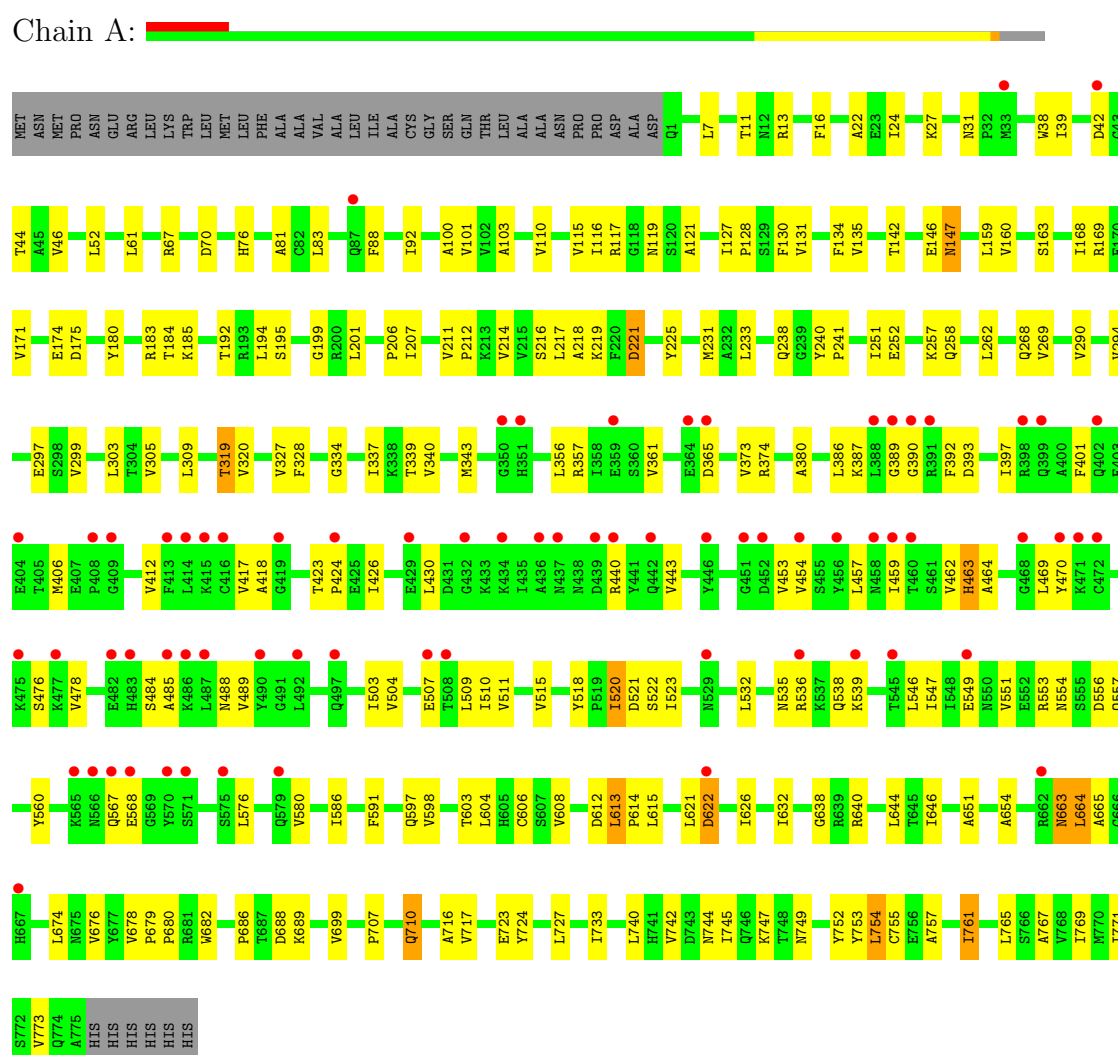
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			6	3	3		
6	B	1	Total	C	O	0	0
			6	3	3		

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: Down Syndrome Cell Adhesion Molecule (DSCAM) isoform 1.30.30, N-terminal eight Ig domains



- Molecule 1: Down Syndrome Cell Adhesion Molecule (DSCAM) isoform 1.30.30, N-terminal eight Ig domains

Chain B: 



CYS LYS ALA ALA ASP GLY PHE PRO PRO PRO GLN VAL THR TRP LYS LYS LYS LYS VAL GLY ASP THR PRO GLY GLU TYR LYS ASP LEU LYS SER ASP ASN ILE ILE ARG VAL VAL GLU GLU GLY GLY THR LEU LEU HIS VAL ASP ASN ILE GLN LYS LYS THR ASN ASN GLU GLY TYR TYR LEU CYS GLU ILE ILE ASN GLY

ILE
GLY
SER
GLY
LEU
SER
ALA
VAL
ILE
MET
ILE
SER
VAL
GLN
ALA
HIS
HIS
HIS
HIS
HIS
HIS

4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	118.46Å 177.61Å 434.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	12.00 – 4.19 11.99 – 4.19	Depositor EDS
% Data completeness (in resolution range)	99.4 (12.00-4.19) 99.4 (11.99-4.19)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.72 (at 4.19Å)	Xtriage
Refinement program	REFMAC 5.4.0061	Depositor
R, R_{free}	0.280 , 0.327 0.284 , 0.331	Depositor DCC
R_{free} test set	1618 reflections (5.24%)	DCC
Wilson B-factor (Å ²)	99.4	Xtriage
Anisotropy	0.178	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.19 , 89.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 32525 reflections	Xtriage
F_o, F_c correlation	0.82	EDS
Total number of atoms	16740	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.38% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, NAG, NDG, SO4

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	0.33	0/6113	0.52	0/8303
1	B	0.38	0/5334	0.54	0/7246
1	C	0.33	0/5334	0.52	0/7246
All	All	0.35	0/16781	0.53	0/22795

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
3	B	1	0

There are no bond length outliers.

There are no bond angle outliers.

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	B	784	NAG	C1

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the

chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5985	0	5928	174	0
1	B	5223	0	5172	128	1
1	C	5223	0	5174	131	1
2	A	56	0	50	3	0
2	B	56	0	50	1	0
3	B	42	0	37	0	0
3	C	42	0	37	1	0
4	B	42	0	37	0	0
4	C	42	0	37	0	0
5	B	5	0	0	0	0
6	A	12	0	16	0	0
6	B	12	0	16	0	0
All	All	16740	0	16554	425	1

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 13.

All (425) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:654:ALA:HB2	1:A:676:VAL:HG12	1.38	1.00
1:A:733:ILE:HG23	1:A:742:VAL:HG22	1.46	0.97
1:B:412:VAL:HB	1:B:459:ILE:HG22	1.53	0.90
1:C:412:VAL:HB	1:C:459:ILE:HG22	1.56	0.87
1:C:504:VAL:HG12	1:C:581:MET:HB2	1.56	0.87
1:C:401:PHE:CE2	1:C:485:ALA:HB3	2.11	0.86
1:A:412:VAL:HB	1:A:459:ILE:HG22	1.58	0.85
1:B:654:ALA:HB2	1:B:676:VAL:HG12	1.59	0.85
1:A:654:ALA:HB2	1:A:676:VAL:CG1	2.08	0.84
1:B:320:VAL:HG21	1:B:361:VAL:HG21	1.61	0.82
1:A:320:VAL:HG21	1:A:361:VAL:HG21	1.62	0.82
1:A:401:PHE:CE2	1:A:485:ALA:HB3	2.14	0.82
1:B:401:PHE:CE2	1:B:485:ALA:HB3	2.15	0.81
1:C:320:VAL:HG21	1:C:361:VAL:HG21	1.62	0.81
1:A:217:LEU:HD23	1:B:217:LEU:HD23	1.62	0.81
1:A:218:ALA:HA	1:B:217:LEU:HD21	1.66	0.78
1:A:217:LEU:HD21	1:B:218:ALA:HA	1.64	0.78
1:C:417:VAL:HG22	1:C:454:VAL:HG22	1.65	0.77
1:A:699:VAL:HG13	1:A:740:LEU:HB3	1.65	0.77
1:C:596:ALA:HB2	1:C:602:LEU:HD21	1.65	0.77
1:A:417:VAL:HG22	1:A:454:VAL:HG22	1.68	0.76

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:504:VAL:HG11	1:C:665:ALA:HB3	1.67	0.75
1:B:503:ILE:HG21	1:B:551:VAL:HG21	1.70	0.74
1:A:217:LEU:CD2	1:B:217:LEU:HD23	2.18	0.74
1:A:217:LEU:HD23	1:B:217:LEU:CD2	2.17	0.74
1:C:373:VAL:HG23	1:C:380:ALA:HB3	1.69	0.74
1:B:417:VAL:HG22	1:B:454:VAL:HG22	1.70	0.74
1:B:76:HIS:HB3	1:B:100:ALA:HB3	1.68	0.74
1:C:532:LEU:HD23	1:C:546:LEU:HD13	1.68	0.73
1:A:373:VAL:HG23	1:A:380:ALA:HB3	1.70	0.73
1:B:127:ILE:HD13	1:B:135:VAL:HG12	1.71	0.72
1:A:651:ALA:HA	1:A:676:VAL:HG11	1.72	0.71
1:B:373:VAL:HG23	1:B:380:ALA:HB3	1.71	0.71
1:A:503:ILE:HG21	1:A:551:VAL:HG21	1.72	0.71
1:A:532:LEU:HD21	1:A:546:LEU:HD22	1.71	0.71
1:C:76:HIS:HB3	1:C:100:ALA:HB3	1.71	0.71
1:C:503:ILE:HG21	1:C:551:VAL:HG21	1.71	0.71
1:B:632:ILE:CG2	1:B:644:LEU:HD11	2.21	0.71
1:A:76:HIS:HB3	1:A:100:ALA:HB3	1.73	0.71
1:C:632:ILE:CG2	1:C:644:LEU:HD11	2.20	0.71
1:A:597:GLN:OE1	1:A:761:ILE:HG22	1.91	0.70
1:C:127:ILE:HD13	1:C:135:VAL:HG12	1.73	0.70
1:A:532:LEU:CD2	1:A:546:LEU:HD22	2.22	0.70
1:C:430:LEU:HD12	1:C:470:TYR:CZ	2.28	0.69
1:B:412:VAL:HB	1:B:459:ILE:CG2	2.22	0.69
1:A:612:ASP:O	1:A:614:PRO:HD2	1.93	0.69
1:B:612:ASP:O	1:B:614:PRO:HD2	1.93	0.68
1:A:225:TYR:HB2	1:A:231:MET:HE3	1.74	0.68
1:A:586:ILE:HA	1:A:608:VAL:HG22	1.76	0.67
1:B:586:ILE:HA	1:B:608:VAL:HG22	1.76	0.67
1:A:632:ILE:CG2	1:A:644:LEU:HD11	2.24	0.67
1:C:612:ASP:O	1:C:614:PRO:HD2	1.94	0.67
1:A:67:ARG:HH11	2:A:782:NAG:H81	1.60	0.67
1:A:319:THR:HG22	1:A:389:GLY:CA	2.24	0.67
1:A:127:ILE:HD13	1:A:135:VAL:HG12	1.76	0.66
1:B:476:SER:OG	1:B:478:VAL:HG12	1.96	0.66
1:C:532:LEU:CD2	1:C:546:LEU:HD13	2.26	0.65
1:B:535:ASN:C	1:B:535:ASN:HD22	2.00	0.65
1:A:532:LEU:HD21	1:A:546:LEU:CD2	2.27	0.64
1:B:430:LEU:HD12	1:B:470:TYR:CZ	2.32	0.64
1:B:225:TYR:HB2	1:B:231:MET:HE3	1.79	0.64
1:A:430:LEU:HD12	1:A:470:TYR:CZ	2.33	0.64
1:B:168:ILE:HD12	1:B:201:LEU:HD11	1.80	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:476:SER:OG	1:C:478:VAL:HG12	1.98	0.64
1:C:231:MET:CE	1:C:305:VAL:HG22	2.29	0.63
1:A:476:SER:OG	1:A:478:VAL:HG12	1.99	0.63
1:A:211:VAL:HG22	1:A:294:VAL:CG1	2.29	0.63
1:C:168:ILE:HD12	1:C:201:LEU:HD11	1.80	0.63
1:A:231:MET:CE	1:A:305:VAL:HG22	2.29	0.63
1:A:412:VAL:HB	1:A:459:ILE:CG2	2.28	0.63
1:A:532:LEU:O	1:A:538:GLN:OE1	2.17	0.63
1:A:676:VAL:HG13	1:A:676:VAL:O	1.99	0.62
1:B:211:VAL:HG22	1:B:294:VAL:CG1	2.30	0.62
1:C:412:VAL:HB	1:C:459:ILE:CG2	2.27	0.62
1:B:251:ILE:HD11	1:B:258:GLN:HG3	1.81	0.61
1:A:110:VAL:HG12	1:A:199:GLY:HA3	1.82	0.61
1:C:110:VAL:HG12	1:C:199:GLY:HA3	1.83	0.61
1:C:211:VAL:HG22	1:C:294:VAL:CG1	2.30	0.61
1:A:423:THR:CG2	1:A:453:VAL:HG23	2.31	0.60
1:A:168:ILE:HD12	1:A:201:LEU:HD11	1.83	0.60
1:A:717:VAL:H	1:A:723:GLU:CD	2.03	0.60
1:B:110:VAL:HG12	1:B:199:GLY:HA3	1.83	0.60
1:C:251:ILE:HD11	1:C:258:GLN:HG3	1.82	0.59
1:C:592:GLU:O	1:C:593:GLU:C	2.40	0.59
1:A:747:LYS:HA	1:A:773:VAL:HG21	1.84	0.59
1:A:251:ILE:HD11	1:A:258:GLN:HG3	1.84	0.59
1:B:231:MET:CE	1:B:305:VAL:HG22	2.32	0.59
1:A:231:MET:HE1	1:A:305:VAL:HG22	1.84	0.59
1:C:423:THR:CG2	1:C:453:VAL:HG23	2.33	0.59
1:B:83:LEU:HD13	1:B:92:ILE:CG2	2.33	0.58
1:A:707:PRO:CD	1:A:761:ILE:HD11	2.33	0.58
1:A:591:PHE:CE1	1:A:604:LEU:HD13	2.39	0.58
1:B:340:VAL:HG22	1:B:373:VAL:HG12	1.86	0.58
1:B:231:MET:HE1	1:B:305:VAL:HG22	1.84	0.58
1:C:262:LEU:HD21	1:C:268:GLN:HB2	1.86	0.58
1:A:262:LEU:HD21	1:A:268:GLN:HB2	1.85	0.57
1:C:121:ALA:HB2	1:C:171:VAL:HG21	1.86	0.57
1:B:121:ALA:HB2	1:B:171:VAL:HG21	1.87	0.57
1:A:185:LYS:HB2	1:A:192:THR:HG22	1.87	0.57
1:A:678:VAL:HG13	1:A:679:PRO:HD2	1.87	0.57
1:B:146:GLU:C	1:B:147:ASN:HD22	2.08	0.57
1:B:262:LEU:HD21	1:B:268:GLN:HB2	1.87	0.56
1:B:532:LEU:CD2	1:B:546:LEU:HD22	2.36	0.56
1:B:488:ASN:HB3	1:B:518:TYR:HB2	1.86	0.56
1:C:225:TYR:HB2	1:C:231:MET:HE3	1.86	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:423:THR:CG2	1:B:453:VAL:HG23	2.35	0.56
1:A:511:VAL:HG21	1:A:576:LEU:HD22	1.87	0.56
1:C:551:VAL:HG12	1:C:580:VAL:HG13	1.87	0.56
1:C:586:ILE:HD11	1:C:606:CYS:SG	2.45	0.56
1:C:83:LEU:HD13	1:C:92:ILE:CG2	2.36	0.56
1:C:254:THR:HG22	1:C:593:GLU:O	2.05	0.56
1:C:511:VAL:HG21	1:C:576:LEU:HD22	1.88	0.56
1:A:121:ALA:HB2	1:A:171:VAL:HG21	1.88	0.56
1:A:504:VAL:HG11	1:A:665:ALA:O	2.06	0.56
1:A:680:PRO:HB2	1:A:765:LEU:HD13	1.87	0.55
1:A:83:LEU:HB2	1:A:92:ILE:HG22	1.88	0.55
1:A:488:ASN:HB3	1:A:518:TYR:HB2	1.88	0.55
1:A:211:VAL:HG22	1:A:294:VAL:HG12	1.87	0.55
1:B:211:VAL:HG22	1:B:294:VAL:HG12	1.89	0.55
1:C:586:ILE:HA	1:C:608:VAL:HG22	1.87	0.55
1:C:488:ASN:HB3	1:C:518:TYR:HB2	1.88	0.55
1:A:83:LEU:HD13	1:A:92:ILE:CG2	2.37	0.55
1:A:654:ALA:CB	1:A:676:VAL:HG12	2.26	0.55
1:A:340:VAL:HG22	1:A:373:VAL:HG12	1.89	0.55
1:B:185:LYS:HB2	1:B:192:THR:HG22	1.89	0.55
1:B:83:LEU:HB2	1:B:92:ILE:HG22	1.88	0.55
1:A:146:GLU:C	1:A:147:ASN:HD22	2.09	0.54
1:B:591:PHE:CE1	1:B:604:LEU:HD13	2.43	0.54
1:C:146:GLU:C	1:C:147:ASN:HD22	2.11	0.54
1:A:418:ALA:CB	1:A:426:ILE:HD11	2.37	0.54
1:C:83:LEU:HB2	1:C:92:ILE:HG22	1.89	0.54
1:A:217:LEU:CD2	1:B:217:LEU:CD2	2.84	0.54
1:C:211:VAL:HG22	1:C:294:VAL:HG12	1.88	0.54
1:B:397:ILE:O	1:B:397:ILE:HD12	2.08	0.54
1:C:654:ALA:HB2	1:C:676:VAL:HG12	1.89	0.54
1:B:83:LEU:HD13	1:B:92:ILE:HG23	1.90	0.54
1:A:225:TYR:HD1	1:A:231:MET:HE2	1.73	0.54
1:C:322:PHE:O	1:C:478:VAL:HG23	2.08	0.54
1:B:418:ALA:CB	1:B:426:ILE:HD11	2.38	0.53
1:B:518:TYR:O	1:B:518:TYR:CD1	2.61	0.53
1:C:185:LYS:HB2	1:C:192:THR:HG22	1.90	0.53
1:C:212:PRO:HA	1:C:238:GLN:O	2.09	0.53
1:C:340:VAL:HG22	1:C:373:VAL:HG12	1.90	0.53
1:A:504:VAL:CG1	1:A:665:ALA:HB1	2.39	0.53
1:A:532:LEU:CD2	1:A:546:LEU:HD13	2.38	0.53
1:B:567:GLN:O	1:B:568:GLU:HG3	2.09	0.53
1:B:206:PRO:O	1:B:207:ILE:HD13	2.09	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:532:LEU:CD2	1:C:546:LEU:HD22	2.38	0.52
1:C:418:ALA:CB	1:C:426:ILE:HD11	2.39	0.52
1:C:518:TYR:CD1	1:C:518:TYR:O	2.62	0.52
1:B:38:TRP:O	1:B:46:VAL:HG22	2.09	0.52
1:A:397:ILE:HD12	1:A:397:ILE:O	2.09	0.52
1:B:212:PRO:HA	1:B:238:GLN:O	2.08	0.52
1:B:520:ILE:HD13	1:B:521:ASP:N	2.25	0.52
1:B:406:MET:SD	1:B:462:VAL:HG11	2.49	0.52
1:B:328:PHE:HD2	1:B:356:LEU:HD12	1.74	0.52
1:C:591:PHE:CZ	1:C:604:LEU:HD13	2.43	0.52
1:B:169:ARG:NH2	1:B:269:VAL:HG13	2.25	0.52
1:C:591:PHE:CE1	1:C:604:LEU:HD13	2.44	0.52
1:C:397:ILE:HD12	1:C:397:ILE:O	2.09	0.52
1:A:551:VAL:HG12	1:A:580:VAL:HG13	1.91	0.52
1:A:716:ALA:HA	1:A:723:GLU:CG	2.40	0.52
1:B:515:VAL:HG21	1:B:523:ILE:HD11	1.91	0.52
1:A:319:THR:HG22	1:A:389:GLY:N	2.24	0.52
1:C:504:VAL:HG13	1:C:581:MET:HE3	1.92	0.51
1:A:212:PRO:HA	1:A:238:GLN:O	2.10	0.51
1:C:101:VAL:HG21	1:C:134:PHE:CZ	2.46	0.51
1:C:520:ILE:HD13	1:C:521:ASP:N	2.25	0.51
1:C:225:TYR:HD1	1:C:231:MET:HE2	1.74	0.51
1:A:598:VAL:CG1	1:A:678:VAL:HG22	2.40	0.51
1:C:83:LEU:HD13	1:C:92:ILE:HG23	1.92	0.51
1:B:511:VAL:HG21	1:B:576:LEU:HD22	1.93	0.51
1:A:520:ILE:HD13	1:A:521:ASP:N	2.26	0.51
1:A:688:ASP:N	1:A:769:ILE:HD11	2.26	0.51
1:A:211:VAL:HG22	1:A:294:VAL:HG11	1.93	0.50
1:A:83:LEU:HD13	1:A:92:ILE:HG23	1.93	0.50
1:C:328:PHE:HD2	1:C:356:LEU:HD12	1.76	0.50
1:A:532:LEU:HD23	1:A:546:LEU:HD13	1.93	0.50
1:B:211:VAL:HG22	1:B:294:VAL:HG11	1.93	0.50
1:C:505:ALA:HB2	1:C:582:VAL:HA	1.93	0.50
1:C:231:MET:HE1	1:C:305:VAL:HG22	1.93	0.50
1:C:309:LEU:HD22	1:C:337:ILE:CD1	2.42	0.50
1:B:309:LEU:HD22	1:B:337:ILE:CD1	2.41	0.50
1:A:603:THR:HG21	1:B:607:SER:CB	2.42	0.50
1:C:169:ARG:NH2	1:C:269:VAL:HG13	2.27	0.50
1:A:257:LYS:HE3	2:A:785:NAG:H81	1.94	0.50
1:A:67:ARG:NH1	2:A:782:NAG:H81	2.26	0.50
1:B:7:LEU:HD12	1:B:27:LYS:HE3	1.93	0.50
1:A:7:LEU:HD12	1:A:27:LYS:HE3	1.94	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:328:PHE:HD2	1:A:356:LEU:HD12	1.77	0.50
1:A:309:LEU:HD22	1:A:337:ILE:CD1	2.41	0.49
1:B:42:ASP:OD1	1:B:44:THR:HG22	2.12	0.49
1:C:663:ASN:O	1:C:664:LEU:C	2.51	0.49
1:A:183:ARG:HG3	1:A:194:LEU:HD23	1.94	0.49
1:A:101:VAL:HG21	1:A:134:PHE:CZ	2.48	0.49
1:C:225:TYR:CD1	1:C:231:MET:HE2	2.46	0.49
1:B:532:LEU:O	1:B:538:GLN:OE1	2.30	0.49
1:C:175:ASP:C	1:C:177:TYR:H	2.15	0.49
1:A:515:VAL:HG21	1:A:523:ILE:HD11	1.93	0.49
1:A:327:VAL:HG22	1:A:357:ARG:CD	2.43	0.49
1:A:682:TRP:CD1	1:A:765:LEU:HD23	2.48	0.49
1:C:505:ALA:CB	1:C:582:VAL:HA	2.43	0.49
1:B:240:TYR:HA	1:B:241:PRO:C	2.32	0.49
1:B:183:ARG:HG3	1:B:194:LEU:HD23	1.95	0.49
1:A:753:TYR:CD2	1:A:771:ILE:HD12	2.48	0.49
1:B:101:VAL:HG21	1:B:134:PHE:CZ	2.47	0.49
1:B:532:LEU:HD12	1:B:532:LEU:O	2.13	0.49
1:C:632:ILE:HG23	1:C:646:ILE:HG12	1.93	0.48
1:A:689:LYS:O	1:A:771:ILE:HA	2.13	0.48
1:C:42:ASP:OD1	1:C:44:THR:HG22	2.13	0.48
1:C:38:TRP:O	1:C:46:VAL:HG22	2.13	0.48
1:B:663:ASN:O	1:B:664:LEU:C	2.51	0.48
1:A:42:ASP:OD1	1:A:44:THR:HG22	2.13	0.48
1:A:169:ARG:NH2	1:A:269:VAL:HG13	2.27	0.48
1:C:532:LEU:HD21	1:C:546:LEU:CD2	2.44	0.48
1:A:682:TRP:NE1	1:A:765:LEU:HD23	2.28	0.48
1:A:233:LEU:HD21	1:A:303:LEU:HD13	1.95	0.48
1:C:211:VAL:HG22	1:C:294:VAL:HG11	1.94	0.48
1:B:615:LEU:HD13	1:B:640:ARG:HB2	1.94	0.48
1:B:327:VAL:HG22	1:B:357:ARG:CD	2.44	0.48
1:C:327:VAL:HG22	1:C:357:ARG:CD	2.44	0.48
1:B:535:ASN:C	1:B:535:ASN:ND2	2.67	0.48
1:C:532:LEU:HD21	1:C:546:LEU:HD22	1.95	0.47
1:A:240:TYR:HA	1:A:241:PRO:C	2.34	0.47
1:C:532:LEU:O	1:C:538:GLN:OE1	2.32	0.47
1:A:632:ILE:HG23	1:A:646:ILE:HG12	1.96	0.47
1:B:92:ILE:HD11	1:B:343:MET:SD	2.54	0.47
1:A:686:PRO:HG2	1:A:769:ILE:HD13	1.96	0.47
1:A:214:VAL:HG13	1:A:297:GLU:HG2	1.95	0.47
1:C:363:LYS:HA	1:C:388:LEU:HD11	1.96	0.47
1:A:319:THR:CG2	1:A:389:GLY:O	2.62	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:761:ILE:CD1	1:A:761:ILE:N	2.78	0.47
1:B:532:LEU:HD23	1:B:546:LEU:HD13	1.95	0.47
1:B:632:ILE:HG23	1:B:646:ILE:HG12	1.95	0.47
1:B:214:VAL:HG13	1:B:297:GLU:HG2	1.97	0.47
1:C:7:LEU:HD12	1:C:27:LYS:HE3	1.94	0.47
1:A:319:THR:HG22	1:A:389:GLY:O	2.14	0.47
1:B:430:LEU:HD23	1:B:430:LEU:C	2.35	0.47
1:A:664:LEU:O	1:A:665:ALA:HB3	2.15	0.47
1:B:290:VAL:HG12	1:B:297:GLU:O	2.14	0.47
1:C:240:TYR:HA	1:C:241:PRO:C	2.35	0.47
1:A:733:ILE:HG12	1:A:742:VAL:HG13	1.96	0.47
1:A:551:VAL:HG12	1:A:580:VAL:CG1	2.45	0.47
1:B:418:ALA:HB2	1:B:426:ILE:HD11	1.97	0.47
1:B:457:LEU:C	1:B:457:LEU:HD12	2.35	0.47
1:B:469:LEU:HD11	1:B:484:SER:HB3	1.96	0.47
1:B:365:ASP:O	1:B:386:LEU:HD23	2.15	0.47
1:A:532:LEU:HD11	1:A:560:TYR:HE2	1.80	0.46
1:A:115:VAL:HG11	1:A:121:ALA:HB2	1.97	0.46
1:C:430:LEU:C	1:C:430:LEU:HD23	2.36	0.46
1:A:603:THR:HG21	1:B:607:SER:HB3	1.97	0.46
1:C:206:PRO:O	1:C:207:ILE:HD13	2.15	0.46
1:A:757:ALA:HB3	1:A:765:LEU:HB2	1.97	0.46
1:B:515:VAL:HG11	1:B:523:ILE:CD1	2.46	0.46
1:B:130:PHE:CD1	1:B:131:VAL:HG13	2.51	0.46
1:A:615:LEU:HD13	1:A:640:ARG:HB2	1.97	0.46
1:C:115:VAL:HG21	1:C:171:VAL:HG11	1.98	0.46
1:A:327:VAL:HG22	1:A:357:ARG:HD3	1.97	0.46
1:A:406:MET:SD	1:A:462:VAL:HG11	2.55	0.46
1:A:225:TYR:CD1	1:A:231:MET:HE2	2.49	0.46
1:C:613:LEU:CB	1:C:614:PRO:CD	2.94	0.46
1:A:591:PHE:CZ	1:A:674:LEU:HD12	2.51	0.46
1:A:567:GLN:O	1:A:568:GLU:HG3	2.15	0.46
1:C:621:LEU:HD23	1:C:622:ASP:N	2.31	0.46
1:A:206:PRO:O	1:A:207:ILE:HD13	2.15	0.46
1:B:225:TYR:HD1	1:B:231:MET:HE2	1.81	0.46
1:C:130:PHE:CD1	1:C:131:VAL:HG13	2.51	0.46
1:B:233:LEU:HD21	1:B:303:LEU:HD13	1.97	0.46
1:C:615:LEU:HD13	1:C:640:ARG:HB2	1.97	0.46
1:C:365:ASP:O	1:C:386:LEU:HD23	2.16	0.46
1:C:52:LEU:HD21	1:C:70:ASP:HB3	1.98	0.46
1:A:365:ASP:O	1:A:386:LEU:HD23	2.16	0.46
1:A:38:TRP:O	1:A:46:VAL:HG22	2.16	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:745:ILE:HD12	1:A:749:ASN:HD22	1.81	0.46
1:C:183:ARG:HG3	1:C:194:LEU:HD23	1.97	0.46
1:C:532:LEU:HD11	1:C:560:TYR:CE2	2.51	0.46
1:B:121:ALA:HB3	1:B:168:ILE:HB	1.98	0.46
1:B:83:LEU:HD13	1:B:92:ILE:HG22	1.98	0.46
1:A:557:GLN:HB2	1:A:580:VAL:HB	1.96	0.45
1:B:534:ILE:HD11	1:B:538:GLN:HE22	1.80	0.45
1:A:621:LEU:O	1:A:622:ASP:C	2.54	0.45
1:B:535:ASN:O	1:B:536:ARG:C	2.54	0.45
1:B:443:VAL:HG22	1:B:457:LEU:HD13	1.98	0.45
1:A:52:LEU:HD21	1:A:70:ASP:HB3	1.99	0.45
1:C:532:LEU:HD11	1:C:560:TYR:HE2	1.80	0.45
1:C:430:LEU:HD12	1:C:470:TYR:CE2	2.51	0.45
1:B:613:LEU:CB	1:B:614:PRO:CD	2.94	0.45
1:A:754:LEU:CD2	1:A:754:LEU:C	2.85	0.45
1:C:567:GLN:O	1:C:568:GLU:HG3	2.15	0.45
1:A:613:LEU:CB	1:A:614:PRO:CD	2.94	0.45
1:A:586:ILE:HD11	1:A:606:CYS:SG	2.57	0.45
1:B:535:ASN:O	1:B:535:ASN:ND2	2.49	0.45
1:C:233:LEU:HD21	1:C:303:LEU:HD13	1.97	0.45
1:C:327:VAL:HG22	1:C:357:ARG:HD3	1.99	0.45
1:A:621:LEU:HD23	1:A:622:ASP:N	2.32	0.45
1:C:92:ILE:HD11	1:C:343:MET:SD	2.57	0.45
1:C:621:LEU:O	1:C:622:ASP:C	2.55	0.45
1:A:443:VAL:HG22	1:A:457:LEU:HD13	1.98	0.45
1:A:231:MET:CE	1:A:303:LEU:HD21	2.47	0.45
1:A:430:LEU:HD23	1:A:430:LEU:C	2.37	0.45
1:B:591:PHE:CZ	1:B:674:LEU:HD12	2.51	0.45
1:B:327:VAL:HG22	1:B:357:ARG:HD3	1.99	0.45
1:C:539:LYS:HB2	1:C:547:ILE:HG23	1.99	0.45
1:C:214:VAL:HG13	1:C:297:GLU:HG2	1.99	0.45
1:A:707:PRO:HD2	1:A:761:ILE:HD11	1.99	0.45
1:B:290:VAL:HG13	1:B:290:VAL:O	2.17	0.45
1:A:663:ASN:O	1:A:664:LEU:C	2.55	0.45
1:A:518:TYR:O	1:A:518:TYR:CD1	2.69	0.45
1:B:52:LEU:HD21	1:B:70:ASP:HB3	1.98	0.45
1:B:309:LEU:HD11	1:B:375:ASN:ND2	2.32	0.44
1:C:373:VAL:CG2	1:C:380:ALA:HB3	2.44	0.44
1:C:418:ALA:HB2	1:C:426:ILE:HD11	2.00	0.44
1:A:539:LYS:HB2	1:A:547:ILE:HG23	1.99	0.44
1:B:116:ILE:O	1:B:117:ARG:C	2.55	0.44
1:A:130:PHE:CD1	1:A:131:VAL:HG13	2.52	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:469:LEU:HD11	1:C:484:SER:HB3	2.00	0.44
1:A:319:THR:HG22	1:A:389:GLY:HA2	1.98	0.44
1:A:115:VAL:HG21	1:A:171:VAL:HG11	1.99	0.44
1:B:231:MET:CE	1:B:303:LEU:HD21	2.47	0.44
1:A:518:TYR:C	1:A:520:ILE:H	2.20	0.44
1:B:664:LEU:O	1:B:665:ALA:HB3	2.17	0.44
1:A:551:VAL:CG1	1:A:580:VAL:HG13	2.48	0.44
1:A:24:ILE:HD11	1:A:61:LEU:HD23	2.00	0.44
1:A:184:THR:O	1:A:192:THR:HA	2.18	0.44
1:B:621:LEU:HD23	1:B:622:ASP:N	2.33	0.44
1:A:469:LEU:HD11	1:A:484:SER:HB3	1.99	0.44
1:B:119:ASN:N	1:B:119:ASN:HD22	2.16	0.44
1:A:119:ASN:N	1:A:119:ASN:HD22	2.16	0.44
1:A:319:THR:HG23	1:A:387:LYS:HB3	2.00	0.44
1:C:184:THR:O	1:C:192:THR:HA	2.18	0.43
1:C:219:LYS:HA	1:C:299:VAL:HG12	2.00	0.43
1:C:417:VAL:CG2	1:C:454:VAL:HG22	2.42	0.43
1:C:115:VAL:HG11	1:C:121:ALA:HB2	2.00	0.43
1:A:598:VAL:HG11	1:A:678:VAL:HG22	2.01	0.43
1:C:515:VAL:HG21	1:C:523:ILE:HD11	1.99	0.43
1:C:24:ILE:HD11	1:C:61:LEU:HD23	2.00	0.43
1:B:184:THR:O	1:B:192:THR:HA	2.18	0.43
1:C:363:LYS:HA	1:C:388:LEU:CD1	2.48	0.43
1:A:507:GLU:O	1:A:551:VAL:HG23	2.19	0.43
1:A:418:ALA:HB2	1:A:426:ILE:HD11	1.99	0.43
1:B:621:LEU:O	1:B:622:ASP:C	2.55	0.43
1:A:159:LEU:HD12	1:A:160:VAL:N	2.34	0.43
1:C:309:LEU:HD11	1:C:375:ASN:ND2	2.34	0.43
1:C:664:LEU:O	1:C:665:ALA:HB3	2.19	0.42
1:B:632:ILE:HG22	1:B:644:LEU:HD11	2.00	0.42
1:B:586:ILE:HD11	1:B:606:CYS:SG	2.58	0.42
1:C:231:MET:CE	1:C:303:LEU:HD21	2.49	0.42
1:C:83:LEU:HD13	1:C:92:ILE:HG22	2.01	0.42
1:A:92:ILE:HD11	1:A:343:MET:SD	2.58	0.42
1:B:219:LYS:HA	1:B:299:VAL:HG12	2.00	0.42
1:C:319:THR:HG22	1:C:389:GLY:CA	2.49	0.42
1:A:147:ASN:N	1:A:147:ASN:HD22	2.17	0.42
1:A:290:VAL:HG12	1:A:297:GLU:O	2.19	0.42
1:B:225:TYR:CD1	1:B:231:MET:HE2	2.54	0.42
1:A:258:GLN:HE21	1:A:710:GLN:CD	2.22	0.42
1:C:443:VAL:HG22	1:C:457:LEU:HD13	2.01	0.42
1:A:319:THR:HG23	1:A:387:LYS:CB	2.49	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:233:LEU:O	1:B:272:THR:HG23	2.20	0.42
1:B:518:TYR:C	1:B:520:ILE:H	2.22	0.42
1:A:418:ALA:HB3	1:A:426:ILE:HD11	2.02	0.42
1:A:478:VAL:O	1:A:478:VAL:HG22	2.19	0.42
1:B:507:GLU:O	1:B:551:VAL:HG23	2.19	0.42
1:B:373:VAL:CG2	1:B:380:ALA:HB3	2.44	0.42
1:C:632:ILE:HG22	1:C:644:LEU:HD11	2.00	0.42
1:C:290:VAL:O	1:C:290:VAL:HG13	2.20	0.42
1:B:159:LEU:HD12	1:B:160:VAL:N	2.35	0.42
1:C:119:ASN:HD22	1:C:119:ASN:N	2.17	0.42
1:B:231:MET:HE2	1:B:303:LEU:HD11	2.01	0.42
1:A:424:PRO:O	1:A:453:VAL:HG21	2.19	0.42
1:B:424:PRO:O	1:B:453:VAL:HG21	2.19	0.42
1:B:115:VAL:HG21	1:B:171:VAL:HG11	2.02	0.42
1:C:168:ILE:CD1	1:C:201:LEU:HD11	2.49	0.42
1:C:147:ASN:HD22	1:C:147:ASN:N	2.18	0.42
1:C:290:VAL:HG12	1:C:297:GLU:O	2.19	0.42
1:A:390:GLY:C	1:A:392:PHE:N	2.72	0.42
1:A:231:MET:HE2	1:A:303:LEU:HD11	2.01	0.41
1:A:515:VAL:HG11	1:A:523:ILE:CD1	2.50	0.41
1:A:128:PRO:HB2	1:A:131:VAL:HG22	2.02	0.41
1:A:16:PHE:CG	1:A:22:ALA:HB2	2.55	0.41
1:B:539:LYS:HB2	1:B:547:ILE:HG23	2.02	0.41
1:C:518:TYR:C	1:C:520:ILE:H	2.24	0.41
1:C:159:LEU:HD12	1:C:160:VAL:N	2.35	0.41
1:A:116:ILE:O	1:A:117:ARG:C	2.59	0.41
1:A:221:ASP:HB2	1:B:217:LEU:HG	2.02	0.41
1:A:707:PRO:HD3	1:A:761:ILE:HD11	2.02	0.41
1:C:457:LEU:C	1:C:457:LEU:HD12	2.40	0.41
1:B:16:PHE:CG	1:B:22:ALA:HB2	2.54	0.41
1:C:16:PHE:CG	1:C:22:ALA:HB2	2.56	0.41
1:A:258:GLN:NE2	1:A:710:GLN:OE1	2.53	0.41
1:C:138:VAL:HG21	1:C:185:LYS:HB2	2.02	0.41
1:C:101:VAL:HG21	1:C:134:PHE:CE2	2.55	0.41
1:B:551:VAL:CG1	1:B:580:VAL:HG22	2.50	0.41
1:A:463:HIS:O	1:A:489:VAL:HG11	2.20	0.41
1:C:406:MET:SD	1:C:462:VAL:HG11	2.60	0.41
1:A:754:LEU:HD23	1:A:767:ALA:O	2.20	0.41
1:B:19:SER:OG	2:B:782:NAG:N2	2.54	0.41
1:A:219:LYS:HA	1:A:299:VAL:HG12	2.02	0.41
1:B:233:LEU:HD12	1:B:273:LEU:HD23	2.03	0.41
1:C:478:VAL:HG22	1:C:478:VAL:O	2.20	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:423:THR:HA	1:A:424:PRO:HD3	1.96	0.41
1:B:532:LEU:HD21	1:B:546:LEU:CD2	2.51	0.41
1:A:290:VAL:HG13	1:A:290:VAL:O	2.20	0.41
1:B:14:ILE:HA	1:B:14:ILE:HD13	1.97	0.41
1:B:403:GLU:HG3	1:B:404:GLU:N	2.36	0.41
1:C:39:ILE:HG13	1:C:81:ALA:HB3	2.02	0.41
1:A:727:LEU:HD23	1:A:733:ILE:HG21	2.03	0.41
1:C:322:PHE:CB	1:C:478:VAL:HG22	2.51	0.41
1:C:322:PHE:HB3	1:C:478:VAL:HG22	2.02	0.40
1:C:424:PRO:O	1:C:453:VAL:HG21	2.22	0.40
1:A:83:LEU:HD13	1:A:92:ILE:HG22	2.02	0.40
1:A:142:THR:HG22	1:A:180:TYR:HD1	1.86	0.40
1:A:417:VAL:CG2	1:A:454:VAL:HG22	2.45	0.40
1:B:478:VAL:O	1:B:478:VAL:HG22	2.21	0.40
1:C:518:TYR:O	1:C:518:TYR:CG	2.74	0.40
1:A:716:ALA:HA	1:A:723:GLU:HG3	2.03	0.40
1:A:752:TYR:HA	1:A:769:ILE:O	2.21	0.40
1:A:309:LEU:HD23	1:A:334:GLY:HA3	2.04	0.40
1:A:373:VAL:CG2	1:A:380:ALA:HB3	2.45	0.40
1:C:233:LEU:O	1:C:272:THR:HG23	2.20	0.40
1:A:39:ILE:HG13	1:A:81:ALA:HB3	2.03	0.40
1:C:403:GLU:HG3	1:C:404:GLU:N	2.35	0.40
1:B:430:LEU:HD12	1:B:470:TYR:CE2	2.57	0.40
1:B:251:ILE:O	1:B:252:GLU:C	2.60	0.40
1:B:147:ASN:HD22	1:B:147:ASN:N	2.17	0.40
3:C:782:NAG:O3	3:C:783:NAG:O5	2.33	0.40

All (1) 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	Distance(Å)	Clash(Å)
1:B:492:LEU:N	1:C:407:GLU:OE1[8_455]	2.04	0.16

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	773/816 (95%)	696 (90%)	64 (8%)	13 (2%)	14	71
1	B	674/816 (83%)	605 (90%)	56 (8%)	13 (2%)	12	68
1	C	674/816 (83%)	600 (89%)	62 (9%)	12 (2%)	13	69
All	All	2121/2448 (87%)	1901 (90%)	182 (9%)	38 (2%)	13	69

All (38) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	613	LEU
1	A	626	ILE
1	B	613	LEU
1	B	626	ILE
1	C	613	LEU
1	C	626	ILE
1	A	216	SER
1	A	638	GLY
1	A	724	TYR
1	B	216	SER
1	B	392	PHE
1	B	638	GLY
1	C	216	SER
1	C	638	GLY
1	A	103	ALA
1	A	174	GLU
1	A	252	GLU
1	A	622	ASP
1	A	664	LEU
1	B	103	ALA
1	B	252	GLU
1	B	622	ASP
1	B	664	LEU
1	C	103	ALA
1	C	174	GLU
1	C	252	GLU
1	C	593	GLU
1	C	622	ASP
1	C	664	LEU
1	A	744	ASN
1	B	174	GLU
1	B	464	ALA
1	B	612	ASP
1	C	612	ASP

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Mol	Chain	Res	Type
1	A	464	ALA
1	A	553	ARG
1	B	553	ARG
1	C	553	ARG

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	654/687 (95%)	625 (96%)	29 (4%)	39	82
1	B	572/687 (83%)	548 (96%)	24 (4%)	40	83
1	C	572/687 (83%)	548 (96%)	24 (4%)	40	83
All	All	1798/2061 (87%)	1721 (96%)	77 (4%)	40	83

All (77) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	THR
1	A	13	ARG
1	A	31	ASN
1	A	88	PHE
1	A	147	ASN
1	A	163	SER
1	A	175	ASP
1	A	195	SER
1	A	221	ASP
1	A	319	THR
1	A	339	THR
1	A	374	ARG
1	A	393	ASP
1	A	440	ARG
1	A	463	HIS
1	A	509	LEU
1	A	510	ILE
1	A	520	ILE
1	A	522	SER

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Mol	Chain	Res	Type
1	A	535	ASN
1	A	536	ARG
1	A	549	GLU
1	A	554	ASN
1	A	556	ASP
1	A	663	ASN
1	A	710	GLN
1	A	754	LEU
1	A	755	CYS
1	A	761	ILE
1	B	11	THR
1	B	13	ARG
1	B	31	ASN
1	B	88	PHE
1	B	147	ASN
1	B	175	ASP
1	B	195	SER
1	B	221	ASP
1	B	319	THR
1	B	339	THR
1	B	374	ARG
1	B	393	ASP
1	B	440	ARG
1	B	463	HIS
1	B	509	LEU
1	B	510	ILE
1	B	520	ILE
1	B	522	SER
1	B	535	ASN
1	B	536	ARG
1	B	549	GLU
1	B	554	ASN
1	B	556	ASP
1	B	663	ASN
1	C	11	THR
1	C	13	ARG
1	C	31	ASN
1	C	88	PHE
1	C	147	ASN
1	C	175	ASP
1	C	195	SER
1	C	221	ASP

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Mol	Chain	Res	Type
1	C	319	THR
1	C	339	THR
1	C	374	ARG
1	C	393	ASP
1	C	440	ARG
1	C	463	HIS
1	C	509	LEU
1	C	510	ILE
1	C	520	ILE
1	C	522	SER
1	C	535	ASN
1	C	536	ARG
1	C	549	GLU
1	C	554	ASN
1	C	556	ASP
1	C	663	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	31	ASN
1	A	147	ASN
1	A	258	GLN
1	A	402	GLN
1	A	554	ASN
1	A	732	ASN
1	B	31	ASN
1	B	147	ASN
1	B	402	GLN
1	B	535	ASN
1	B	554	ASN
1	B	579	GLN
1	C	31	ASN
1	C	147	ASN
1	C	167	HIS
1	C	402	GLN
1	C	554	ASN
1	C	579	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

20 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	$\# Z > 2$
2	NAG	A	782	1,2	12,14,15	0.56	0	15,19,21	0.98	1 (6%)
2	NAG	A	783	2	12,14,15	0.56	0	15,19,21	1.03	1 (6%)
2	NAG	A	784	1,2	12,14,15	0.54	0	15,19,21	1.06	1 (6%)
2	NAG	A	785	2	12,14,15	0.59	0	15,19,21	1.12	1 (6%)
2	NAG	B	782	1,2	12,14,15	0.81	1 (8%)	15,19,21	0.83	0
2	NAG	B	783	2	12,14,15	0.80	1 (8%)	15,19,21	1.22	1 (6%)
3	NAG	B	784	1,3	12,14,15	0.66	0	15,19,21	0.94	0
3	NAG	B	785	3	12,14,15	0.62	0	15,19,21	1.01	2 (13%)
3	NAG	B	786	3	12,14,15	0.62	0	15,19,21	0.89	0
4	NDG	B	787	1,4	12,14,15	0.87	0	15,19,21	1.90	4 (26%)
4	NAG	B	788	4	12,14,15	0.72	0	15,19,21	1.35	3 (20%)
4	NAG	B	789	4	12,14,15	0.61	0	15,19,21	0.90	0
2	NAG	B	790	1,2	12,14,15	0.75	0	15,19,21	1.35	3 (20%)
2	NAG	B	791	2	12,14,15	0.67	1 (8%)	15,19,21	1.32	3 (20%)
3	NAG	C	782	1,3	12,14,15	0.53	0	15,19,21	1.09	2 (13%)
3	NAG	C	783	3	12,14,15	0.71	1 (8%)	15,19,21	1.28	2 (13%)
3	NAG	C	784	3	12,14,15	0.62	0	15,19,21	0.79	0
4	NDG	C	785	1,4	12,14,15	0.55	0	15,19,21	0.76	0
4	NAG	C	786	4	12,14,15	0.72	1 (8%)	15,19,21	1.15	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	C	787	4	12,14,15	0.69	0	15,19,21	1.04	1 (6%)

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	NAG	A	782	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	783	2	-	0/6/23/26	0/1/1/1
2	NAG	A	784	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	785	2	-	2/6/23/26	0/1/1/1
2	NAG	B	782	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	783	2	-	0/6/23/26	0/1/1/1
3	NAG	B	784	1,3	1/1/5/7	0/6/23/26	0/1/1/1
3	NAG	B	785	3	-	0/6/23/26	0/1/1/1
3	NAG	B	786	3	-	0/6/23/26	0/1/1/1
4	NDG	B	787	1,4	-	0/6/23/26	0/1/1/1
4	NAG	B	788	4	-	0/6/23/26	0/1/1/1
4	NAG	B	789	4	-	0/6/23/26	0/1/1/1
2	NAG	B	790	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	791	2	-	0/6/23/26	0/1/1/1
3	NAG	C	782	1,3	-	0/6/23/26	0/1/1/1
3	NAG	C	783	3	-	0/6/23/26	0/1/1/1
3	NAG	C	784	3	-	0/6/23/26	0/1/1/1
4	NDG	C	785	1,4	-	0/6/23/26	0/1/1/1
4	NAG	C	786	4	-	0/6/23/26	0/1/1/1
4	NAG	C	787	4	-	0/6/23/26	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	782	NAG	O5-C5	-2.58	1.40	1.45
2	B	783	NAG	O5-C5	-2.27	1.41	1.45
4	C	786	NAG	O5-C5	-2.22	1.41	1.45
3	C	783	NAG	O5-C5	-2.12	1.41	1.45
2	B	791	NAG	O5-C5	-2.04	1.41	1.45

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	787	NDG	O-C5-C6	3.66	110.83	106.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	787	NDG	C3-C4-C5	3.43	116.33	110.20
3	C	783	NAG	O5-C5-C4	-3.35	106.40	110.65
2	B	791	NAG	O5-C5-C4	-3.30	106.47	110.65
4	B	788	NAG	O5-C5-C6	3.28	110.42	106.98
4	B	787	NDG	C2-N2-C7	2.93	128.02	123.09
3	C	783	NAG	O5-C5-C6	2.87	109.99	106.98
2	A	783	NAG	O5-C5-C6	2.81	109.93	106.98
2	A	785	NAG	O5-C5-C6	2.81	109.92	106.98
4	B	787	NDG	C4-C3-C2	2.70	117.92	111.32
2	B	790	NAG	O5-C5-C4	-2.68	107.25	110.65
2	B	791	NAG	O5-C5-C6	2.64	109.75	106.98
3	B	785	NAG	C2-N2-C7	-2.58	118.75	123.09
2	A	784	NAG	O5-C5-C4	2.57	113.92	110.65
4	C	787	NAG	O5-C5-C6	2.58	109.68	106.98
2	B	783	NAG	O5-C5-C6	2.55	109.66	106.98
2	B	790	NAG	C4-C3-C2	2.49	117.42	111.32
3	C	782	NAG	O5-C5-C6	2.48	109.59	106.98
2	B	790	NAG	O5-C5-C6	2.44	109.54	106.98
2	A	782	NAG	O5-C5-C4	2.36	113.65	110.65
4	B	788	NAG	O5-C5-C4	-2.35	107.67	110.65
4	B	788	NAG	C4-C3-C2	2.34	117.05	111.32
4	C	786	NAG	C3-C2-N2	-2.14	108.50	111.76
3	C	782	NAG	C4-C3-C2	-2.14	106.08	111.32
2	B	791	NAG	C3-C2-N2	-2.07	108.60	111.76
3	B	785	NAG	O5-C5-C6	2.04	109.13	106.98

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	B	784	NAG	C1

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	785	NAG	O7-C7-N2-C2
2	A	785	NAG	C8-C7-N2-C2

There are no ring outliers.

5.6 Ligand geometry ⓘ

5 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	$\# Z > 2$
6	GOL	A	786	-	5,5,5	0.33	0	5,5,5	0.36	0
6	GOL	A	787	-	5,5,5	0.35	0	5,5,5	0.31	0
5	SO4	B	792	-	4,4,4	0.26	0	6,6,6	0.12	0
6	GOL	B	793	-	5,5,5	0.36	0	5,5,5	0.21	0
6	GOL	B	794	-	5,5,5	0.38	0	5,5,5	0.33	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
6	GOL	A	786	-	-	0/4/4/4	0/0/0/0
6	GOL	A	787	-	-	0/4/4/4	0/0/0/0
5	SO4	B	792	-	-	0/0/0/0	0/0/0/0
6	GOL	B	793	-	-	0/4/4/4	0/0/0/0
6	GOL	B	794	-	-	0/4/4/4	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.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	775/816 (94%)	0.55	72 (9%) 9 12	27, 55, 89, 101	0
1	B	676/816 (82%)	-0.13	0 100 100	16, 42, 82, 93	0
1	C	676/816 (82%)	0.55	49 (7%) 15 17	25, 53, 101, 108	0
All	All	2127/2448 (86%)	0.33	121 (5%) 23 22	16, 50, 93, 108	0

All (121) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	567	GLN	6.6
1	A	439	ASP	5.8
1	A	477	LYS	5.7
1	A	492	LEU	5.0
1	A	570	TYR	5.0
1	A	390	GLY	5.0
1	A	486	LYS	4.8
1	A	490	TYR	4.5
1	C	177	TYR	4.5
1	A	446	TYR	4.4
1	A	482	GLU	4.4
1	A	429	GLU	4.2
1	A	472	CYS	4.2
1	C	184	THR	4.2
1	C	114	HIS	4.1
1	A	389	GLY	4.1
1	C	185	LYS	3.9
1	A	571	SER	3.9
1	A	451	GLY	3.9
1	C	117	ARG	3.9
1	A	436	ALA	3.9
1	C	205	GLU	3.9
1	A	408	PRO	3.8

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Mol	Chain	Res	Type	RSRZ
1	A	471	LYS	3.8
1	A	458	ASN	3.8
1	A	459	ILE	3.8
1	A	442	GLN	3.7
1	A	536	ARG	3.7
1	A	398	ARG	3.6
1	A	432	GLY	3.5
1	C	622	ASP	3.5
1	A	483	HIS	3.5
1	A	565	LYS	3.4
1	C	180	TYR	3.4
1	C	125	CYS	3.4
1	C	174	GLU	3.3
1	A	549	GLU	3.3
1	C	200	ARG	3.3
1	A	399	GLN	3.2
1	A	413	PHE	3.2
1	A	470	TYR	3.2
1	C	198	LYS	3.2
1	A	434	LYS	3.1
1	C	199	GLY	3.1
1	C	258	GLN	3.1
1	A	415	LYS	3.1
1	C	181	GLN	3.1
1	A	662	ARG	3.1
1	A	409	GLY	3.1
1	C	13	ARG	3.0
1	A	622	ASP	3.0
1	A	416	CYS	3.0
1	A	575	SER	3.0
1	A	456	TYR	3.0
1	C	108	ALA	3.0
1	C	204	THR	2.9
1	A	350	GLY	2.9
1	C	182	CYS	2.8
1	A	545	THR	2.8
1	C	109	ASP	2.8
1	C	136	GLU	2.7
1	A	497	GLN	2.7
1	A	452	ASP	2.7
1	A	351	HIS	2.7
1	A	359	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	437	ASN	2.7
1	A	440	ARG	2.7
1	C	158	TYR	2.7
1	A	419	GLY	2.6
1	A	579	GLN	2.6
1	A	487	LEU	2.6
1	A	539	LYS	2.6
1	C	155	ASP	2.6
1	A	454	VAL	2.6
1	C	192	THR	2.5
1	C	124	LYS	2.5
1	C	367	GLY	2.5
1	A	529	ASN	2.5
1	A	388	LEU	2.5
1	A	568	GLU	2.5
1	A	414	LEU	2.5
1	A	468	GLY	2.5
1	A	460	THR	2.4
1	A	424	PRO	2.4
1	C	26	CYS	2.4
1	C	296	GLY	2.4
1	C	85	ARG	2.4
1	C	135	VAL	2.4
1	C	173	PRO	2.4
1	A	475	LYS	2.3
1	A	402	GLN	2.3
1	C	156	GLY	2.3
1	C	186	HIS	2.3
1	C	107	GLU	2.3
1	C	33	MET	2.3
1	A	485	ALA	2.3
1	C	115	VAL	2.3
1	C	623	GLY	2.2
1	A	391	ARG	2.2
1	A	364	GLU	2.2
1	A	508	THR	2.2
1	A	667	HIS	2.2
1	A	87	GLN	2.2
1	C	126	LEU	2.2
1	A	507	GLU	2.2
1	C	238	GLN	2.2
1	C	178	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	193	ARG	2.2
1	C	128	PRO	2.2
1	A	33	MET	2.2
1	C	239	GLY	2.2
1	A	42	ASP	2.1
1	A	365	ASP	2.1
1	A	566	ASN	2.1
1	C	291	ASN	2.1
1	C	175	ASP	2.1
1	C	106	TYR	2.1
1	A	404	GLU	2.0
1	C	111	ASN	2.0
1	C	157	LYS	2.0
1	C	113	GLU	2.0

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

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

6.3 Carbohydrates ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	NAG	B	791	14/15	0.42	5.99	71,72,73,73	0
4	NAG	B	788	14/15	0.36	5.15	77,80,81,81	0
2	NAG	B	790	14/15	0.45	3.12	64,66,68,70	0
3	NAG	B	785	14/15	0.28	3.00	44,50,51,51	0
2	NAG	A	783	14/15	0.38	2.95	52,53,53,54	0
2	NAG	A	784	14/15	0.37	2.68	62,65,66,66	0
4	NAG	B	789	14/15	0.47	2.51	83,84,85,86	0
3	NAG	B	784	14/15	0.27	1.99	38,44,48,48	0
2	NAG	A	785	14/15	0.34	1.95	66,66,67,67	0
4	NDG	B	787	14/15	0.27	1.05	60,64,68,72	0
4	NDG	C	785	14/15	0.25	0.78	63,64,67,67	0
2	NAG	B	782	14/15	0.21	0.33	46,47,49,51	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	NAG	C	784	14/15	0.36	0.15	53,53,55,55	0
3	NAG	C	782	14/15	0.24	0.04	42,45,46,46	0
2	NAG	A	782	14/15	0.20	-0.16	50,52,52,53	0
3	NAG	C	783	14/15	0.21	-1.17	46,49,50,51	0
4	NAG	C	787	14/15	0.36	-	66,67,67,67	0
2	NAG	B	783	14/15	0.41	-	54,56,59,59	0
4	NAG	C	786	14/15	0.31	-	66,66,67,67	0
3	NAG	B	786	14/15	0.58	-	52,53,54,54	0

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, 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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
6	GOL	A	786	6/6	0.27	3.80	25,27,27,27	0
6	GOL	B	794	6/6	0.27	2.83	41,41,42,44	0
6	GOL	B	793	6/6	0.19	1.86	23,23,24,24	0
6	GOL	A	787	6/6	0.24	1.20	22,22,22,23	0
5	SO4	B	792	5/5	0.14	-1.07	20,21,21,24	0

6.5 Other polymers

There are no such residues in this entry.