



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 09:00 PM GMT

PDB ID : 4UM8
Title : Crystal structure of alpha V beta 6
Authors : Dong, X.; Springer, T.A.
Deposited on : 2014-05-15
Resolution : 2.85 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

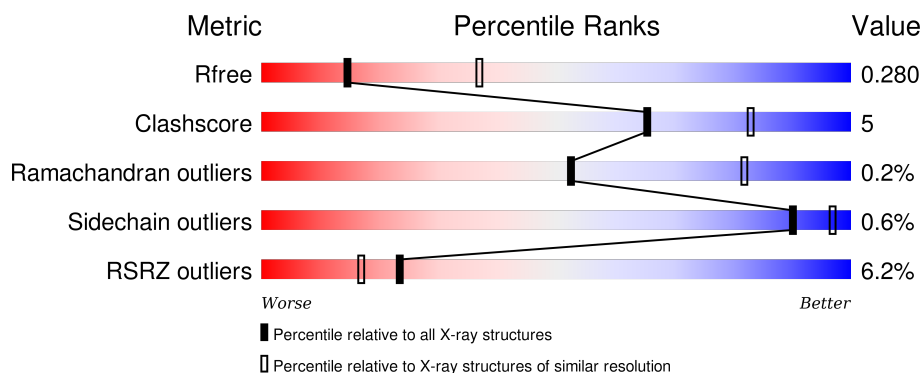
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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	2228 (2.90-2.82)
Clashscore	102246	2499 (2.90-2.82)
Ramachandran outliers	100387	2439 (2.90-2.82)
Sidechain outliers	100360	2442 (2.90-2.82)
RSRZ outliers	91569	2236 (2.90-2.82)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	681	<div> <div>2%</div> <div>77%</div> <div>10%</div> <div>13%</div> </div>
1	C	681	<div> <div>8%</div> <div>73%</div> <div>13%</div> <div>14%</div> </div>
2	B	788	<div> <div>4%</div> <div>47%</div> <div>6%</div> <div>46%</div> </div>
2	D	788	<div> <div>3%</div> <div>45%</div> <div>7%</div> <div>47%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	SO4	A	1598	-	-	-	X
6	CA	A	2002	-	-	-	X
7	NAG	D	3370	-	-	-	X
7	MAN	D	3373	-	-	-	X
9	NAG	C	3266	X	-	-	-

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 16497 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 INTEGRIN ALPHA-V.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	591	Total	C	N	O	S	0	0	0
			4579	2904	776	878	21			
1	C	588	Total	C	N	O	S	0	0	0
			4559	2893	773	872	21			

There are 174 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	596	THR	-	EXPRESSION TAG	UNP P06756
A	597	GLY	-	EXPRESSION TAG	UNP P06756
A	598	GLY	-	EXPRESSION TAG	UNP P06756
A	599	LEU	-	EXPRESSION TAG	UNP P06756
A	600	GLU	-	EXPRESSION TAG	UNP P06756
A	601	VAL	-	EXPRESSION TAG	UNP P06756
A	602	LEU	-	EXPRESSION TAG	UNP P06756
A	603	PHE	-	EXPRESSION TAG	UNP P06756
A	604	GLN	-	EXPRESSION TAG	UNP P06756
A	605	GLY	-	EXPRESSION TAG	UNP P06756
A	606	PRO	-	EXPRESSION TAG	UNP P06756
A	607	GLY	-	EXPRESSION TAG	UNP P06756
A	608	GLU	-	EXPRESSION TAG	UNP P06756
A	609	ASN	-	EXPRESSION TAG	UNP P06756
A	610	ALA	-	EXPRESSION TAG	UNP P06756
A	611	GLN	-	EXPRESSION TAG	UNP P06756
A	612	LEU	-	EXPRESSION TAG	UNP P06756
A	613	GLU	-	EXPRESSION TAG	UNP P06756
A	614	LYS	-	EXPRESSION TAG	UNP P06756
A	615	GLU	-	EXPRESSION TAG	UNP P06756
A	616	LEU	-	EXPRESSION TAG	UNP P06756
A	617	GLN	-	EXPRESSION TAG	UNP P06756
A	618	ALA	-	EXPRESSION TAG	UNP P06756
A	619	LEU	-	EXPRESSION TAG	UNP P06756
A	620	GLU	-	EXPRESSION TAG	UNP P06756

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Chain	Residue	Modelled	Actual	Comment	Reference
A	621	LYS	-	EXPRESSION TAG	UNP P06756
A	622	GLU	-	EXPRESSION TAG	UNP P06756
A	623	ASN	-	EXPRESSION TAG	UNP P06756
A	624	ALA	-	EXPRESSION TAG	UNP P06756
A	625	GLN	-	EXPRESSION TAG	UNP P06756
A	626	LEU	-	EXPRESSION TAG	UNP P06756
A	627	GLU	-	EXPRESSION TAG	UNP P06756
A	628	TRP	-	EXPRESSION TAG	UNP P06756
A	629	GLU	-	EXPRESSION TAG	UNP P06756
A	630	LEU	-	EXPRESSION TAG	UNP P06756
A	631	GLN	-	EXPRESSION TAG	UNP P06756
A	632	ALA	-	EXPRESSION TAG	UNP P06756
A	633	LEU	-	EXPRESSION TAG	UNP P06756
A	634	GLU	-	EXPRESSION TAG	UNP P06756
A	635	LYS	-	EXPRESSION TAG	UNP P06756
A	636	GLU	-	EXPRESSION TAG	UNP P06756
A	637	LEU	-	EXPRESSION TAG	UNP P06756
A	638	ALA	-	EXPRESSION TAG	UNP P06756
A	639	GLN	-	EXPRESSION TAG	UNP P06756
A	640	THR	-	EXPRESSION TAG	UNP P06756
A	641	THR	-	EXPRESSION TAG	UNP P06756
A	642	GLY	-	EXPRESSION TAG	UNP P06756
A	643	TRP	-	EXPRESSION TAG	UNP P06756
A	644	ARG	-	EXPRESSION TAG	UNP P06756
A	645	GLY	-	EXPRESSION TAG	UNP P06756
A	646	GLY	-	EXPRESSION TAG	UNP P06756
A	647	HIS	-	EXPRESSION TAG	UNP P06756
A	648	VAL	-	EXPRESSION TAG	UNP P06756
A	649	VAL	-	EXPRESSION TAG	UNP P06756
A	650	GLU	-	EXPRESSION TAG	UNP P06756
A	651	GLY	-	EXPRESSION TAG	UNP P06756
A	652	LEU	-	EXPRESSION TAG	UNP P06756
A	653	ALA	-	EXPRESSION TAG	UNP P06756
A	654	GLY	-	EXPRESSION TAG	UNP P06756
A	655	GLU	-	EXPRESSION TAG	UNP P06756
A	656	LEU	-	EXPRESSION TAG	UNP P06756
A	657	GLU	-	EXPRESSION TAG	UNP P06756
A	658	GLN	-	EXPRESSION TAG	UNP P06756
A	659	LEU	-	EXPRESSION TAG	UNP P06756
A	660	ARG	-	EXPRESSION TAG	UNP P06756
A	661	ALA	-	EXPRESSION TAG	UNP P06756
A	662	ARG	-	EXPRESSION TAG	UNP P06756

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Chain	Residue	Modelled	Actual	Comment	Reference
A	663	LEU	-	EXPRESSION TAG	UNP P06756
A	664	GLU	-	EXPRESSION TAG	UNP P06756
A	665	HIS	-	EXPRESSION TAG	UNP P06756
A	666	HIS	-	EXPRESSION TAG	UNP P06756
A	667	PRO	-	EXPRESSION TAG	UNP P06756
A	668	GLN	-	EXPRESSION TAG	UNP P06756
A	669	GLY	-	EXPRESSION TAG	UNP P06756
A	670	GLN	-	EXPRESSION TAG	UNP P06756
A	671	ARG	-	EXPRESSION TAG	UNP P06756
A	672	GLU	-	EXPRESSION TAG	UNP P06756
A	673	PRO	-	EXPRESSION TAG	UNP P06756
A	674	ALA	-	EXPRESSION TAG	UNP P06756
A	675	GLY	-	EXPRESSION TAG	UNP P06756
A	676	HIS	-	EXPRESSION TAG	UNP P06756
A	677	HIS	-	EXPRESSION TAG	UNP P06756
A	678	HIS	-	EXPRESSION TAG	UNP P06756
A	679	HIS	-	EXPRESSION TAG	UNP P06756
A	680	HIS	-	EXPRESSION TAG	UNP P06756
A	681	HIS	-	EXPRESSION TAG	UNP P06756
A	400	CYS	MET	ENGINEERED MUTATION	UNP P06756
C	596	THR	-	EXPRESSION TAG	UNP P06756
C	597	GLY	-	EXPRESSION TAG	UNP P06756
C	598	GLY	-	EXPRESSION TAG	UNP P06756
C	599	LEU	-	EXPRESSION TAG	UNP P06756
C	600	GLU	-	EXPRESSION TAG	UNP P06756
C	601	VAL	-	EXPRESSION TAG	UNP P06756
C	602	LEU	-	EXPRESSION TAG	UNP P06756
C	603	PHE	-	EXPRESSION TAG	UNP P06756
C	604	GLN	-	EXPRESSION TAG	UNP P06756
C	605	GLY	-	EXPRESSION TAG	UNP P06756
C	606	PRO	-	EXPRESSION TAG	UNP P06756
C	607	GLY	-	EXPRESSION TAG	UNP P06756
C	608	GLU	-	EXPRESSION TAG	UNP P06756
C	609	ASN	-	EXPRESSION TAG	UNP P06756
C	610	ALA	-	EXPRESSION TAG	UNP P06756
C	611	GLN	-	EXPRESSION TAG	UNP P06756
C	612	LEU	-	EXPRESSION TAG	UNP P06756
C	613	GLU	-	EXPRESSION TAG	UNP P06756
C	614	LYS	-	EXPRESSION TAG	UNP P06756
C	615	GLU	-	EXPRESSION TAG	UNP P06756
C	616	LEU	-	EXPRESSION TAG	UNP P06756
C	617	GLN	-	EXPRESSION TAG	UNP P06756

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Chain	Residue	Modelled	Actual	Comment	Reference
C	618	ALA	-	EXPRESSION TAG	UNP P06756
C	619	LEU	-	EXPRESSION TAG	UNP P06756
C	620	GLU	-	EXPRESSION TAG	UNP P06756
C	621	LYS	-	EXPRESSION TAG	UNP P06756
C	622	GLU	-	EXPRESSION TAG	UNP P06756
C	623	ASN	-	EXPRESSION TAG	UNP P06756
C	624	ALA	-	EXPRESSION TAG	UNP P06756
C	625	GLN	-	EXPRESSION TAG	UNP P06756
C	626	LEU	-	EXPRESSION TAG	UNP P06756
C	627	GLU	-	EXPRESSION TAG	UNP P06756
C	628	TRP	-	EXPRESSION TAG	UNP P06756
C	629	GLU	-	EXPRESSION TAG	UNP P06756
C	630	LEU	-	EXPRESSION TAG	UNP P06756
C	631	GLN	-	EXPRESSION TAG	UNP P06756
C	632	ALA	-	EXPRESSION TAG	UNP P06756
C	633	LEU	-	EXPRESSION TAG	UNP P06756
C	634	GLU	-	EXPRESSION TAG	UNP P06756
C	635	LYS	-	EXPRESSION TAG	UNP P06756
C	636	GLU	-	EXPRESSION TAG	UNP P06756
C	637	LEU	-	EXPRESSION TAG	UNP P06756
C	638	ALA	-	EXPRESSION TAG	UNP P06756
C	639	GLN	-	EXPRESSION TAG	UNP P06756
C	640	THR	-	EXPRESSION TAG	UNP P06756
C	641	THR	-	EXPRESSION TAG	UNP P06756
C	642	GLY	-	EXPRESSION TAG	UNP P06756
C	643	TRP	-	EXPRESSION TAG	UNP P06756
C	644	ARG	-	EXPRESSION TAG	UNP P06756
C	645	GLY	-	EXPRESSION TAG	UNP P06756
C	646	GLY	-	EXPRESSION TAG	UNP P06756
C	647	HIS	-	EXPRESSION TAG	UNP P06756
C	648	VAL	-	EXPRESSION TAG	UNP P06756
C	649	VAL	-	EXPRESSION TAG	UNP P06756
C	650	GLU	-	EXPRESSION TAG	UNP P06756
C	651	GLY	-	EXPRESSION TAG	UNP P06756
C	652	LEU	-	EXPRESSION TAG	UNP P06756
C	653	ALA	-	EXPRESSION TAG	UNP P06756
C	654	GLY	-	EXPRESSION TAG	UNP P06756
C	655	GLU	-	EXPRESSION TAG	UNP P06756
C	656	LEU	-	EXPRESSION TAG	UNP P06756
C	657	GLU	-	EXPRESSION TAG	UNP P06756
C	658	GLN	-	EXPRESSION TAG	UNP P06756
C	659	LEU	-	EXPRESSION TAG	UNP P06756

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Chain	Residue	Modelled	Actual	Comment	Reference
C	660	ARG	-	EXPRESSION TAG	UNP P06756
C	661	ALA	-	EXPRESSION TAG	UNP P06756
C	662	ARG	-	EXPRESSION TAG	UNP P06756
C	663	LEU	-	EXPRESSION TAG	UNP P06756
C	664	GLU	-	EXPRESSION TAG	UNP P06756
C	665	HIS	-	EXPRESSION TAG	UNP P06756
C	666	HIS	-	EXPRESSION TAG	UNP P06756
C	667	PRO	-	EXPRESSION TAG	UNP P06756
C	668	GLN	-	EXPRESSION TAG	UNP P06756
C	669	GLY	-	EXPRESSION TAG	UNP P06756
C	670	GLN	-	EXPRESSION TAG	UNP P06756
C	671	ARG	-	EXPRESSION TAG	UNP P06756
C	672	GLU	-	EXPRESSION TAG	UNP P06756
C	673	PRO	-	EXPRESSION TAG	UNP P06756
C	674	ALA	-	EXPRESSION TAG	UNP P06756
C	675	GLY	-	EXPRESSION TAG	UNP P06756
C	676	HIS	-	EXPRESSION TAG	UNP P06756
C	677	HIS	-	EXPRESSION TAG	UNP P06756
C	678	HIS	-	EXPRESSION TAG	UNP P06756
C	679	HIS	-	EXPRESSION TAG	UNP P06756
C	680	HIS	-	EXPRESSION TAG	UNP P06756
C	681	HIS	-	EXPRESSION TAG	UNP P06756
C	400	CYS	MET	ENGINEERED MUTATION	UNP P06756

- Molecule 2 is a protein called INTEGRIN BETA-6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	423	Total	C	N	O	S	0	0	0
			3252	2051	548	628	25			
2	D	414	Total	C	N	O	S	0	0	0
			3202	2020	539	618	25			

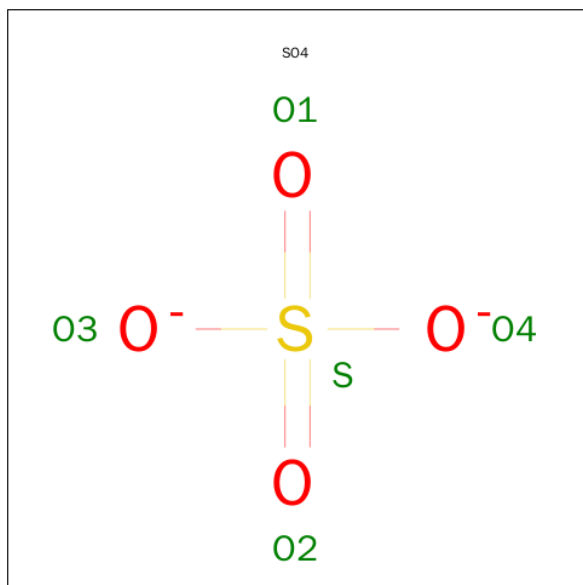
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	270	CYS	ILE	ENGINEERED MUTATION	UNP P18564
D	270	CYS	ILE	ENGINEERED MUTATION	UNP P18564

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Cl 1 1	0	0
3	C	2	Total Cl 2 2	0	0

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 5 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Ni 1 1	0	0

- Molecule 6 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	1	Total Ca 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	4	Total 4	Ca 4	0	0
6	D	1	Total 1	Ca 1	0	0
6	C	4	Total 4	Ca 4	0	0

- Molecule 7 is a polymer of unknown type called SUGAR (4-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	4	Total 50	C 28	N 2	O 20	0	0
7	C	4	Total 50	C 28	N 2	O 20	0	0
7	D	4	Total 50	C 28	N 2	O 20	0	0

- Molecule 8 is a polymer of unknown type called SUGAR (5-MER).

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

- Molecule 9 is a polymer of unknown type called SUGAR (6-MER).

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

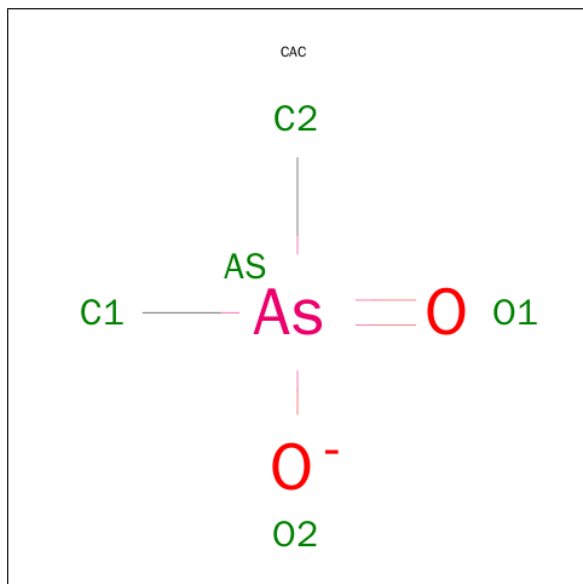
- Molecule 10 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	A	3	Total 39	C 22	N 2	O 15	0	0
10	C	3	Total 39	C 22	N 2	O 15	0	0

- Molecule 11 is a polymer of unknown type called SUGAR (2-MER).

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

- Molecule 12 is CACODYLATE ION (three-letter code: CAC) (formula: $\text{C}_2\text{H}_6\text{AsO}_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
12	B	1	Total	As	C	O	0	0
			5	1	2	2		
12	D	1	Total	As	C	O	0	0
			5	1	2	2		

- Molecule 13 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	B	1	Total	Mg	0	0
			1	1		
13	D	1	Total	Mg	0	0
			1	1		

- Molecule 14 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $\text{C}_8\text{H}_{15}\text{NO}_6$).



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

- Molecule 15 is a polymer of unknown type called SUGAR (7-MER).

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

- Molecule 16 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	A	65	Total	O	0	0
			65	65		
16	B	32	Total	O	0	0
			32	32		
16	C	38	Total	O	0	0
			38	38		
16	D	26	Total	O	0	0
			26	26		

Chain B:

Position	Most Conserved Amino Acid	Information Content (bits)
1	GLY	0.14
2	GLY	0.13
3	GLY	0.12
4	GLY	0.11
5	GLY	0.10
6	GLY	0.09
7	GLY	0.08
8	GLY	0.07
9	GLY	0.06
10	GLY	0.05
11	GLY	0.04
12	GLY	0.03
13	GLY	0.02
14	GLY	0.01
15	GLY	0.01
16	GLY	0.01
17	GLY	0.01
18	GLY	0.01
19	GLY	0.01
20	GLY	0.01

[illegible]

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

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

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	184.45Å 170.01Å 102.39Å 90.00° 98.68° 90.00°	Depositor
Resolution (Å)	48.66 – 2.85 48.66 – 2.85	Depositor EDS
% Data completeness (in resolution range)	96.4 (48.66-2.85) 96.4 (48.66-2.85)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.34 (at 2.86Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.238 , 0.281 0.238 , 0.280	Depositor DCC
R_{free} test set	1796 reflections (2.57%)	DCC
Wilson B-factor (Å ²)	61.1	Xtriage
Anisotropy	0.384	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 75.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	0 of 69928 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	16497	wwPDB-VP
Average B, all atoms (Å ²)	86.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.31% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NI, MG, BMA, NAG, CL, CA, SO4, CAC, MAN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.21	0/4682	0.39	0/6339
1	C	0.21	0/4660	0.37	0/6305
2	B	0.21	0/3308	0.40	0/4481
2	D	0.21	0/3258	0.39	0/4413
All	All	0.21	0/15908	0.39	0/21538

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
9	C	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
9	C	3266	NAG	C1

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	4579	0	4426	34	1
1	C	4559	0	4408	51	1
2	B	3252	0	3234	35	0
2	D	3202	0	3176	36	0
3	A	1	0	0	0	0
3	C	2	0	0	0	0
4	A	15	0	0	1	0
5	A	1	0	0	0	0
6	A	4	0	0	0	0
6	B	1	0	0	0	0
6	C	4	0	0	0	0
6	D	1	0	0	0	0
7	A	50	0	43	1	0
7	C	50	0	43	1	0
7	D	50	0	43	2	0
8	A	122	0	104	1	0
9	A	72	0	61	1	0
9	C	72	0	61	1	0
10	A	39	0	34	1	0
10	C	39	0	34	0	0
11	A	28	0	25	0	0
11	C	56	0	50	0	0
12	B	5	0	0	0	0
12	D	5	0	0	0	0
13	B	1	0	0	0	0
13	D	1	0	0	0	0
14	B	14	0	13	0	0
14	D	28	0	26	0	0
15	C	83	0	70	2	0
16	A	65	0	0	0	0
16	B	32	0	0	0	0
16	C	38	0	0	0	0
16	D	26	0	0	1	0
All	All	16497	0	15851	160	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 160 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:109:ARG:NH2	2:B:397:THR:OG1	2.19	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:220:ASP:N	2:B:220:ASP:OD1	2.24	0.70
1:C:116:THR:HG22	1:C:118:MET:H	1.55	0.70
1:A:480:LYS:HB2	1:A:533:MET:HB3	1.74	0.70
1:A:116:THR:HG22	1:A:118:MET:H	1.57	0.70

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	Interatomic distance (Å)	Clash overlap (Å)
1:A:452:SER:OG	1:C:452:SER:OG[4_555]	2.19	0.01

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	587/681 (86%)	562 (96%)	25 (4%)	0	100	100
1	C	580/681 (85%)	557 (96%)	23 (4%)	0	100	100
2	B	417/788 (53%)	397 (95%)	18 (4%)	2 (0%)	34	67
2	D	406/788 (52%)	389 (96%)	16 (4%)	1 (0%)	52	82
All	All	1990/2938 (68%)	1905 (96%)	82 (4%)	3 (0%)	52	82

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	365	ASP
2	B	161	VAL
2	D	161	VAL

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	485/555 (87%)	483 (100%)	2 (0%)	93	98
1	C	483/555 (87%)	480 (99%)	3 (1%)	90	97
2	B	371/685 (54%)	367 (99%)	4 (1%)	80	94
2	D	368/685 (54%)	367 (100%)	1 (0%)	94	98
All	All	1707/2480 (69%)	1697 (99%)	10 (1%)	90	97

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	397	THR
2	B	414	ARG
1	C	463	LEU
2	B	369	LEU
1	C	275	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	352	GLN
1	A	474	ASN
1	C	152	GLN
1	C	207	GLN
2	D	304	GLN

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 ⓘ

53 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
7	NAG	A	3044	1,7	14,14,15	0.30	0	15,19,21	0.42	0
7	NAG	A	3045	7	14,14,15	0.32	0	15,19,21	0.55	0
7	BMA	A	3046	7	11,11,12	0.59	0	14,15,17	0.84	0
7	MAN	A	3047	7	11,11,12	0.74	0	14,15,17	1.03	2 (14%)
8	NAG	A	3260	1,8	14,14,15	0.18	0	15,19,21	0.25	0
8	NAG	A	3261	8	14,14,15	0.21	0	15,19,21	0.26	0
8	BMA	A	3262	8	11,11,12	0.79	0	14,15,17	0.83	0
8	MAN	A	3263	8	11,11,12	0.86	0	14,15,17	1.09	1 (7%)
8	MAN	A	3264	8	11,11,12	0.70	0	14,15,17	0.99	2 (14%)
9	NAG	A	3266	1,9	14,14,15	1.14	1 (7%)	15,19,21	0.97	1 (6%)
9	NAG	A	3267	9	14,14,15	0.46	0	15,19,21	0.23	0
9	BMA	A	3268	9	11,11,12	0.79	1 (9%)	14,15,17	0.81	0
9	MAN	A	3269	9	11,11,12	0.74	1 (9%)	14,15,17	0.93	1 (7%)
9	MAN	A	3270	9	11,11,12	0.77	1 (9%)	14,15,17	0.94	1 (7%)
9	MAN	A	3271	9	11,11,12	0.76	1 (9%)	14,15,17	0.97	2 (14%)
10	NAG	A	3458	1,10	14,14,15	0.30	0	15,19,21	0.45	0
10	NAG	A	3459	10	14,14,15	0.29	0	15,19,21	0.51	0
10	BMA	A	3460	10	11,11,12	0.82	0	14,15,17	1.10	2 (14%)
8	NAG	A	3524	1,8	14,14,15	0.36	0	15,19,21	0.49	0
8	NAG	A	3525	8	14,14,15	0.28	0	15,19,21	0.36	0
8	BMA	A	3526	8	11,11,12	0.61	0	14,15,17	1.08	2 (14%)
8	MAN	A	3527	8	11,11,12	0.72	0	14,15,17	1.30	2 (14%)
8	MAN	A	3528	8	11,11,12	0.61	0	14,15,17	1.14	2 (14%)
11	NAG	A	3585	1,11	14,14,15	0.33	0	15,19,21	0.36	0
11	NAG	A	3586	11	14,14,15	0.29	0	15,19,21	0.39	0
10	NAG	C	3044	1,10	14,14,15	0.51	0	15,19,21	0.49	0
10	NAG	C	3045	10	14,14,15	0.41	0	15,19,21	0.71	1 (6%)
10	BMA	C	3046	10	11,11,12	0.54	0	14,15,17	1.03	1 (7%)
11	NAG	C	3260	1,11	14,14,15	0.26	0	15,19,21	0.31	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
11	NAG	C	3261	11	14,14,15	0.22	0	15,19,21	0.35	0
9	NAG	C	3266	1,9	14,14,15	1.71	2 (14%)	15,19,21	1.34	2 (13%)
9	NAG	C	3267	9	14,14,15	0.41	0	15,19,21	0.24	0
9	BMA	C	3268	9	11,11,12	0.71	0	14,15,17	0.78	0
9	MAN	C	3269	9	11,11,12	0.77	1 (9%)	14,15,17	0.90	1 (7%)
9	MAN	C	3270	9	11,11,12	0.69	0	14,15,17	1.05	2 (14%)
9	MAN	C	3271	9	11,11,12	0.67	0	14,15,17	1.01	2 (14%)
7	NAG	C	3458	1,7	14,14,15	0.33	0	15,19,21	0.59	0
7	NAG	C	3459	7	14,14,15	0.36	0	15,19,21	0.45	0
7	BMA	C	3460	7	11,11,12	1.01	1 (9%)	14,15,17	1.32	2 (14%)
7	MAN	C	3461	7	11,11,12	1.12	2 (18%)	14,15,17	1.24	3 (21%)
15	NAG	C	3524	1,15	14,14,15	1.03	2 (14%)	15,19,21	0.83	1 (6%)
15	NAG	C	3525	15	14,14,15	0.58	1 (7%)	15,19,21	0.71	1 (6%)
15	BMA	C	3526	15	11,11,12	1.02	1 (9%)	14,15,17	1.61	4 (28%)
15	MAN	C	3527	15	11,11,12	0.79	0	14,15,17	1.47	2 (14%)
15	MAN	C	3528	15	11,11,12	0.98	1 (9%)	14,15,17	0.87	1 (7%)
15	MAN	C	3529	15	11,11,12	0.72	0	14,15,17	0.97	2 (14%)
15	MAN	C	3530	15	11,11,12	0.58	0	14,15,17	1.13	2 (14%)
11	NAG	C	3585	1,11	14,14,15	0.38	0	15,19,21	0.22	0
11	NAG	C	3586	11	14,14,15	0.28	0	15,19,21	0.35	0
7	NAG	D	3370	2,7	14,14,15	0.60	1 (7%)	15,19,21	0.41	0
7	NAG	D	3371	7	14,14,15	0.33	0	15,19,21	0.65	0
7	BMA	D	3372	7	11,11,12	0.57	0	14,15,17	1.17	1 (7%)
7	MAN	D	3373	7	11,11,12	0.73	0	14,15,17	1.02	2 (14%)

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
7	NAG	A	3044	1,7	-	0/6/23/26	0/1/1/1
7	NAG	A	3045	7	-	0/6/23/26	0/1/1/1
7	BMA	A	3046	7	-	0/2/19/22	0/1/1/1
7	MAN	A	3047	7	-	0/2/19/22	0/1/1/1
8	NAG	A	3260	1,8	-	0/6/23/26	0/1/1/1
8	NAG	A	3261	8	-	0/6/23/26	0/1/1/1
8	BMA	A	3262	8	-	0/2/19/22	0/1/1/1
8	MAN	A	3263	8	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	MAN	A	3264	8	-	0/2/19/22	0/1/1/1
9	NAG	A	3266	1,9	-	0/6/23/26	0/1/1/1
9	NAG	A	3267	9	-	0/6/23/26	0/1/1/1
9	BMA	A	3268	9	-	0/2/19/22	0/1/1/1
9	MAN	A	3269	9	-	0/2/19/22	0/1/1/1
9	MAN	A	3270	9	-	0/2/19/22	0/1/1/1
9	MAN	A	3271	9	-	0/2/19/22	0/1/1/1
10	NAG	A	3458	1,10	-	0/6/23/26	0/1/1/1
10	NAG	A	3459	10	-	0/6/23/26	0/1/1/1
10	BMA	A	3460	10	-	0/2/19/22	0/1/1/1
8	NAG	A	3524	1,8	-	0/6/23/26	0/1/1/1
8	NAG	A	3525	8	-	0/6/23/26	0/1/1/1
8	BMA	A	3526	8	-	0/2/19/22	0/1/1/1
8	MAN	A	3527	8	-	0/2/19/22	1/1/1/1
8	MAN	A	3528	8	-	0/2/19/22	0/1/1/1
11	NAG	A	3585	1,11	-	0/6/23/26	0/1/1/1
11	NAG	A	3586	11	-	0/6/23/26	0/1/1/1
10	NAG	C	3044	1,10	-	0/6/23/26	0/1/1/1
10	NAG	C	3045	10	-	0/6/23/26	0/1/1/1
10	BMA	C	3046	10	-	0/2/19/22	0/1/1/1
11	NAG	C	3260	1,11	-	0/6/23/26	0/1/1/1
11	NAG	C	3261	11	-	0/6/23/26	0/1/1/1
9	NAG	C	3266	1,9	1/1/5/7	0/6/23/26	0/1/1/1
9	NAG	C	3267	9	-	0/6/23/26	0/1/1/1
9	BMA	C	3268	9	-	0/2/19/22	0/1/1/1
9	MAN	C	3269	9	-	0/2/19/22	0/1/1/1
9	MAN	C	3270	9	-	0/2/19/22	0/1/1/1
9	MAN	C	3271	9	-	0/2/19/22	0/1/1/1
7	NAG	C	3458	1,7	-	0/6/23/26	0/1/1/1
7	NAG	C	3459	7	-	0/6/23/26	0/1/1/1
7	BMA	C	3460	7	-	0/2/19/22	0/1/1/1
7	MAN	C	3461	7	-	0/2/19/22	0/1/1/1
15	NAG	C	3524	1,15	-	0/6/23/26	0/1/1/1
15	NAG	C	3525	15	-	0/6/23/26	0/1/1/1
15	BMA	C	3526	15	-	0/2/19/22	0/1/1/1
15	MAN	C	3527	15	-	0/2/19/22	0/1/1/1
15	MAN	C	3528	15	-	0/2/19/22	0/1/1/1
15	MAN	C	3529	15	-	0/2/19/22	0/1/1/1
15	MAN	C	3530	15	-	0/2/19/22	0/1/1/1
11	NAG	C	3585	1,11	-	0/6/23/26	0/1/1/1
11	NAG	C	3586	11	-	0/6/23/26	0/1/1/1
7	NAG	D	3370	2,7	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	D	3371	7	-	0/6/23/26	0/1/1/1
7	BMA	D	3372	7	-	0/2/19/22	0/1/1/1
7	MAN	D	3373	7	-	0/2/19/22	0/1/1/1

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	C	3266	NAG	O5-C1	-5.89	1.33	1.43
9	A	3266	NAG	O5-C1	-4.10	1.36	1.43
15	C	3524	NAG	O5-C1	-3.08	1.38	1.43
15	C	3528	MAN	O5-C1	-2.56	1.39	1.43
9	C	3266	NAG	C1-C2	-2.29	1.49	1.52

The worst 5 of 48 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	C	3266	NAG	C1-O5-C5	-3.12	108.29	112.25
10	A	3460	BMA	O2-C2-C3	-2.82	104.45	110.12
15	C	3526	BMA	C1-C2-C3	-2.41	106.69	109.54
15	C	3526	BMA	C3-C4-C5	-2.40	106.02	110.20
9	C	3271	MAN	O2-C2-C3	-2.29	105.52	110.12

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
9	C	3266	NAG	C1

There are no torsion outliers.

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	3527	MAN	C1-C2-C3-C4-C5-O5

18 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	3046	BMA	1	0
7	A	3047	MAN	1	0
9	A	3268	BMA	1	0
9	A	3270	MAN	1	0
10	A	3459	NAG	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	A	3460	BMA	1	0
8	A	3526	BMA	1	0
8	A	3527	MAN	1	0
9	C	3268	BMA	1	0
9	C	3270	MAN	1	0
7	C	3459	NAG	1	0
7	C	3460	BMA	1	0
15	C	3524	NAG	1	0
15	C	3525	NAG	1	0
15	C	3526	BMA	1	0
15	C	3527	MAN	1	0
7	D	3372	BMA	1	0
7	D	3373	MAN	2	0

5.6 Ligand geometry

Of 24 ligands modelled in this entry, 16 are monoatomic - leaving 8 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	SO4	A	1596	-	4,4,4	0.23	0	6,6,6	0.08	0
4	SO4	A	1597	-	4,4,4	0.23	0	6,6,6	0.09	0
4	SO4	A	1598	-	4,4,4	0.24	0	6,6,6	0.08	0
12	CAC	B	1442	-	0,4,4	0.00	-	0,6,6	0.00	-
14	NAG	B	3243	2	14,14,15	0.30	0	15,19,21	0.27	0
12	CAC	D	1442	-	0,4,4	0.00	-	0,6,6	0.00	-
14	NAG	D	3080	2	14,14,15	0.39	0	15,19,21	0.55	0
14	NAG	D	3243	2	14,14,15	0.30	0	15,19,21	0.28	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
4	SO4	A	1596	-	-	0/0/0/0	0/0/0/0
4	SO4	A	1597	-	-	0/0/0/0	0/0/0/0
4	SO4	A	1598	-	-	0/0/0/0	0/0/0/0
12	CAC	B	1442	-	-	0/0/0/0	0/0/0/0
14	NAG	B	3243	2	-	0/6/23/26	0/1/1/1
12	CAC	D	1442	-	-	0/0/0/0	0/0/0/0
14	NAG	D	3080	2	-	0/6/23/26	0/1/1/1
14	NAG	D	3243	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1596	SO4	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, 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	591/681 (86%)	-0.00	11 (1%) 70 66	34, 64, 109, 185	0
1	C	588/681 (86%)	0.57	53 (9%) 12 7	52, 100, 155, 201	0
2	B	423/788 (53%)	0.41	35 (8%) 14 9	25, 70, 166, 245	0
2	D	414/788 (52%)	0.33	27 (6%) 22 16	33, 77, 150, 205	0
All	All	2016/2938 (68%)	0.32	126 (6%) 23 17	25, 78, 150, 245	0

The worst 5 of 126 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	8	LEU	7.6
2	B	58	ILE	7.4
2	B	55	LEU	7.2
1	C	129	PHE	7.1
2	B	50	ALA	6.8

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

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

6.3 Carbohydrates [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
7	NAG	D	3370	14/15	0.64	0.44	5.25	120,139,148,162	0
7	MAN	D	3373	11/12	0.70	0.37	3.40	153,162,169,169	0
15	MAN	C	3528	11/12	0.73	0.33	1.86	131,142,151,152	0
15	MAN	C	3530	11/12	0.71	0.27	1.75	128,136,161,170	0
10	NAG	A	3459	14/15	0.74	0.24	1.17	132,155,172,174	0
10	NAG	A	3458	14/15	0.82	0.24	1.06	105,125,137,138	0
7	NAG	C	3459	14/15	0.73	0.22	0.58	117,137,149,149	0
10	NAG	C	3044	14/15	0.86	0.21	0.39	88,102,119,139	0
7	NAG	C	3458	14/15	0.92	0.20	-0.03	81,104,118,130	0
7	NAG	A	3044	14/15	0.93	0.16	-0.14	40,72,97,108	0
9	NAG	A	3266	14/15	0.96	0.17	-0.48	50,64,81,97	0
8	NAG	A	3260	14/15	0.95	0.13	-0.49	60,82,102,102	0
11	NAG	A	3585	14/15	0.94	0.18	-1.10	89,112,120,132	0
9	NAG	C	3266	14/15	0.87	0.18	-1.12	73,84,104,108	0
11	NAG	C	3260	14/15	0.88	0.23	-	83,105,113,120	0
10	NAG	C	3045	14/15	0.88	0.31	-	119,136,147,154	0
9	MAN	A	3269	11/12	0.82	0.27	-	104,115,137,152	0
9	MAN	A	3271	11/12	0.90	0.19	-	110,121,130,130	0
7	MAN	A	3047	11/12	0.64	0.22	-	138,152,165,166	0
7	BMA	C	3460	11/12	0.66	0.30	-	149,163,235,236	0
8	NAG	A	3524	14/15	0.89	0.17	-	78,105,117,118	0
10	BMA	A	3460	11/12	0.68	0.42	-	175,182,191,192	0
9	BMA	C	3268	11/12	0.87	0.19	-	112,117,158,163	0
8	BMA	A	3526	11/12	0.79	0.29	-	135,141,150,154	0
8	NAG	A	3261	14/15	0.87	0.23	-	99,123,133,148	0
9	MAN	C	3270	11/12	0.80	0.38	-	166,172,177,180	0
7	BMA	A	3046	11/12	0.67	0.25	-	137,148,165,170	0
9	MAN	C	3269	11/12	0.89	0.28	-	103,111,115,117	0
8	MAN	A	3528	11/12	0.75	0.42	-	152,163,169,172	0
8	NAG	A	3525	14/15	0.87	0.23	-	100,119,131,142	0
9	BMA	A	3268	11/12	0.82	0.16	-	93,117,134,137	0
7	MAN	C	3461	11/12	0.80	0.25	-	95,155,172,173	0
11	NAG	C	3586	14/15	0.65	0.38	-	149,155,163,168	0
15	MAN	C	3527	11/12	0.80	0.28	-	130,139,148,152	0
15	NAG	C	3525	14/15	0.58	0.41	-	134,143,150,152	0
15	BMA	C	3526	11/12	0.81	0.21	-	120,130,140,143	0
7	NAG	D	3371	14/15	0.80	0.23	-	153,165,173,182	0
8	MAN	A	3263	11/12	0.68	0.28	-	161,170,185,192	0
11	NAG	C	3585	14/15	0.91	0.19	-	89,106,134,139	0
8	MAN	A	3527	11/12	0.51	0.34	-	144,157,163,168	0
11	NAG	A	3586	14/15	0.79	0.37	-	124,147,157,161	0
9	MAN	A	3270	11/12	0.87	0.20	-	119,137,139,139	0
15	MAN	C	3529	11/12	0.71	0.29	-	118,135,150,152	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
7	NAG	A	3045	14/15	0.79	0.23	-	103,130,141,149	0
7	BMA	D	3372	11/12	0.68	0.48	-	168,186,195,202	0
15	NAG	C	3524	14/15	0.86	0.30	-	103,121,128,139	0
8	BMA	A	3262	11/12	0.69	0.27	-	149,158,166,171	0
9	MAN	C	3271	11/12	0.81	0.47	-	178,185,187,188	0
10	BMA	C	3046	11/12	0.61	0.18	-	125,146,155,161	0
11	NAG	C	3261	14/15	0.78	0.32	-	111,124,129,133	0
8	MAN	A	3264	11/12	0.62	0.56	-	169,187,191,194	0
9	NAG	A	3267	14/15	0.94	0.17	-	59,69,92,107	0
9	NAG	C	3267	14/15	0.92	0.21	-	69,88,101,105	0

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
6	CA	A	2002	1/1	0.46	0.52	16.22	219,219,219,219	0
4	SO4	A	1598	5/5	0.82	0.46	6.28	155,156,156,157	5
4	SO4	A	1597	5/5	0.94	0.25	1.66	133,133,136,140	0
6	CA	A	2003	1/1	0.95	0.19	1.46	71,71,71,71	0
12	CAC	D	1442	5/5	0.91	0.26	0.89	28,51,133,223	0
6	CA	D	2003	1/1	0.98	0.19	0.79	90,90,90,90	0
6	CA	A	2001	1/1	0.99	0.14	-0.58	76,76,76,76	0
6	CA	A	2004	1/1	0.95	0.13	-0.74	58,58,58,58	0
6	CA	C	2002	1/1	0.81	0.11	-1.06	106,106,106,106	0
12	CAC	B	1442	5/5	0.96	0.16	-1.06	37,68,85,295	0
6	CA	B	2003	1/1	0.98	0.10	-1.40	64,64,64,64	0
13	MG	B	2001	1/1	0.88	0.13	-1.79	63,63,63,63	0
6	CA	C	2004	1/1	0.70	0.07	-1.94	151,151,151,151	0
6	CA	C	2001	1/1	0.78	0.07	-1.98	104,104,104,104	0
13	MG	D	2001	1/1	0.90	0.15	-2.75	117,117,117,117	0
6	CA	C	2003	1/1	0.79	0.04	-3.16	115,115,115,115	0
5	NI	A	1599	1/1	0.97	0.04	-	97,97,97,97	0
4	SO4	A	1596	5/5	0.99	0.11	-	64,65,71,72	5
14	NAG	D	3080	14/15	0.79	0.31	-	94,127,134,139	0
14	NAG	D	3243	14/15	0.90	0.36	-	104,128,144,152	0
3	CL	A	1595	1/1	0.88	0.10	-	75,75,75,75	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
14	NAG	B	3243	14/15	0.88	0.29	-	100,112,118,118	0
3	CL	C	1596	1/1	0.90	0.14	-	96,96,96,96	0
3	CL	C	1595	1/1	0.77	0.11	-	111,111,111,111	1

6.5 Other polymers [i](#)

There are no such residues in this entry.