



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:42 PM GMT

PDB ID : 1YAE
Title : Structure of the Kainate Receptor Subunit GluR6 Agonist Binding Domain
Complexed with Domoic Acid
Authors : Nanao, M.H.; Green, T.; Stern-Bach, Y.; Heinemann, S.F.; Choe, S.
Deposited on : 2004-12-17
Resolution : 3.11 Å(reported)

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

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

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

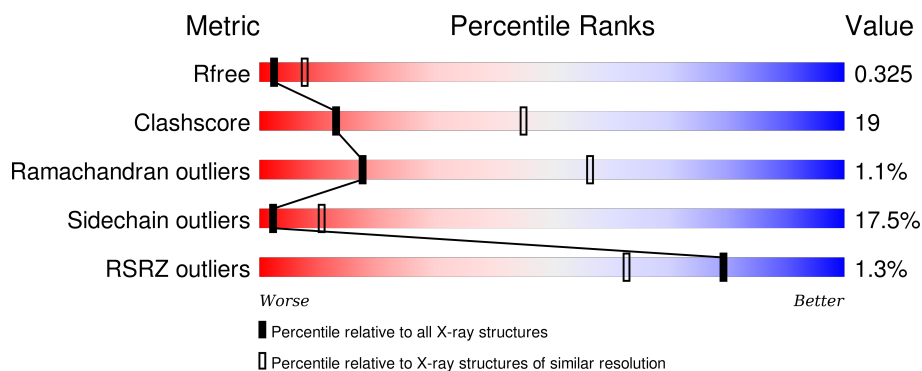
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.11 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	1112 (3.16-3.08)
Clashscore	102246	1218 (3.16-3.08)
Ramachandran outliers	100387	1175 (3.16-3.08)
Sidechain outliers	100360	1175 (3.16-3.08)
RSRZ outliers	91569	1114 (3.16-3.08)

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	312	<div> <div>2%</div> <div>50% 28% 5% 16%</div> </div>
1	B	312	<div> <div>47% 29% 8% 16%</div> </div>
1	C	312	<div> <div>49% 29% 18%</div> </div>
1	D	312	<div> <div>43% 34% 6% 17%</div> </div>
1	E	312	<div> <div>2%</div> <div>46% 28% 7% 18%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	312	

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	NAG	A	1	X	-	-	-
3	NAG	C	1302	X	-	-	-
3	NAG	D	1401	X	-	-	-
3	NAG	D	1402	X	-	-	-
3	NAG	E	1502	X	-	-	-
3	NAG	F	1601	X	-	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12512 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 Glutamate receptor, ionotropic kainate 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	261	Total	C	N	O	S	0	0	0
			2079	1324	346	397	12			
1	B	261	Total	C	N	O	S	0	0	0
			2082	1325	347	398	12			
1	C	257	Total	C	N	O	S	0	0	0
			2053	1309	341	392	11			
1	D	259	Total	C	N	O	S	0	0	0
			2067	1316	344	395	12			
1	E	257	Total	C	N	O	S	0	0	0
			2056	1312	341	392	11			
1	F	226	Total	C	N	O	S	0	0	0
			1815	1163	297	344	11			

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	653	GLY	-	LINKER	GB 56280
A	654	GLY	-	LINKER	GB 56280
A	655	SER	-	LINKER	GB 56280
A	656	LEU	-	LINKER	GB 56280
A	657	VAL	-	LINKER	GB 56280
A	658	PRO	-	LINKER	GB 56280
A	659	ARG	-	LINKER	GB 56280
A	660	GLY	-	LINKER	GB 56280
A	661	SER	-	LINKER	GB 56280
B	653	GLY	-	LINKER	GB 56280
B	654	GLY	-	LINKER	GB 56280
B	655	SER	-	LINKER	GB 56280
B	656	LEU	-	LINKER	GB 56280
B	657	VAL	-	LINKER	GB 56280
B	658	PRO	-	LINKER	GB 56280
B	659	ARG	-	LINKER	GB 56280
B	660	GLY	-	LINKER	GB 56280

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Chain	Residue	Modelled	Actual	Comment	Reference
B	661	SER	-	LINKER	GB 56280
C	653	GLY	-	LINKER	GB 56280
C	654	GLY	-	LINKER	GB 56280
C	655	SER	-	LINKER	GB 56280
C	656	LEU	-	LINKER	GB 56280
C	657	VAL	-	LINKER	GB 56280
C	658	PRO	-	LINKER	GB 56280
C	659	ARG	-	LINKER	GB 56280
C	660	GLY	-	LINKER	GB 56280
C	661	SER	-	LINKER	GB 56280
D	653	GLY	-	LINKER	GB 56280
D	654	GLY	-	LINKER	GB 56280
D	655	SER	-	LINKER	GB 56280
D	656	LEU	-	LINKER	GB 56280
D	657	VAL	-	LINKER	GB 56280
D	658	PRO	-	LINKER	GB 56280
D	659	ARG	-	LINKER	GB 56280
D	660	GLY	-	LINKER	GB 56280
D	661	SER	-	LINKER	GB 56280
E	653	GLY	-	LINKER	GB 56280
E	654	GLY	-	LINKER	GB 56280
E	655	SER	-	LINKER	GB 56280
E	656	LEU	-	LINKER	GB 56280
E	657	VAL	-	LINKER	GB 56280
E	658	PRO	-	LINKER	GB 56280
E	659	ARG	-	LINKER	GB 56280
E	660	GLY	-	LINKER	GB 56280
E	661	SER	-	LINKER	GB 56280
F	653	GLY	-	LINKER	GB 56280
F	654	GLY	-	LINKER	GB 56280
F	655	SER	-	LINKER	GB 56280
F	656	LEU	-	LINKER	GB 56280
F	657	VAL	-	LINKER	GB 56280
F	658	PRO	-	LINKER	GB 56280
F	659	ARG	-	LINKER	GB 56280
F	660	GLY	-	LINKER	GB 56280
F	661	SER	-	LINKER	GB 56280

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

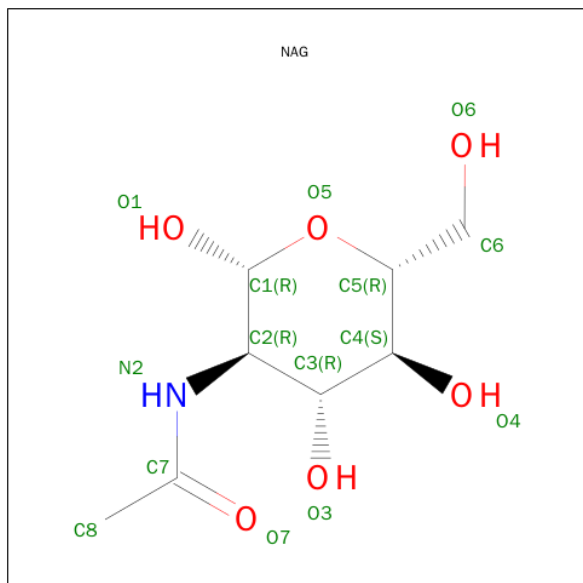
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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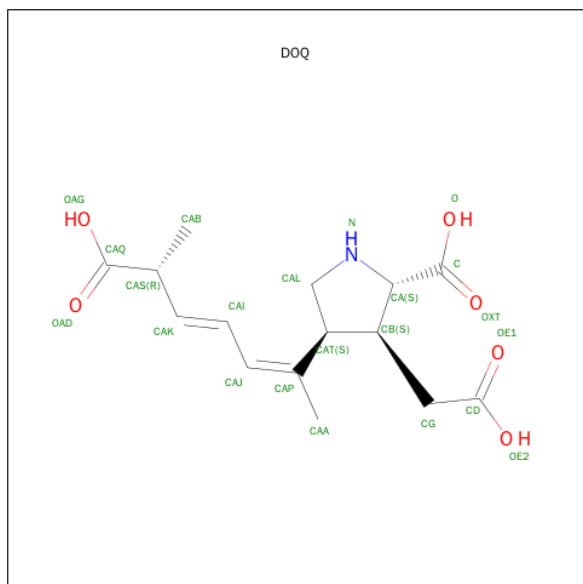
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	2	Total	C	N	O	
			24	14	1	9	
						0	0

- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 4 is (2S,3S,4S)-2-CARBOXY-4-[(1Z,3E,5R)-5-CARBOXY-1-METHYL-1,3-HEXADIENYL]-3-PYRROLIDINEACETIC ACID (three-letter code: DOQ) (formula: C₁₅H₂₁NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			22	15	1	6		
4	B	1	Total	C	N	O	0	0
			22	15	1	6		
4	C	1	Total	C	N	O	0	0
			22	15	1	6		
4	D	1	Total	C	N	O	0	0
			22	15	1	6		
4	E	1	Total	C	N	O	0	0
			22	15	1	6		
4	F	1	Total	C	N	O	0	0
			22	15	1	6		

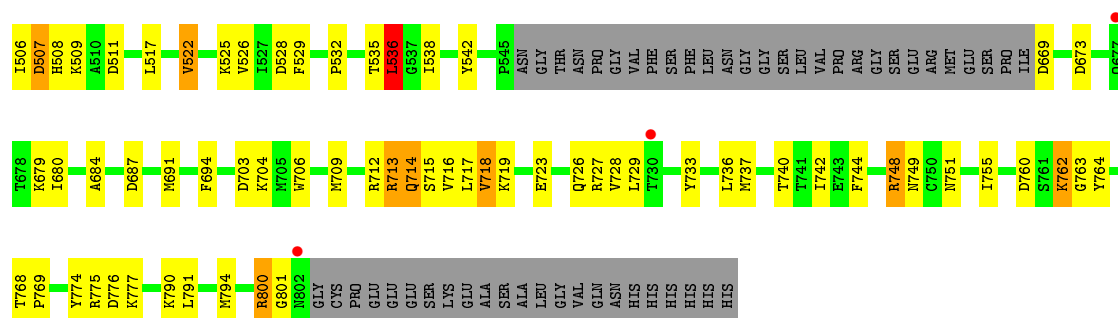
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	13	Total	O	0	0
			13	13		
5	B	19	Total	O	0	0
			19	19		
5	C	14	Total	O	0	0
			14	14		
5	D	16	Total	O	0	0
			16	16		

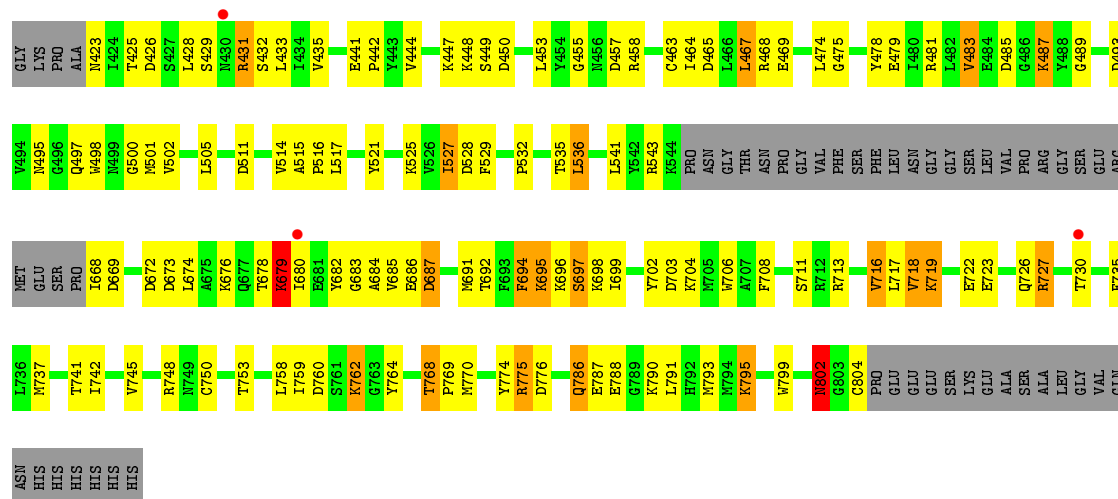
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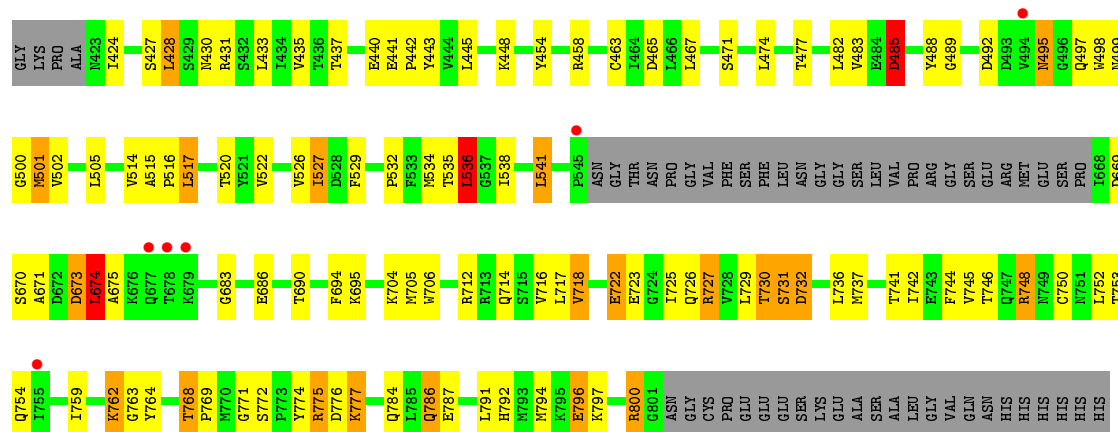
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	E	9	Total	O	0	0
			9	9		
5	F	7	Total	O	0	0
			7	7		



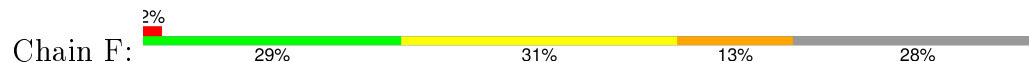
- Molecule 1: Glutamate receptor, ionotropic kainate 2



- Molecule 1: Glutamate receptor, ionotropic kainate 2



- Molecule 1: Glutamate receptor, ionotropic kainate 2



I778	T779	I780	A781	I782	L783	Q784	L785	Q786	E787	E788	G789	K790	L791	H792	M793	K797	R800	GLY	ASN	CYS	PRO	GLU	GLU	GLU	SER	LYS	GLU	ALA	SER	ALA	LEU	GLY	VAL	GLN	ASN	HIS	HIS	HIS	HIS	HIS																
S710	S711	R712	R713	Q714	S715	VAL	L717	V718	N721	E722	E723	G724	I725	Q726	R727	V728	L729	T730	S731	D732	F735	L736	W737	T740	T741	I742	V745	T746	Q747	R748	N749	C750	W751	L752	T753	Q754	I755	L758	I759	D760	S761	K762	G763	Y764	T768	G771	S772	P773	Y774	R775	D776	K777				
THR	ASN	PRO	GLY	VAL	PHE	SER	PHE	LEU	ASN	GLY	SER	LEU	VAL	PRO	ARG	GLY	SER	GLU	ARG	MET	GLU	SER	PRO	ILE	ASP	SER	ALA	ASP	ASP	LEU	ALA	LYS	GLN	THR	LYS	I680	G683	A684	V685	E686	D687	F694	LYS	LYS	SER	LYS	ILE	SER	THR	TYR	ASP	K704	H705	W706	M709	
D485	G486	F487	Y488	G489	A490	Q491	D492	D493	V494	Q497	W498	N499	G500	M501	V502	R503	E504	L505	I506	ASP	HIS	LYS	ALA	D511	L512	A513	V514	A515	P516	L517	A518	I519	V522	K525	VAL	I527	D528	F529	S530	K531	P532	F533	M534	T535	L536	G537	I538	S539	I540	T541	Y542	ARG	LYS	PRO	ASN	GLY
GLY	LYS	PRO	ALA	I423	I424	T425	D426	S427	L428	S429	N430	R431	S432	L433	I434	V435	T436	T437	I438	L439	E440	P442	Y443	V444	K447	D450	Y454	D457	R458	F459	E460	C463	I464	D465	L466	L467	R468	E469	L470	S471	T472	I473	L474	G475	F476	T477	Y478	E479	I480	R481	L482	V483	E484			

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	246.36Å 106.57Å 172.69Å 90.00° 133.19° 90.00°	Depositor
Resolution (Å)	45.00 – 3.11 44.49 – 3.11	Depositor EDS
% Data completeness (in resolution range)	94.3 (45.00-3.11) 94.4 (44.49-3.11)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.83 (at 3.12Å)	Xtriage
Refinement program	REFMAC 5.2.0003	Depositor
R, R_{free}	0.275 , 0.334 0.269 , 0.325	Depositor DCC
R_{free} test set	2817 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	69.4	Xtriage
Anisotropy	0.176	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 48.5	EDS
Estimated twinning fraction	0.006 for h+2*l,k,-h-l 0.008 for h,-k,-h-l 0.021 for -h-2*l,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 55645 reflections	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	12512	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.17% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² 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: DOQ, NAG, FUC

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	0.47	0/2116	0.83	6/2850 (0.2%)
1	B	0.46	0/2119	0.87	10/2855 (0.4%)
1	C	0.46	0/2090	0.85	10/2816 (0.4%)
1	D	0.58	2/2103 (0.1%)	0.87	11/2832 (0.4%)
1	E	0.51	0/2093	0.85	8/2820 (0.3%)
1	F	0.63	0/1845	0.86	4/2482 (0.2%)
All	All	0.52	2/12366 (0.0%)	0.86	49/16655 (0.3%)

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
2	A	1	0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	697	SER	CB-OG	-11.88	1.26	1.42
1	D	696	LYS	CB-CG	7.02	1.71	1.52

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	545	PRO	CA-N-CD	-12.18	94.44	111.50
1	B	732	ASP	CB-CG-OD2	6.29	123.96	118.30
1	B	493	ASP	CB-CG-OD2	6.19	123.87	118.30
1	D	694	PHE	CB-CG-CD1	-6.05	116.57	120.80
1	D	750	CYS	CA-CB-SG	-5.97	103.25	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	465	ASP	CB-CG-OD2	5.95	123.66	118.30
1	D	776	ASP	CB-CG-OD2	5.89	123.61	118.30
1	E	536	LEU	CA-CB-CG	5.74	128.50	115.30
1	C	482	LEU	CA-CB-CG	5.73	128.47	115.30
1	A	426	ASP	CB-CG-OD2	5.72	123.44	118.30
1	C	465	ASP	CB-CG-OD2	5.71	123.43	118.30
1	C	703	ASP	CB-CG-OD2	5.66	123.39	118.30
1	F	732	ASP	CB-CG-OD2	5.65	123.39	118.30
1	A	485	ASP	CB-CG-OD2	5.63	123.37	118.30
1	C	492	ASP	CB-CG-OD2	5.63	123.36	118.30
1	C	457	ASP	CB-CG-OD2	5.59	123.33	118.30
1	B	457	ASP	CB-CG-OD2	5.54	123.29	118.30
1	B	445	LEU	CA-CB-CG	5.53	128.03	115.30
1	B	465	ASP	CB-CG-OD2	5.52	123.26	118.30
1	B	673	ASP	CB-CG-OD2	5.50	123.25	118.30
1	B	528	ASP	CB-CG-OD2	5.49	123.24	118.30
1	E	776	ASP	CB-CG-OD2	5.49	123.24	118.30
1	E	492	ASP	CB-CG-OD2	5.47	123.23	118.30
1	B	541	LEU	CA-CB-CG	5.47	127.89	115.30
1	D	465	ASP	CB-CG-OD2	5.39	123.15	118.30
1	E	669	ASP	CB-CG-OD2	5.38	123.14	118.30
1	D	673	ASP	CB-CG-OD2	5.38	123.14	118.30
1	D	511	ASP	CB-CG-OD2	5.38	123.14	118.30
1	C	776	ASP	CB-CG-OD2	5.37	123.14	118.30
1	C	687	ASP	CB-CG-OD2	5.36	123.12	118.30
1	E	485	ASP	CB-CG-OD2	5.34	123.11	118.30
1	E	732	ASP	CB-CG-OD2	5.33	123.09	118.30
1	F	776	ASP	CB-CG-OD2	5.30	123.07	118.30
1	B	669	ASP	CB-CG-OD2	5.30	123.07	118.30
1	C	536	LEU	CA-CB-CG	5.27	127.41	115.30
1	E	674	LEU	CA-CB-CG	5.24	127.35	115.30
1	D	703	ASP	CB-CG-OD2	5.23	123.00	118.30
1	A	536	LEU	CA-CB-CG	5.20	127.25	115.30
1	A	507	ASP	CB-CG-OD2	5.18	122.96	118.30
1	C	511	ASP	CB-CG-OD2	5.17	122.96	118.30
1	D	669	ASP	CB-CG-OD2	5.17	122.95	118.30
1	A	465	ASP	CB-CG-OD2	5.12	122.91	118.30
1	A	673	ASP	CB-CG-OD2	5.11	122.90	118.30
1	D	426	ASP	CB-CG-OD2	5.09	122.88	118.30
1	D	687	ASP	CB-CG-OD2	5.09	122.88	118.30
1	D	760	ASP	CB-CG-OD2	5.06	122.85	118.30
1	F	485	ASP	CB-CG-OD2	5.05	122.85	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	450	ASP	CB-CG-OD2	5.01	122.81	118.30
1	C	760	ASP	CB-CG-OD2	5.00	122.80	118.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	1	NAG	C1

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2079	0	2084	66	0
1	B	2082	0	2082	90	0
1	C	2053	0	2054	57	0
1	D	2067	0	2069	71	0
1	E	2056	0	2065	79	0
1	F	1815	0	1809	121	0
2	A	24	0	22	1	0
3	B	28	0	26	3	0
3	C	28	0	26	0	0
3	D	28	0	26	2	0
3	E	28	0	26	0	0
3	F	14	0	13	1	0
4	A	22	0	18	2	0
4	B	22	0	18	2	0
4	C	22	0	18	0	0
4	D	22	0	18	1	0
4	E	22	0	18	1	0
4	F	22	0	18	2	0
5	A	13	0	0	0	0
5	B	19	0	0	0	0
5	C	14	0	0	1	0
5	D	16	0	0	1	0
5	E	9	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	F	7	0	0	3	0
All	All	12512	0	12410	473	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 19.

All (473) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:498:TRP:CE3	1:F:502:VAL:HG11	1.66	1.28
1:F:506:ILE:HD13	1:F:506:ILE:C	1.67	1.11
1:E:727:ARG:HG2	1:E:727:ARG:HH11	1.18	1.09
1:F:498:TRP:HE3	1:F:502:VAL:HG11	0.99	1.08
1:F:447:LYS:HG2	1:F:460:GLU:HG3	1.40	1.01
1:A:505:LEU:HB2	1:A:527:ILE:HD11	1.41	1.01
1:C:748:ARG:HG3	1:C:748:ARG:HH11	1.24	1.00
1:E:775:ARG:HH11	1:E:775:ARG:HG2	1.25	0.99
1:F:506:ILE:CD1	1:F:506:ILE:C	2.29	0.98
1:F:506:ILE:HD13	1:F:506:ILE:O	1.66	0.95
1:B:498:TRP:O	1:B:503:ARG:HG2	1.70	0.92
1:F:443:TYR:HB3	1:F:463:CYS:SG	2.09	0.91
1:E:502:VAL:HG13	1:E:527:ILE:HD13	1.52	0.89
1:F:498:TRP:HB3	1:F:502:VAL:HG12	1.56	0.87
1:B:426:ASP:HB3	1:B:429:SER:HB2	1.54	0.87
1:E:437:THR:HA	1:E:501:MET:HE1	1.57	0.86
1:D:449:SER:OG	1:D:453:LEU:HD11	1.75	0.86
1:B:482:LEU:HD23	1:B:482:LEU:H	1.38	0.85
1:F:439:LEU:HG	1:F:482:LEU:HD21	1.60	0.84
1:F:541:LEU:HB2	1:F:737:MET:HE3	1.58	0.83
1:F:800:ARG:HB3	1:F:800:ARG:NH1	1.92	0.83
1:E:437:THR:HA	1:E:501:MET:CE	2.10	0.82
1:F:498:TRP:CE3	1:F:502:VAL:CG1	2.58	0.81
1:A:802:ASN:H	1:A:802:ASN:ND2	1.75	0.80
1:E:775:ARG:NH1	1:E:775:ARG:HG2	1.96	0.80
1:F:500:GLY:O	1:F:504:GLU:HG2	1.81	0.79
1:D:684:ALA:HB3	1:D:691:MET:HE2	1.62	0.79
1:B:544:LYS:HE3	1:B:750:CYS:O	1.83	0.78
1:B:744:PHE:HB2	1:B:799:TRP:CZ3	2.19	0.78
1:F:536:LEU:HG	1:F:762:LYS:HB3	1.63	0.78
1:D:444:VAL:HG13	1:D:464:ILE:HD11	1.66	0.78
1:B:538:ILE:HB	1:B:759:ILE:HB	1.66	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:695:LYS:HG3	1:D:706:TRP:CZ2	2.19	0.77
1:E:775:ARG:HH11	1:E:775:ARG:CG	1.97	0.77
1:F:469:GLU:HA	1:F:469:GLU:OE1	1.83	0.76
1:F:540:ILE:HG22	1:F:755:ILE:HB	1.65	0.76
1:F:463:CYS:HB3	1:F:514:VAL:HG12	1.69	0.76
1:E:529:PHE:O	1:E:775:ARG:HD2	1.88	0.74
1:F:531:LYS:HB2	1:F:779:THR:HG23	1.70	0.74
1:E:727:ARG:NH1	1:E:727:ARG:HG2	1.93	0.74
1:C:482:LEU:CD2	1:C:482:LEU:H	2.01	0.74
1:F:505:LEU:HD23	1:F:506:ILE:N	2.03	0.73
1:F:424:ILE:HA	1:F:427:SER:HB3	1.69	0.73
1:F:541:LEU:HD21	1:F:752:LEU:HB3	1.70	0.72
1:E:694:PHE:HB3	1:E:706:TRP:HB2	1.72	0.72
1:D:786:GLN:HG2	1:D:791:LEU:HD12	1.70	0.72
1:E:727:ARG:CG	1:E:727:ARG:HH11	1.98	0.71
1:B:541:LEU:HG	1:B:737:MET:CE	2.20	0.71
1:F:519:ILE:HG22	1:F:529:PHE:CG	2.25	0.71
1:B:482:LEU:CD2	1:B:482:LEU:H	2.02	0.71
1:D:447:LYS:NZ	1:D:457:ASP:O	2.24	0.70
1:D:429:SER:HA	1:D:475:GLY:O	1.91	0.70
1:A:670:SER:HB3	1:A:673:ASP:H	1.54	0.70
1:A:669:ASP:HA	1:A:755:ILE:HG23	1.72	0.70
1:F:447:LYS:HG2	1:F:460:GLU:CG	2.19	0.69
1:F:498:TRP:HB3	1:F:502:VAL:CG1	2.22	0.69
1:F:505:LEU:HD11	1:F:527:ILE:HB	1.75	0.69
1:D:536:LEU:HD22	1:D:762:LYS:HB3	1.75	0.69
1:E:686:GLU:HG2	1:E:717:LEU:HB3	1.75	0.69
1:E:737:MET:HG3	1:E:742:ILE:HG13	1.75	0.69
1:A:430:ASN:HB3	1:A:431:ARG:HH11	1.58	0.69
1:D:543:ARG:HH21	3:D:1402:NAG:HN2	1.39	0.69
1:A:672:ASP:N	1:A:672:ASP:OD1	2.26	0.68
1:D:428:LEU:HD12	1:D:474:LEU:HD13	1.74	0.68
1:D:793:MET:SD	1:F:454:TYR:HB2	2.33	0.68
1:E:744:PHE:O	1:E:748:ARG:HG3	1.93	0.68
1:F:425:THR:OG1	3:F:1601:NAG:H62	1.93	0.68
1:F:519:ILE:HG22	1:F:529:PHE:CD2	2.29	0.68
1:D:695:LYS:HG3	1:D:706:TRP:CH2	2.29	0.67
1:B:505:LEU:HD22	1:B:769:PRO:HD3	1.77	0.67
1:C:489:GLY:HA2	1:C:500:GLY:H	1.60	0.67
1:B:541:LEU:HG	1:B:737:MET:HE2	1.75	0.66
1:F:447:LYS:CG	1:F:460:GLU:HG3	2.23	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:489:GLY:HA2	1:B:500:GLY:H	1.60	0.66
1:D:489:GLY:HA2	1:D:500:GLY:H	1.59	0.66
1:A:768:THR:HG23	1:A:772:SER:HB3	1.78	0.66
1:C:498:TRP:NE1	1:C:526:VAL:HG21	2.11	0.66
1:C:505:LEU:HD22	1:C:769:PRO:HD3	1.78	0.65
1:F:800:ARG:HH11	1:F:800:ARG:HB3	1.62	0.65
1:D:515:ALA:HB1	1:D:516:PRO:HD2	1.78	0.64
1:D:543:ARG:NH2	3:D:1402:NAG:HN2	1.95	0.64
1:D:431:ARG:CG	1:D:431:ARG:HH11	2.10	0.64
1:B:507:ASP:HB3	1:B:509:LYS:HE2	1.79	0.64
1:F:541:LEU:HB2	1:F:737:MET:CE	2.26	0.64
1:C:800:ARG:HD3	1:C:801:GLY:H	1.62	0.64
1:E:489:GLY:HA2	1:E:500:GLY:H	1.63	0.64
1:B:435:VAL:HG11	1:B:467:LEU:HD11	1.80	0.63
1:A:489:GLY:HA2	1:A:500:GLY:H	1.64	0.63
1:E:718:VAL:HG22	1:E:723:GLU:HB3	1.80	0.63
1:B:744:PHE:HB2	1:B:799:TRP:CE3	2.34	0.63
1:B:540:ILE:HD13	1:B:736:LEU:HD23	1.80	0.63
1:A:695:LYS:HD3	1:A:706:TRP:CZ2	2.33	0.63
1:B:482:LEU:N	1:B:482:LEU:CD2	2.63	0.62
1:C:536:LEU:HD22	1:C:762:LYS:HB3	1.82	0.62
1:B:737:MET:HE3	1:B:742:ILE:HA	1.81	0.62
1:D:768:THR:HG21	1:D:775:ARG:HB3	1.81	0.62
1:D:431:ARG:HG2	1:D:431:ARG:HH11	1.64	0.61
1:F:774:TYR:O	1:F:778:ILE:HG12	1.99	0.61
1:F:768:THR:CG2	1:F:772:SER:HB3	2.31	0.61
1:F:505:LEU:C	1:F:505:LEU:HD23	2.21	0.61
1:A:726:GLN:HG2	1:B:722:GLU:HB3	1.83	0.61
1:E:694:PHE:CZ	1:E:736:LEU:HD13	2.35	0.60
1:C:744:PHE:O	1:C:748:ARG:HG2	2.02	0.60
1:A:430:ASN:HB3	1:A:431:ARG:NH1	2.16	0.60
1:F:786:GLN:HB2	1:F:791:LEU:HD12	1.81	0.60
1:B:795:LYS:O	1:B:799:TRP:HD1	1.85	0.60
1:A:803:GLY:O	1:A:804:CYS:SG	2.59	0.60
2:A:1:NAG:H61	2:A:2:FUC:H5	1.84	0.60
1:C:748:ARG:CG	1:C:748:ARG:HH11	2.05	0.60
1:D:698:LYS:HB2	1:E:454:TYR:CE1	2.37	0.60
1:D:674:LEU:HD22	1:D:682:TYR:CD2	2.37	0.60
1:A:454:TYR:O	1:A:457:ASP:HB3	2.02	0.59
1:E:495:ASN:HD21	1:E:497:GLN:NE2	2.00	0.59
1:A:768:THR:HG21	1:A:775:ARG:HB2	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:727:ARG:HA	1:B:730:THR:HG22	1.83	0.59
1:C:451:LYS:HB2	1:C:452:PRO:HD2	1.83	0.59
1:A:505:LEU:CB	1:A:527:ILE:HD11	2.24	0.59
1:F:423:ASN:OD1	1:F:424:ILE:N	2.36	0.58
1:E:532:PRO:HA	1:E:764:TYR:O	2.03	0.58
1:F:517:LEU:HD12	1:F:529:PHE:CE1	2.38	0.58
1:B:428:LEU:HD11	1:B:474:LEU:HB3	1.83	0.58
1:A:483:VAL:CG2	1:A:501:MET:HG3	2.32	0.58
1:F:758:LEU:O	1:F:759:ILE:HG13	2.03	0.58
1:E:428:LEU:HD11	1:E:474:LEU:HD13	1.84	0.58
1:C:529:PHE:O	1:C:775:ARG:HD2	2.04	0.58
1:B:698:LYS:HE2	1:D:788:GLU:HG3	1.86	0.58
1:B:463:CYS:HB3	1:B:514:VAL:HG12	1.86	0.57
1:F:515:ALA:HB1	1:F:516:PRO:HD2	1.85	0.57
1:C:482:LEU:HD23	1:C:482:LEU:H	1.69	0.57
1:D:716:VAL:HG12	1:D:717:LEU:HD23	1.87	0.57
1:D:463:CYS:HB3	1:D:514:VAL:HG12	1.86	0.57
1:B:445:LEU:CD2	1:B:460:GLU:HG3	2.34	0.57
1:A:506:ILE:C	1:A:508:HIS:H	2.08	0.57
1:B:424:ILE:HA	1:B:427:SER:OG	2.04	0.57
1:F:491:GLN:NE2	1:F:491:GLN:H	2.03	0.57
1:C:718:VAL:HG22	1:C:723:GLU:HG2	1.87	0.56
1:C:679:LYS:HG3	1:C:680:ILE:HG13	1.87	0.56
1:C:498:TRP:HE1	1:C:526:VAL:HG21	1.69	0.56
1:B:544:LYS:HG2	1:B:753:THR:OG1	2.05	0.56
1:E:694:PHE:CE2	1:E:736:LEU:HD13	2.39	0.56
1:E:495:ASN:HD21	1:E:497:GLN:HG3	1.70	0.56
1:B:803:GLY:O	1:B:804:CYS:HB2	2.05	0.56
1:C:694:PHE:HB3	1:C:706:TRP:HB2	1.88	0.56
1:C:709:MET:CE	1:C:736:LEU:HD12	2.36	0.56
1:E:726:GLN:O	1:E:730:THR:HB	2.04	0.56
1:A:483:VAL:HG22	1:A:501:MET:HG3	1.87	0.56
1:F:469:GLU:CA	1:F:469:GLU:OE1	2.52	0.56
1:D:423:ASN:N	5:D:72:HOH:O	2.38	0.56
1:B:431:ARG:HD3	1:B:774:TYR:OH	2.06	0.56
1:F:727:ARG:NH1	1:F:731:SER:OG	2.38	0.56
1:E:529:PHE:C	1:E:775:ARG:HD2	2.26	0.56
1:F:435:VAL:HG12	1:F:512:LEU:HB2	1.88	0.56
1:F:718:VAL:HG13	1:F:723:GLU:HB3	1.89	0.55
1:E:440:GLU:OE2	4:E:1503:DOQ:HAA3	2.05	0.55
1:A:498:TRP:O	1:A:503:ARG:HG2	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:722:GLU:HA	1:E:725:ILE:HD12	1.88	0.55
1:E:435:VAL:HG11	1:E:467:LEU:HD11	1.89	0.55
1:E:443:TYR:HB3	1:E:463:CYS:SG	2.45	0.55
1:B:528:ASP:HB2	1:B:768:THR:HG22	1.89	0.55
1:B:498:TRP:CE3	1:B:502:VAL:HG11	2.41	0.55
1:C:713:ARG:HB3	1:C:714:GLN:HE21	1.71	0.55
1:F:467:LEU:HA	1:F:470:LEU:HD12	1.87	0.54
1:F:483:VAL:HG13	1:F:486:GLY:HA2	1.89	0.54
1:C:443:TYR:OH	1:C:740:THR:HG23	2.07	0.54
1:C:748:ARG:HG3	1:C:748:ARG:NH1	2.04	0.54
1:C:492:ASP:OD1	1:C:494:VAL:HG12	2.07	0.54
1:C:503:ARG:HA	1:C:506:ILE:HD12	1.89	0.54
1:F:424:ILE:HG22	1:F:777:LYS:HD2	1.90	0.54
1:C:528:ASP:HB3	1:C:775:ARG:HD3	1.90	0.54
1:D:435:VAL:HG21	1:D:467:LEU:HD11	1.90	0.54
1:B:538:ILE:HG12	1:B:760:ASP:OD1	2.08	0.53
1:B:789:GLY:HA3	1:D:699:ILE:HD11	1.90	0.53
1:A:454:TYR:CD1	1:F:723:GLU:HG2	2.44	0.53
1:E:483:VAL:HG22	1:E:501:MET:HG3	1.91	0.53
1:B:541:LEU:HG	1:B:737:MET:HE1	1.91	0.53
1:F:485:ASP:OD1	1:F:485:ASP:C	2.45	0.53
1:F:519:ILE:HG23	1:F:764:TYR:O	2.09	0.53
1:A:434:ILE:HG23	1:A:510:ALA:HA	1.90	0.53
1:B:740:THR:HG23	1:B:741:THR:N	2.22	0.53
1:C:522:VAL:O	1:C:525:LYS:HG2	2.08	0.53
1:F:538:ILE:HB	1:F:759:ILE:HB	1.91	0.53
1:A:727:ARG:NH1	1:A:731:SER:OG	2.41	0.53
1:E:437:THR:O	1:E:483:VAL:HG23	2.09	0.53
1:E:534:MET:O	1:E:763:GLY:HA2	2.09	0.53
1:A:749:ASN:ND2	1:A:751:ASN:H	2.07	0.52
1:F:712:ARG:HH11	1:F:712:ARG:HB3	1.73	0.52
1:B:740:THR:O	1:B:799:TRP:CZ3	2.62	0.52
1:F:778:ILE:HG22	1:F:782:ILE:HD11	1.91	0.52
1:F:429:SER:O	1:F:431:ARG:N	2.42	0.52
1:C:737:MET:HG3	1:C:742:ILE:HG13	1.91	0.52
1:F:426:ASP:O	1:F:428:LEU:N	2.42	0.52
1:B:751:ASN:N	1:B:751:ASN:OD1	2.42	0.52
1:B:477:THR:HB	1:C:714:GLN:HG3	1.92	0.52
1:A:802:ASN:HD22	1:A:802:ASN:H	1.56	0.52
1:B:544:LYS:CG	1:B:753:THR:OG1	2.58	0.52
1:E:683:GLY:HA3	1:E:716:VAL:HG13	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:517:LEU:HD23	1:D:529:PHE:CE1	2.45	0.52
1:A:675:ALA:HB2	1:A:705:MET:HG2	1.91	0.52
1:C:749:ASN:OD1	1:C:751:ASN:HB2	2.09	0.52
1:B:694:PHE:HB3	1:B:706:TRP:HB2	1.92	0.51
1:E:495:ASN:ND2	1:E:497:GLN:HG3	2.25	0.51
1:C:482:LEU:HD22	1:C:482:LEU:H	1.74	0.51
1:D:428:LEU:CD1	1:D:774:TYR:HD1	2.24	0.51
1:E:431:ARG:HG2	1:E:774:TYR:OH	2.10	0.51
1:C:532:PRO:HA	1:C:764:TYR:O	2.11	0.51
1:B:436:THR:HG23	1:B:501:MET:HG2	1.93	0.51
1:E:502:VAL:HG13	1:E:527:ILE:CD1	2.33	0.51
1:A:749:ASN:HD22	1:A:751:ASN:H	1.59	0.51
1:F:683:GLY:HA2	1:F:709:MET:SD	2.51	0.51
1:B:428:LEU:CD1	1:B:474:LEU:HB3	2.40	0.51
1:B:795:LYS:O	1:B:799:TRP:CD1	2.63	0.50
1:C:713:ARG:HG3	1:C:717:LEU:HD12	1.91	0.50
1:F:800:ARG:CZ	1:F:800:ARG:HB3	2.41	0.50
1:D:694:PHE:HB3	1:D:706:TRP:HB2	1.93	0.50
1:E:737:MET:HG3	1:E:742:ILE:CG1	2.39	0.50
1:C:715:SER:O	1:C:727:ARG:NH2	2.39	0.50
1:E:505:LEU:HD22	1:E:769:PRO:HD3	1.93	0.50
1:F:747:GLN:NE2	1:F:800:ARG:HB2	2.25	0.50
1:B:740:THR:CG2	1:B:741:THR:N	2.74	0.50
1:A:454:TYR:CE1	1:F:723:GLU:HG2	2.46	0.50
1:B:544:LYS:N	1:B:751:ASN:O	2.37	0.50
1:F:471:SER:HA	1:F:476:PHE:CE1	2.46	0.50
1:A:460:GLU:HA	1:A:464:ILE:HG21	1.93	0.50
1:F:721:ASN:O	1:F:725:ILE:HG12	2.12	0.50
1:A:802:ASN:HD22	1:A:802:ASN:N	2.09	0.50
1:F:680:ILE:N	5:F:4:HOH:O	2.44	0.50
1:F:694:PHE:N	1:F:694:PHE:CD1	2.78	0.50
1:B:686:GLU:HG2	1:B:717:LEU:HD13	1.94	0.50
1:F:768:THR:HG23	1:F:772:SER:HB3	1.94	0.49
1:A:521:TYR:CZ	1:A:525:LYS:HD2	2.47	0.49
1:B:502:VAL:HG13	1:B:527:ILE:HD13	1.94	0.49
1:C:430:ASN:HB2	1:C:431:ARG:HH11	1.77	0.49
1:A:495:ASN:ND2	1:A:497:GLN:HB2	2.27	0.49
1:F:435:VAL:HG23	1:F:480:ILE:HA	1.94	0.49
1:A:537:GLY:HA3	1:A:758:LEU:HD12	1.95	0.49
1:F:437:THR:OG1	1:F:444:VAL:HG21	2.13	0.49
1:B:540:ILE:CD1	1:B:736:LEU:HD23	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:709:MET:HE1	1:C:736:LEU:HD12	1.95	0.49
1:F:489:GLY:HA3	1:F:502:VAL:HB	1.95	0.49
1:E:437:THR:HA	1:E:501:MET:HE3	1.92	0.49
1:B:506:ILE:C	1:B:508:HIS:H	2.16	0.49
1:B:507:ASP:CB	1:B:509:LYS:HE2	2.42	0.49
1:B:793:MET:HG3	1:E:454:TYR:HB2	1.95	0.49
1:B:506:ILE:O	1:B:508:HIS:HD2	1.95	0.49
1:F:729:LEU:HG	1:F:752:LEU:HD21	1.95	0.49
1:D:498:TRP:CE3	1:D:502:VAL:HG11	2.48	0.49
1:F:686:GLU:HB3	1:F:717:LEU:HB3	1.95	0.49
1:D:718:VAL:HG13	1:D:723:GLU:HB3	1.95	0.49
1:F:489:GLY:HA2	1:F:499:ASN:O	2.13	0.48
1:A:542:TYR:HB2	1:A:755:ILE:HD12	1.95	0.48
1:E:441:GLU:HG2	1:E:744:PHE:CE2	2.48	0.48
1:F:694:PHE:HD1	1:F:694:PHE:H	1.61	0.48
1:F:505:LEU:CD1	1:F:527:ILE:HB	2.43	0.48
1:C:431:ARG:HG2	1:C:774:TYR:OH	2.13	0.48
1:B:498:TRP:CH2	1:B:522:VAL:HG12	2.48	0.48
1:B:445:LEU:CD2	1:B:460:GLU:CG	2.91	0.48
1:D:485:ASP:O	1:D:487:LYS:HD3	2.13	0.48
1:E:499:ASN:OD1	1:E:500:GLY:N	2.46	0.48
1:B:749:ASN:HB3	1:B:752:LEU:HD12	1.96	0.48
1:A:669:ASP:HA	1:A:755:ILE:CG2	2.40	0.48
1:D:684:ALA:HB3	1:D:691:MET:CE	2.38	0.48
1:A:469:GLU:O	1:A:473:ILE:HG12	2.14	0.48
1:A:749:ASN:HD21	1:A:751:ASN:HB2	1.77	0.48
1:D:483:VAL:CG2	1:D:501:MET:HG3	2.44	0.48
1:F:506:ILE:CD1	1:F:506:ILE:O	2.49	0.47
1:F:505:LEU:O	1:F:506:ILE:C	2.53	0.47
1:A:528:ASP:CB	1:A:768:THR:HG22	2.44	0.47
1:B:503:ARG:HD2	1:B:507:ASP:OD2	2.14	0.47
1:E:671:ALA:HB2	1:E:759:ILE:HD11	1.95	0.47
1:F:519:ILE:CD1	1:F:532:PRO:HG3	2.44	0.47
1:F:491:GLN:H	1:F:491:GLN:HE21	1.61	0.47
1:D:455:GLY:O	1:D:458:ARG:HG2	2.15	0.47
1:A:436:THR:HG23	1:A:501:MET:HG2	1.97	0.47
1:A:675:ALA:HB2	1:A:705:MET:CG	2.45	0.47
1:E:753:THR:HG22	1:E:754:GLN:N	2.30	0.47
1:B:672:ASP:O	1:B:676:LYS:HG2	2.15	0.47
1:D:795:LYS:O	1:D:799:TRP:HB2	2.14	0.47
1:A:487:LYS:HD3	1:A:499:ASN:ND2	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:441:GLU:HG3	1:F:442:PRO:HA	1.97	0.47
1:F:737:MET:HG2	1:F:742:ILE:HG12	1.95	0.47
1:D:428:LEU:HD13	1:D:774:TYR:CD1	2.50	0.47
1:D:702:TYR:CE1	1:D:759:ILE:HG23	2.50	0.47
1:F:436:THR:HA	1:F:481:ARG:O	2.15	0.47
1:A:786:GLN:HB2	1:A:791:LEU:HD12	1.96	0.47
1:F:778:ILE:O	1:F:782:ILE:HG13	2.16	0.46
1:B:698:LYS:HE2	1:D:788:GLU:CG	2.45	0.46
1:B:443:TYR:HE1	1:B:534:MET:HE1	1.80	0.46
1:B:740:THR:HG21	1:B:764:TYR:OH	2.15	0.46
1:D:698:LYS:O	1:E:458:ARG:NE	2.48	0.46
1:B:424:ILE:HA	1:B:427:SER:HG	1.79	0.46
1:E:463:CYS:HB3	1:E:514:VAL:HG12	1.98	0.46
1:C:456:ASN:H	1:C:456:ASN:HD22	1.63	0.46
1:B:686:GLU:HG3	1:B:717:LEU:HB3	1.96	0.46
1:C:499:ASN:OD1	1:C:500:GLY:N	2.49	0.46
1:D:718:VAL:CG1	1:D:719:LYS:N	2.78	0.46
1:B:493:ASP:N	1:B:493:ASP:OD1	2.48	0.46
1:D:726:GLN:O	1:D:730:THR:HG23	2.16	0.46
1:A:537:GLY:H	1:A:739:SER:HG	1.64	0.46
1:C:542:TYR:HB3	1:C:755:ILE:HD13	1.97	0.46
1:C:728:VAL:HG22	1:C:733:TYR:O	2.16	0.46
1:E:675:ALA:HB1	1:E:705:MET:HG2	1.96	0.46
1:F:424:ILE:HG12	1:F:780:ILE:HG21	1.98	0.46
1:E:744:PHE:CZ	1:E:748:ARG:HD2	2.51	0.46
1:B:437:THR:OG1	1:B:444:VAL:HG21	2.16	0.46
1:E:538:ILE:HD13	1:E:690:THR:HG23	1.97	0.46
1:E:695:LYS:HA	1:E:706:TRP:CE2	2.50	0.46
1:C:536:LEU:HD13	1:C:763:GLY:H	1.79	0.46
1:E:495:ASN:HD21	1:E:497:GLN:HE21	1.64	0.46
1:C:790:LYS:O	1:C:794:MET:HG3	2.15	0.46
1:F:438:ILE:HG21	1:F:488:TYR:CZ	2.50	0.46
1:D:431:ARG:NH1	1:D:431:ARG:CG	2.74	0.46
1:B:727:ARG:HG3	1:B:727:ARG:O	2.15	0.46
1:A:531:LYS:HE2	1:A:779:THR:HG21	1.98	0.46
1:A:426:ASP:O	1:A:429:SER:HB2	2.16	0.46
1:F:501:MET:HA	1:F:504:GLU:HG3	1.98	0.45
1:F:517:LEU:HD12	1:F:529:PHE:HE1	1.78	0.45
1:A:421:PRO:HB2	1:A:422:ALA:H	1.63	0.45
1:C:800:ARG:NE	1:C:800:ARG:HA	2.31	0.45
1:E:673:ASP:OD1	1:E:674:LEU:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:540:ILE:CG2	1:F:755:ILE:HB	2.40	0.45
1:C:441:GLU:HG2	1:C:445:LEU:HD21	1.98	0.45
1:B:439:LEU:HG	1:B:482:LEU:HD12	1.98	0.45
1:A:528:ASP:HB3	1:A:768:THR:HG22	1.98	0.45
1:C:441:GLU:CG	1:C:445:LEU:HD21	2.47	0.45
1:A:781:ALA:O	1:A:785:LEU:HG	2.17	0.45
1:F:541:LEU:CB	1:F:737:MET:CE	2.93	0.45
1:F:472:THR:HA	5:F:32:HOH:O	2.16	0.45
1:F:497:GLN:HB3	1:F:497:GLN:HE21	1.59	0.45
1:A:694:PHE:HB3	1:A:706:TRP:HB2	1.97	0.45
1:F:538:ILE:HG12	1:F:760:ASP:OD1	2.17	0.45
1:D:683:GLY:HA3	1:D:716:VAL:HG13	1.99	0.45
1:C:482:LEU:CD2	1:C:482:LEU:N	2.72	0.45
1:A:441:GLU:HA	1:A:442:PRO:HA	1.81	0.45
1:A:740:THR:CG2	1:A:741:THR:N	2.79	0.45
1:F:786:GLN:CB	1:F:791:LEU:HD12	2.47	0.45
1:F:428:LEU:HD12	1:F:476:PHE:HB3	1.98	0.45
1:F:797:LYS:HE3	5:F:9:HOH:O	2.16	0.45
1:B:445:LEU:HD21	1:B:460:GLU:HG3	1.99	0.45
1:C:506:ILE:C	1:C:508:HIS:H	2.20	0.45
1:C:712:ARG:O	1:C:716:VAL:HB	2.17	0.45
1:B:543:ARG:CZ	3:B:1202:NAG:HN2	2.29	0.45
1:D:505:LEU:HB2	1:D:527:ILE:HD11	1.97	0.44
1:F:429:SER:HA	1:F:475:GLY:O	2.17	0.44
1:E:424:ILE:HD11	1:E:777:LYS:HG3	2.00	0.44
1:F:737:MET:HE2	1:F:737:MET:HB3	1.69	0.44
1:A:488:TYR:CE2	4:A:1103:DOQ:HAL2	2.53	0.44
1:D:741:THR:O	1:D:745:VAL:HG23	2.17	0.44
1:D:495:ASN:ND2	1:D:497:GLN:HG3	2.32	0.44
1:B:791:LEU:HD23	1:B:794:MET:HE2	2.00	0.44
1:B:538:ILE:HD12	1:B:690:THR:HG23	1.99	0.44
1:E:541:LEU:HD11	1:E:752:LEU:HD13	2.00	0.44
1:D:483:VAL:HG22	1:D:501:MET:HG3	2.00	0.43
1:C:507:ASP:HB2	1:C:509:LYS:HG3	1.99	0.43
1:E:686:GLU:HG2	1:E:717:LEU:CB	2.46	0.43
1:A:483:VAL:HG21	1:A:501:MET:HG3	2.00	0.43
1:A:443:TYR:OH	1:A:740:THR:HG23	2.18	0.43
1:E:520:THR:HG22	1:E:522:VAL:H	1.83	0.43
1:B:683:GLY:HA2	1:B:709:MET:HE2	2.00	0.43
1:B:434:ILE:HD12	1:B:481:ARG:HH21	1.83	0.43
1:B:737:MET:HE2	1:B:742:ILE:HG12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:718:VAL:CG1	1:F:723:GLU:HB3	2.49	0.43
1:E:726:GLN:HA	1:E:729:LEU:HD12	1.99	0.43
1:F:748:ARG:HH11	1:F:748:ARG:HG2	1.81	0.43
1:E:440:GLU:HG3	1:E:488:TYR:OH	2.19	0.43
1:C:456:ASN:N	1:C:456:ASN:HD22	2.17	0.43
1:B:718:VAL:HG22	1:B:723:GLU:HB3	2.01	0.43
1:B:680:ILE:HG23	1:B:732:ASP:OD2	2.18	0.43
1:E:794:MET:O	1:E:797:LYS:HB3	2.19	0.43
1:D:441:GLU:HA	1:D:442:PRO:HA	1.82	0.43
1:E:427:SER:OG	1:E:777:LYS:HE3	2.19	0.43
1:D:802:ASN:OD1	1:D:802:ASN:N	2.37	0.43
1:B:799:TRP:O	1:B:800:ARG:HB2	2.18	0.43
1:D:528:ASP:CB	1:D:768:THR:HG22	2.49	0.43
1:F:790:LYS:O	1:F:791:LEU:C	2.57	0.43
1:C:429:SER:HA	1:C:475:GLY:O	2.19	0.43
1:D:695:LYS:HD3	1:D:706:TRP:CH2	2.53	0.43
1:B:700:SER:HA	1:F:458:ARG:HG2	2.00	0.43
1:B:686:GLU:O	4:B:1203:DOQ:HAB1	2.19	0.42
1:D:708:PHE:CD1	1:D:708:PHE:C	2.91	0.42
1:D:685:VAL:HG23	1:D:735:PHE:HZ	1.84	0.42
1:D:469:GLU:OE2	1:D:790:LYS:HE3	2.19	0.42
1:B:696:LYS:HD2	1:D:787:GLU:OE2	2.19	0.42
1:F:503:ARG:HA	1:F:506:ILE:HG23	2.01	0.42
1:F:539:SER:HB3	1:F:742:ILE:HD12	2.00	0.42
1:D:674:LEU:HD22	1:D:682:TYR:HD2	1.82	0.42
1:B:738:GLU:OE1	4:B:1203:DOQ:HG2	2.19	0.42
1:B:437:THR:OG1	1:B:438:ILE:N	2.51	0.42
1:F:519:ILE:HD11	1:F:532:PRO:HG3	2.01	0.42
1:E:718:VAL:CG2	1:E:723:GLU:HB3	2.47	0.42
4:F:1603:DOQ:HAA1	4:F:1603:DOQ:HAL1	1.89	0.42
1:B:543:ARG:HH22	3:B:1202:NAG:H3	1.85	0.42
1:F:503:ARG:O	1:F:506:ILE:HG13	2.20	0.42
1:A:506:ILE:C	1:A:508:HIS:N	2.72	0.42
1:A:437:THR:OG1	1:A:444:VAL:HG21	2.19	0.42
1:F:685:VAL:HG23	1:F:735:PHE:HZ	1.84	0.42
1:D:479:GLU:CD	1:D:481:ARG:HE	2.22	0.42
1:B:799:TRP:N	1:B:799:TRP:CD1	2.87	0.42
1:B:793:MET:HE2	1:D:699:ILE:HG12	2.00	0.42
1:F:485:ASP:OD1	1:F:486:GLY:N	2.53	0.42
1:A:721:ASN:O	1:A:725:ILE:HG12	2.19	0.42
1:E:731:SER:OG	1:E:732:ASP:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:802:ASN:N	1:A:802:ASN:ND2	2.47	0.42
1:E:474:LEU:HD23	1:E:474:LEU:HA	1.90	0.42
1:C:441:GLU:HA	1:C:442:PRO:HA	1.86	0.42
1:C:684:ALA:HB3	1:C:691:MET:HG2	2.02	0.42
1:C:439:LEU:HD23	1:C:444:VAL:HG12	2.02	0.42
1:A:498:TRP:O	1:A:503:ARG:CG	2.67	0.42
1:F:426:ASP:C	1:F:428:LEU:H	2.23	0.42
1:E:792:HIS:CE1	1:E:796:GLU:OE1	2.73	0.42
1:E:529:PHE:O	1:E:775:ARG:CD	2.64	0.42
1:E:495:ASN:HD21	1:E:497:GLN:CG	2.32	0.41
1:C:436:THR:HA	1:C:481:ARG:O	2.20	0.41
1:F:775:ARG:HG3	1:F:776:ASP:N	2.35	0.41
1:F:491:GLN:H	1:F:491:GLN:CD	2.23	0.41
1:D:467:LEU:HD13	1:D:478:TYR:CE2	2.55	0.41
1:A:429:SER:HA	1:A:475:GLY:O	2.20	0.41
1:F:447:LYS:HD3	1:F:457:ASP:O	2.20	0.41
1:B:538:ILE:HG23	1:B:690:THR:HG23	2.01	0.41
1:D:517:LEU:HD23	1:D:529:PHE:HE1	1.81	0.41
1:D:686:GLU:O	1:D:687:ASP:HB2	2.21	0.41
1:E:768:THR:CG2	1:E:772:SER:HB3	2.50	0.41
1:A:742:ILE:O	1:A:746:THR:HB	2.19	0.41
1:C:448:LYS:HD3	1:C:448:LYS:HA	1.81	0.41
1:D:453:LEU:HB2	1:D:458:ARG:HB3	2.02	0.41
1:F:528:ASP:HB3	1:F:775:ARG:HD3	2.01	0.41
1:F:473:ILE:HG22	1:F:474:LEU:HG	2.02	0.41
1:F:535:THR:HA	1:F:763:GLY:HA2	2.02	0.41
1:B:543:ARG:NH2	3:B:1202:NAG:H3	2.35	0.41
4:A:1103:DOQ:HAL1	4:A:1103:DOQ:HAA1	1.65	0.41
1:D:521:TYR:CE2	1:D:525:LYS:HE2	2.56	0.41
1:F:424:ILE:CG2	1:F:777:LYS:HD2	2.50	0.41
1:A:674:LEU:O	1:A:677:GLN:HG3	2.21	0.41
1:E:441:GLU:HA	1:E:442:PRO:HA	1.82	0.41
1:E:786:GLN:HG2	1:E:791:LEU:HD12	2.03	0.41
4:D:1403:DOQ:HAA1	4:D:1403:DOQ:HAL1	1.78	0.41
1:D:737:MET:HG3	1:D:742:ILE:CG1	2.51	0.41
1:B:740:THR:O	1:B:799:TRP:HZ3	2.03	0.41
1:E:441:GLU:HG2	1:E:744:PHE:HE2	1.85	0.41
1:B:428:LEU:CD1	1:B:476:PHE:HD2	2.34	0.41
1:E:443:TYR:HE1	1:E:534:MET:HE1	1.85	0.41
1:F:740:THR:HG23	1:F:741:THR:N	2.36	0.41
1:E:498:TRP:HE1	1:E:526:VAL:HG11	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:712:ARG:HH11	1:F:712:ARG:CB	2.33	0.41
1:E:498:TRP:NE1	1:E:526:VAL:HG11	2.36	0.41
1:A:672:ASP:C	1:A:674:LEU:N	2.74	0.41
1:B:788:GLU:HG3	1:D:698:LYS:HE2	2.02	0.41
1:E:536:LEU:HD22	1:E:762:LYS:HB3	2.01	0.41
1:E:536:LEU:HD13	1:E:763:GLY:H	1.86	0.41
1:C:503:ARG:NH1	5:C:71:HOH:O	2.54	0.41
1:F:441:GLU:HA	1:F:442:PRO:HA	1.82	0.41
1:A:455:GLY:HA2	1:A:458:ARG:HH21	1.85	0.41
1:C:495:ASN:ND2	1:C:497:GLN:HB2	2.36	0.41
1:D:678:THR:OG1	1:D:679:LYS:HD3	2.20	0.41
1:F:774:TYR:O	1:F:775:ARG:C	2.59	0.41
1:E:515:ALA:O	1:E:517:LEU:N	2.49	0.41
1:F:784:GLN:O	1:F:788:GLU:HG2	2.21	0.41
1:B:498:TRP:HH2	1:B:522:VAL:HG12	1.86	0.40
1:E:726:GLN:NE2	5:E:46:HOH:O	2.13	0.40
1:F:721:ASN:OD1	4:F:1603:DOQ:HAA2	2.21	0.40
1:D:718:VAL:HG13	1:D:719:LYS:N	2.36	0.40
1:F:534:MET:O	1:F:763:GLY:HA2	2.21	0.40
1:E:515:ALA:HB1	1:E:516:PRO:HD2	2.04	0.40
1:F:503:ARG:O	1:F:506:ILE:HG23	2.21	0.40
1:D:505:LEU:HD22	1:D:769:PRO:HD3	2.04	0.40
1:F:741:THR:O	1:F:745:VAL:HG22	2.21	0.40
1:A:435:VAL:HG11	1:A:467:LEU:HD11	2.03	0.40
1:D:532:PRO:HA	1:D:764:TYR:O	2.21	0.40
1:A:433:LEU:O	1:A:478:TYR:HA	2.22	0.40
1:B:747:GLN:NE2	1:B:800:ARG:HA	2.37	0.40
1:E:485:ASP:OD1	1:E:500:GLY:HA2	2.21	0.40
1:D:723:GLU:O	1:D:727:ARG:HB2	2.22	0.40
1:C:456:ASN:N	1:C:456:ASN:ND2	2.69	0.40
1:A:451:LYS:HG3	1:A:451:LYS:H	1.64	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	257/312 (82%)	234 (91%)	21 (8%)	2 (1%)	24	64
1	B	257/312 (82%)	239 (93%)	17 (7%)	1 (0%)	39	77
1	C	253/312 (81%)	239 (94%)	13 (5%)	1 (0%)	39	77
1	D	255/312 (82%)	235 (92%)	17 (7%)	3 (1%)	16	53
1	E	253/312 (81%)	230 (91%)	21 (8%)	2 (1%)	24	64
1	F	214/312 (69%)	186 (87%)	21 (10%)	7 (3%)	5	26
All	All	1489/1872 (80%)	1363 (92%)	110 (7%)	16 (1%)	17	56

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	802	ASN
1	F	430	ASN
1	E	771	GLY
1	F	427	SER
1	F	429	SER
1	F	771	GLY
1	F	775	ARG
1	A	507	ASP
1	D	802	ASN
1	B	800	ARG
1	C	507	ASP
1	D	770	MET
1	D	679	LYS
1	F	759	ILE
1	E	800	ARG
1	F	489	GLY

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	228/270 (84%)	197 (86%)	31 (14%)	5	20
1	B	229/270 (85%)	190 (83%)	39 (17%)	2	11
1	C	225/270 (83%)	193 (86%)	32 (14%)	4	18
1	D	227/270 (84%)	186 (82%)	41 (18%)	2	9
1	E	226/270 (84%)	185 (82%)	41 (18%)	2	9
1	F	199/270 (74%)	149 (75%)	50 (25%)	1	2
All	All	1334/1620 (82%)	1100 (82%)	234 (18%)	2	10

All (234) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	425	THR
1	A	428	LEU
1	A	429	SER
1	A	433	LEU
1	A	450	ASP
1	A	464	ILE
1	A	469	GLU
1	A	479	GLU
1	A	482	LEU
1	A	485	ASP
1	A	493	ASP
1	A	503	ARG
1	A	517	LEU
1	A	527	ILE
1	A	536	LEU
1	A	670	SER
1	A	672	ASP
1	A	678	THR
1	A	680	ILE
1	A	695	LYS
1	A	698	LYS
1	A	715	SER
1	A	746	THR
1	A	749	ASN
1	A	752	LEU
1	A	762	LYS
1	A	768	THR
1	A	790	LYS
1	A	799	TRP
1	A	800	ARG

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Mol	Chain	Res	Type
1	A	802	ASN
1	B	424	ILE
1	B	426	ASP
1	B	428	LEU
1	B	431	ARG
1	B	433	LEU
1	B	445	LEU
1	B	450	ASP
1	B	451	LYS
1	B	467	LEU
1	B	471	SER
1	B	481	ARG
1	B	482	LEU
1	B	483	VAL
1	B	484	GLU
1	B	503	ARG
1	B	509	LYS
1	B	512	LEU
1	B	517	LEU
1	B	527	ILE
1	B	534	MET
1	B	536	LEU
1	B	541	LEU
1	B	545	PRO
1	B	680	ILE
1	B	685	VAL
1	B	686	GLU
1	B	698	LYS
1	B	714	GLN
1	B	716	VAL
1	B	718	VAL
1	B	746	THR
1	B	748	ARG
1	B	750	CYS
1	B	751	ASN
1	B	768	THR
1	B	775	ARG
1	B	780	ILE
1	B	786	GLN
1	B	795	LYS
1	C	425	THR
1	C	449	SER

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Mol	Chain	Res	Type
1	C	456	ASN
1	C	458	ARG
1	C	467	LEU
1	C	482	LEU
1	C	483	VAL
1	C	485	ASP
1	C	493	ASP
1	C	497	GLN
1	C	501	MET
1	C	503	ARG
1	C	517	LEU
1	C	522	VAL
1	C	535	THR
1	C	536	LEU
1	C	538	ILE
1	C	669	ASP
1	C	673	ASP
1	C	704	LYS
1	C	713	ARG
1	C	714	GLN
1	C	718	VAL
1	C	719	LYS
1	C	726	GLN
1	C	729	LEU
1	C	748	ARG
1	C	762	LYS
1	C	768	THR
1	C	777	LYS
1	C	791	LEU
1	C	800	ARG
1	D	425	THR
1	D	431	ARG
1	D	432	SER
1	D	433	LEU
1	D	448	LYS
1	D	450	ASP
1	D	467	LEU
1	D	468	ARG
1	D	483	VAL
1	D	487	LYS
1	D	493	ASP
1	D	527	ILE

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Mol	Chain	Res	Type
1	D	535	THR
1	D	536	LEU
1	D	541	LEU
1	D	668	ILE
1	D	672	ASP
1	D	676	LYS
1	D	679	LYS
1	D	680	ILE
1	D	692	THR
1	D	695	LYS
1	D	697	SER
1	D	704	LYS
1	D	711	SER
1	D	713	ARG
1	D	716	VAL
1	D	718	VAL
1	D	719	LYS
1	D	722	GLU
1	D	727	ARG
1	D	748	ARG
1	D	753	THR
1	D	758	LEU
1	D	762	LYS
1	D	768	THR
1	D	775	ARG
1	D	786	GLN
1	D	795	LYS
1	D	802	ASN
1	D	804	CYS
1	E	428	LEU
1	E	430	ASN
1	E	433	LEU
1	E	445	LEU
1	E	448	LYS
1	E	471	SER
1	E	477	THR
1	E	482	LEU
1	E	485	ASP
1	E	495	ASN
1	E	501	MET
1	E	517	LEU
1	E	527	ILE

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Mol	Chain	Res	Type
1	E	535	THR
1	E	536	LEU
1	E	541	LEU
1	E	670	SER
1	E	673	ASP
1	E	674	LEU
1	E	704	LYS
1	E	712	ARG
1	E	714	GLN
1	E	718	VAL
1	E	722	GLU
1	E	727	ARG
1	E	730	THR
1	E	731	SER
1	E	741	THR
1	E	745	VAL
1	E	746	THR
1	E	748	ARG
1	E	750	CYS
1	E	762	LYS
1	E	768	THR
1	E	775	ARG
1	E	777	LYS
1	E	784	GLN
1	E	786	GLN
1	E	787	GLU
1	E	796	GLU
1	E	800	ARG
1	F	426	ASP
1	F	428	LEU
1	F	430	ASN
1	F	433	LEU
1	F	435	VAL
1	F	437	THR
1	F	450	ASP
1	F	465	ASP
1	F	468	ARG
1	F	469	GLU
1	F	471	SER
1	F	477	THR
1	F	478	TYR
1	F	484	GLU

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Mol	Chain	Res	Type
1	F	485	ASP
1	F	491	GLN
1	F	492	ASP
1	F	494	VAL
1	F	497	GLN
1	F	501	MET
1	F	502	VAL
1	F	503	ARG
1	F	505	LEU
1	F	506	ILE
1	F	522	VAL
1	F	527	ILE
1	F	531	LYS
1	F	535	THR
1	F	536	LEU
1	F	538	ILE
1	F	540	ILE
1	F	542	TYR
1	F	687	ASP
1	F	694	PHE
1	F	706	TRP
1	F	712	ARG
1	F	714	GLN
1	F	723	GLU
1	F	729	LEU
1	F	732	ASP
1	F	737	MET
1	F	745	VAL
1	F	748	ARG
1	F	753	THR
1	F	761	SER
1	F	768	THR
1	F	780	ILE
1	F	782	ILE
1	F	786	GLN
1	F	793	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	456	ASN
1	A	749	ASN

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Mol	Chain	Res	Type
1	A	802	ASN
1	B	508	HIS
1	B	747	GLN
1	B	754	GLN
1	C	456	ASN
1	C	491	GLN
1	C	714	GLN
1	C	784	GLN
1	E	495	ASN
1	E	754	GLN
1	F	430	ASN
1	F	491	GLN
1	F	497	GLN
1	F	747	GLN
1	F	754	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

2 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	1	1,2	14,14,15	0.52	0	15,19,21	1.48	1 (6%)
2	FUC	A	2	2	10,10,11	0.79	0	14,14,16	2.13	6 (42%)

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	1	1,2	1/1/5/7	0/6/23/26	0/1/1/1
2	FUC	A	2	2	-	0/0/17/20	0/1/1/1

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2	FUC	O5-C5-C6	2.26	109.87	106.13
2	A	2	FUC	C3-C4-C5	2.43	113.81	109.72
2	A	2	FUC	C2-C3-C4	2.67	115.58	111.04
2	A	2	FUC	O5-C5-C4	2.85	114.47	109.53
2	A	2	FUC	C1-O5-C5	3.83	118.30	112.38
2	A	2	FUC	C1-C2-C3	4.47	114.83	109.54
2	A	1	NAG	C1-O5-C5	4.99	118.58	112.25

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	1	NAG	C1

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1	NAG	1	0
2	A	2	FUC	1	0

5.6 Ligand geometry

15 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected

value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	DOQ	A	1103	-	11,22,22	2.26	2 (18%)	6,30,30	2.31	3 (50%)
3	NAG	B	1201	1	14,14,15	0.80	1 (7%)	15,19,21	1.31	2 (13%)
3	NAG	B	1202	1	14,14,15	0.57	0	15,19,21	1.73	1 (6%)
4	DOQ	B	1203	-	11,22,22	2.28	1 (9%)	6,30,30	2.66	1 (16%)
3	NAG	C	1301	1	14,14,15	0.71	0	15,19,21	2.06	4 (26%)
3	NAG	C	1302	1	14,14,15	0.71	1 (7%)	15,19,21	1.25	3 (20%)
4	DOQ	C	1303	-	11,22,22	2.74	1 (9%)	6,30,30	1.30	1 (16%)
3	NAG	D	1401	1	14,14,15	0.52	0	15,19,21	1.64	4 (26%)
3	NAG	D	1402	1	14,14,15	0.68	0	15,19,21	1.33	1 (6%)
4	DOQ	D	1403	-	11,22,22	2.67	2 (18%)	6,30,30	1.97	1 (16%)
3	NAG	E	1501	1	14,14,15	0.69	0	15,19,21	1.54	3 (20%)
3	NAG	E	1502	1	14,14,15	0.85	0	15,19,21	1.53	3 (20%)
4	DOQ	E	1503	-	11,22,22	2.46	2 (18%)	6,30,30	2.80	1 (16%)
3	NAG	F	1601	1	14,14,15	0.53	0	15,19,21	1.23	1 (6%)
4	DOQ	F	1603	-	11,22,22	2.36	2 (18%)	6,30,30	2.27	3 (50%)

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	DOQ	A	1103	-	-	0/11/35/35	0/1/1/1
3	NAG	B	1201	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1202	1	-	0/6/23/26	0/1/1/1
4	DOQ	B	1203	-	-	0/11/35/35	0/1/1/1
3	NAG	C	1301	1	-	0/6/23/26	0/1/1/1
3	NAG	C	1302	1	1/1/5/7	0/6/23/26	0/1/1/1
4	DOQ	C	1303	-	-	0/11/35/35	0/1/1/1
3	NAG	D	1401	1	1/1/5/7	0/6/23/26	0/1/1/1
3	NAG	D	1402	1	1/1/5/7	0/6/23/26	0/1/1/1
4	DOQ	D	1403	-	-	0/11/35/35	0/1/1/1
3	NAG	E	1501	1	-	0/6/23/26	0/1/1/1
3	NAG	E	1502	1	1/1/5/7	0/6/23/26	0/1/1/1
4	DOQ	E	1503	-	-	0/11/35/35	0/1/1/1
3	NAG	F	1601	1	1/1/5/7	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	DOQ	F	1603	-	-	0/11/35/35	0/1/1/1

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1103	DOQ	CAA-CAP	2.01	1.54	1.50
4	D	1403	DOQ	CAA-CAP	2.06	1.54	1.50
3	C	1302	NAG	C1-C2	2.15	1.55	1.52
4	F	1603	DOQ	CAA-CAP	2.22	1.54	1.50
4	E	1503	DOQ	CAS-CAK	2.29	1.54	1.51
3	B	1201	NAG	C1-C2	2.31	1.55	1.52
4	A	1103	DOQ	CAJ-CAP	6.77	1.39	1.34
4	F	1603	DOQ	CAJ-CAP	6.87	1.39	1.34
4	B	1203	DOQ	CAJ-CAP	6.97	1.39	1.34
4	E	1503	DOQ	CAJ-CAP	7.21	1.40	1.34
4	C	1303	DOQ	CAJ-CAP	8.19	1.40	1.34
4	D	1403	DOQ	CAJ-CAP	8.23	1.40	1.34

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	1503	DOQ	CAI-CAJ-CAP	-6.29	120.77	127.39
4	B	1203	DOQ	CAI-CAJ-CAP	-5.87	121.21	127.39
4	F	1603	DOQ	CAI-CAJ-CAP	-4.20	122.97	127.39
4	A	1103	DOQ	CAI-CAJ-CAP	-3.74	123.46	127.39
4	D	1403	DOQ	CAI-CAJ-CAP	-3.61	123.59	127.39
4	A	1103	DOQ	CAB-CAS-CAK	-3.11	106.80	111.19
4	A	1103	DOQ	CAJ-CAI-CAK	-2.69	117.37	124.18
4	F	1603	DOQ	CAJ-CAI-CAK	-2.39	118.11	124.18
4	C	1303	DOQ	CAI-CAJ-CAP	-2.33	124.93	127.39
4	F	1603	DOQ	CAB-CAS-CAK	-2.04	108.30	111.19
3	E	1501	NAG	O5-C5-C6	2.03	111.73	107.35
3	D	1401	NAG	C2-N2-C7	2.07	125.70	123.04
3	E	1502	NAG	C2-N2-C7	2.23	125.90	123.04
3	C	1302	NAG	C4-C3-C2	2.24	114.71	111.23
3	C	1302	NAG	O5-C5-C6	2.27	112.26	107.35
3	D	1401	NAG	C4-C3-C2	2.43	115.01	111.23
3	B	1201	NAG	O5-C5-C6	2.45	112.66	107.35
3	B	1201	NAG	C4-C3-C2	2.55	115.19	111.23
3	E	1501	NAG	C3-C4-C5	2.56	114.67	110.20
3	C	1302	NAG	C1-O5-C5	2.62	115.57	112.25
3	C	1301	NAG	O5-C5-C6	2.77	113.35	107.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	1401	NAG	C3-C4-C5	2.87	115.20	110.20
3	F	1601	NAG	C1-O5-C5	3.12	116.21	112.25
3	E	1502	NAG	C3-C4-C5	3.17	115.72	110.20
3	E	1502	NAG	C1-O5-C5	3.37	116.53	112.25
3	C	1301	NAG	C3-C4-C5	3.68	116.62	110.20
3	D	1402	NAG	C2-N2-C7	3.71	127.81	123.04
3	D	1401	NAG	C1-O5-C5	3.95	117.26	112.25
3	C	1301	NAG	C4-C3-C2	4.00	117.45	111.23
3	E	1501	NAG	C1-O5-C5	4.17	117.54	112.25
3	C	1301	NAG	C1-O5-C5	4.26	117.66	112.25
3	B	1202	NAG	C1-O5-C5	6.21	120.13	112.25

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	D	1402	NAG	C1
3	E	1502	NAG	C1
3	D	1401	NAG	C1
3	C	1302	NAG	C1
3	F	1601	NAG	C1

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1103	DOQ	2	0
3	B	1202	NAG	3	0
4	B	1203	DOQ	2	0
3	D	1402	NAG	2	0
4	D	1403	DOQ	1	0
4	E	1503	DOQ	1	0
3	F	1601	NAG	1	0
4	F	1603	DOQ	2	0

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	261/312 (83%)	-0.06	2 (0%) 87 75	24, 58, 73, 77	0
1	B	261/312 (83%)	-0.03	0 100 100	24, 57, 74, 79	0
1	C	257/312 (82%)	-0.02	3 (1%) 81 65	26, 58, 77, 86	0
1	D	259/312 (83%)	-0.03	3 (1%) 81 65	25, 58, 73, 79	0
1	E	257/312 (82%)	0.05	6 (2%) 64 41	26, 58, 81, 93	0
1	F	226/312 (72%)	0.09	6 (2%) 58 35	46, 58, 74, 79	0
All	All	1521/1872 (81%)	-0.00	20 (1%) 79 63	24, 58, 75, 93	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	677	GLN	3.2
1	E	678	THR	3.1
1	E	545	PRO	3.1
1	C	730	THR	2.8
1	E	679	LYS	2.7
1	D	730	THR	2.7
1	C	802	ASN	2.6
1	F	750	CYS	2.4
1	F	424	ILE	2.4
1	D	430	ASN	2.3
1	F	732	ASP	2.3
1	C	677	GLN	2.3
1	F	771	GLY	2.3
1	E	494	VAL	2.2
1	F	751	ASN	2.1
1	A	803	GLY	2.1
1	E	755	ILE	2.1
1	F	711	SER	2.0
1	A	802	ASN	2.0

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Mol	Chain	Res	Type	RSRZ
1	D	680	ILE	2.0

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

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

6.3 Carbohydrates [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	FUC	A	2	10/11	0.89	0.30	-	81,82,82,82	0
2	NAG	A	1	14/15	0.83	0.18	-	78,79,80,80	0

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	NAG	B	1202	14/15	0.82	0.37	1.81	81,82,85,85	0
4	DOQ	E	1503	22/22	0.88	0.27	1.67	50,53,58,59	0
4	DOQ	F	1603	22/22	0.93	0.20	-0.23	59,60,62,64	0
4	DOQ	D	1403	22/22	0.92	0.20	-0.24	41,42,44,44	0
4	DOQ	A	1103	22/22	0.96	0.20	-0.80	35,36,41,42	0
4	DOQ	C	1303	22/22	0.95	0.19	-0.81	42,44,48,49	0
4	DOQ	B	1203	22/22	0.95	0.21	-0.91	33,35,37,38	0
3	NAG	D	1402	14/15	0.83	0.34	-	83,85,87,87	0
3	NAG	C	1301	14/15	0.77	0.22	-	82,84,85,85	0
3	NAG	D	1401	14/15	0.82	0.34	-	84,87,87,88	0
3	NAG	E	1502	14/15	0.72	0.43	-	84,86,88,88	0
3	NAG	B	1201	14/15	0.82	0.26	-	79,80,81,81	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	NAG	C	1302	14/15	0.81	0.36	-	85,88,89,90	0
3	NAG	E	1501	14/15	0.69	0.33	-	85,87,88,88	0
3	NAG	F	1601	14/15	0.81	0.31	-	88,90,91,92	0

6.5 Other polymers [i](#)

There are no such residues in this entry.