



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:15 AM GMT

PDB ID : 3OAX
Title : Crystal structure of bovine rhodopsin with beta-ionone
Authors : Makino, C.L.; Riley, C.K.; Looney, J.; Crouch, R.K.; Okada, T.
Deposited on : 2010-08-05
Resolution : 2.60 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

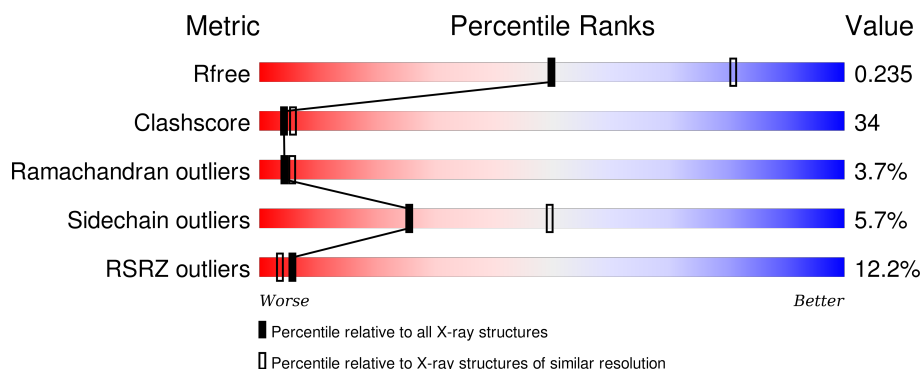
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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	349	
1	B	349	

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
10	ID3	A	6025	-	-	-	X
10	ID3	B	6026	-	-	X	X
12	HTO	B	1401	-	-	-	X
3	RET	B	1296	-	-	-	X
4	PLM	A	1322	-	-	-	X
4	PLM	A	1323	-	-	-	X
4	PLM	B	1322	-	-	-	X
4	PLM	B	1323	-	-	-	X
7	ZN	A	962	-	-	-	X
8	4E6	A	1410	-	-	-	X
8	4E6	B	1407	-	-	-	X
9	HTG	A	1507	-	-	-	X
9	HTG	B	1506	-	-	-	X

2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 6015 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 Rhodopsin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	349	Total	C	N	O	S	0	0	0
			2749	1818	424	481	26			
1	B	349	Total	C	N	O	S	0	0	0
			2749	1818	424	481	26			

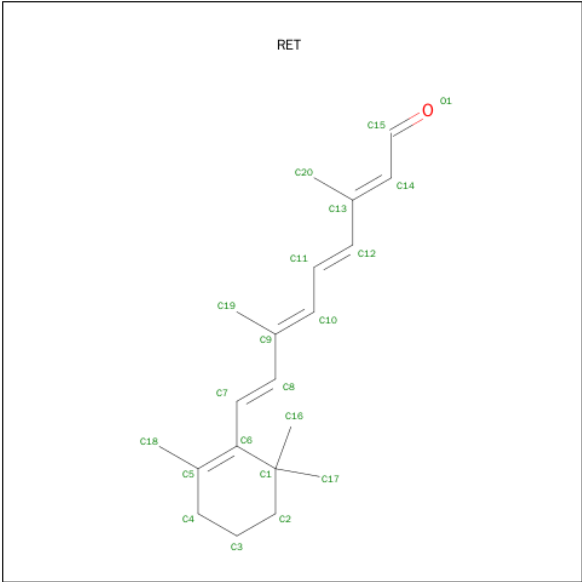
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	ACE	-	ACETYLATION	UNP P02699
B	0	ACE	-	ACETYLATION	UNP P02699

- Molecule 2 is a polymer of unknown type called SUGAR (3-MER).

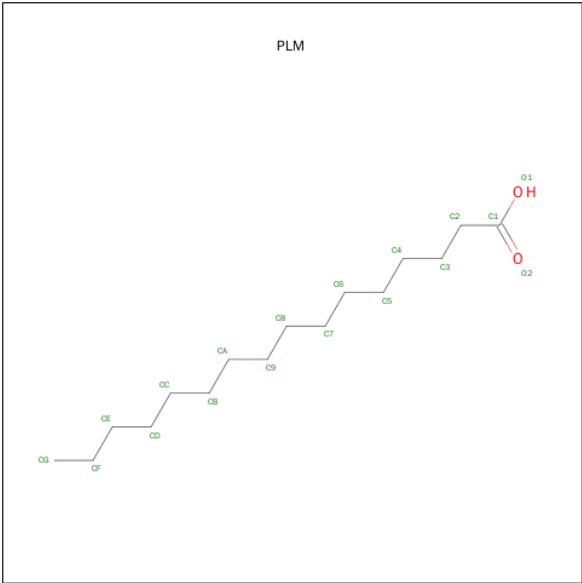
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 3 is RETINAL (three-letter code: RET) (formula: C₂₀H₂₈O).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C		0	0
			20	20			
3	B	1	Total	C		0	0
			20	20			

- Molecule 4 is PALMITIC ACID (three-letter code: PLM) (formula: C₁₆H₃₂O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			17	16	1		
4	A	1	Total	C	O	0	0
			17	16	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			17	16	1		
4	B	1	Total	C	O	0	0
			17	16	1		

- Molecule 5 is a polymer of unknown type called SUGAR (2-MER).

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

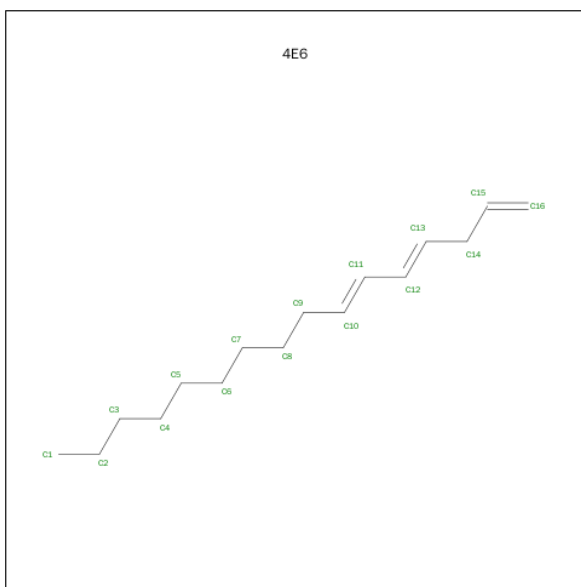
- Molecule 6 is MERCURY (II) ION (three-letter code: HG) (formula: Hg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	3	Total	Hg	0	0
			3	3		
6	A	3	Total	Hg	0	0
			3	3		

- Molecule 7 is ZINC ION (three-letter code: ZN) (formula: Zn).

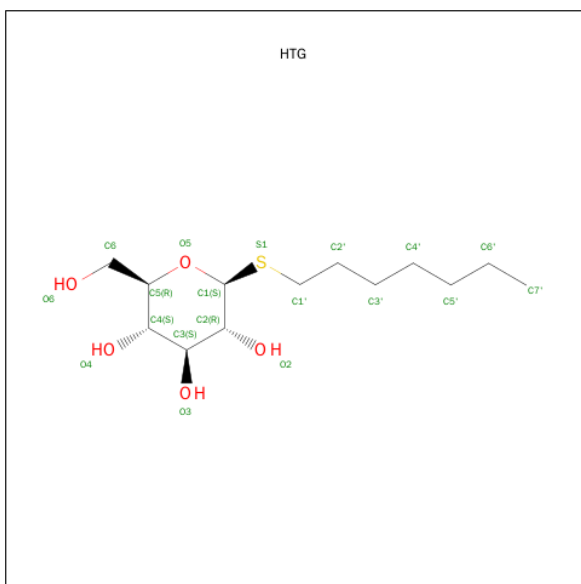
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	3	Total	Zn	0	0
			3	3		
7	A	4	Total	Zn	0	0
			4	4		

- Molecule 8 is (4E,6E)-HEXADECA-1,4,6-TRIENE (three-letter code: 4E6) (formula: C₁₆H₂₈).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	1	Total	C	0	0
			16	16		
8	B	1	Total	C	0	0
			16	16		

- Molecule 9 is HEPTYL 1-THIOHEXOPYRANOSIDE (three-letter code: HTG) (formula: $C_{13}H_{26}O_5S$).



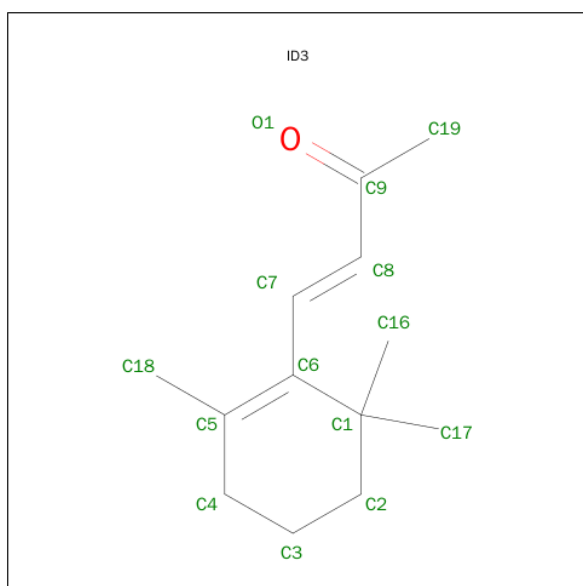
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	A	1	Total	C	O	S	0	0
			19	13	5	1		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	A	1	Total	C	O	S	0	0
			19	13	5	1		
9	B	1	Total	C	O	S	0	0
			19	13	5	1		
9	B	1	Total	C	O	S	0	0
			19	13	5	1		

- Molecule 10 is (3E)-4-(2,6,6-TRIMETHYLCYCLOHEX-1-EN-1-YL)BUT-3-EN-2-ONE (three-letter code: ID3) (formula: C₁₃H₂₀O).

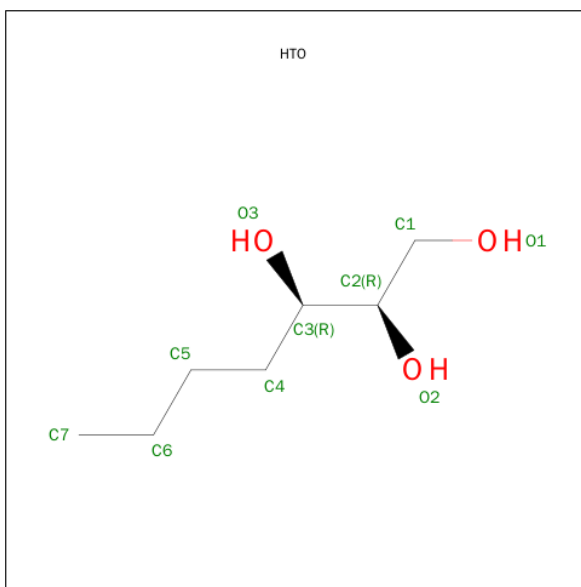


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	A	1	Total	C	O		0	0
			14	13	1			
10	B	1	Total	C	O		0	0
			14	13	1			

- Molecule 11 is a polymer of unknown type called SUGAR (4-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
11	B	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 12 is HEPTANE-1,2,3-TRIOL (three-letter code: HTO) (formula: C₇H₁₆O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	B	1	Total	C	O	0	0
			10	7	3		

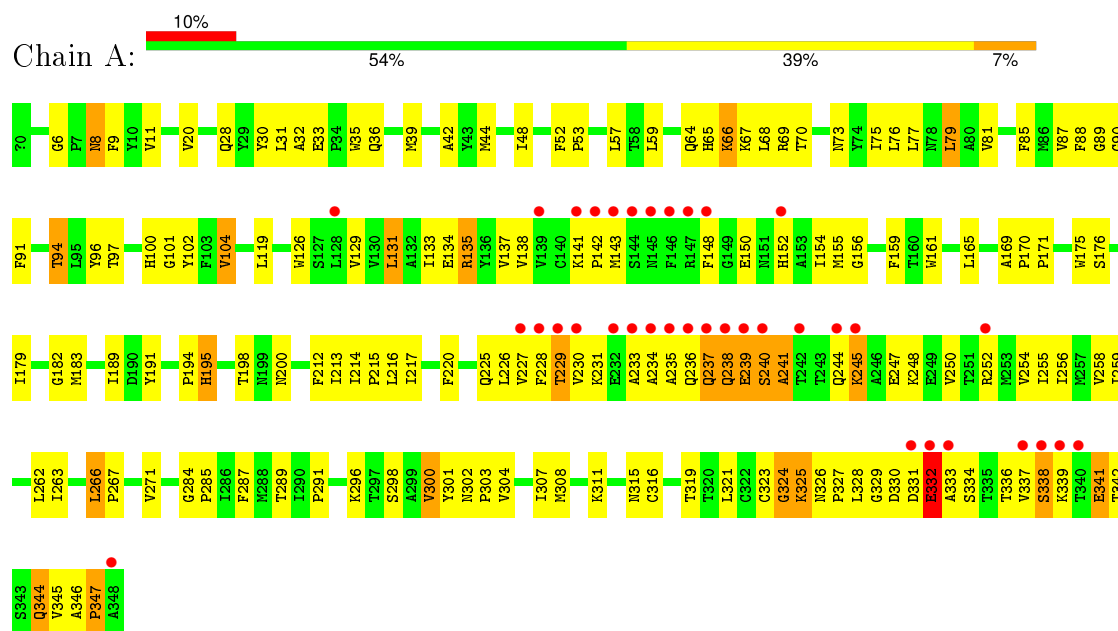
- Molecule 13 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	A	57	Total	O	0	0
			57	57		
13	B	48	Total	O	0	0
			48	48		

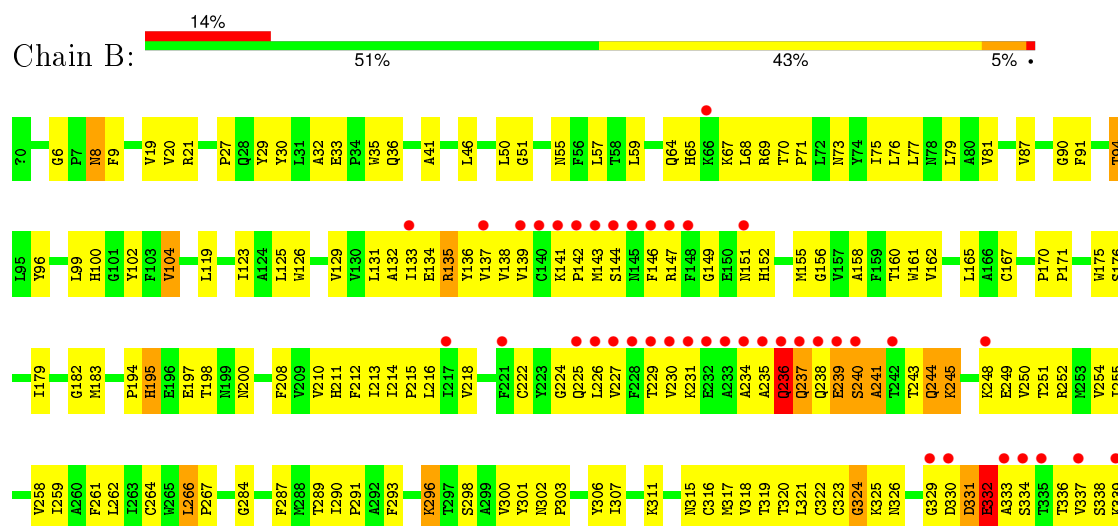
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Rhodopsin



• Molecule 1: Rhodopsin



T340	
E341	
T342	
S343	
Q344	
V345	
A346	
P347	
A348	

4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	96.99 Å 96.99 Å 149.80 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.60 48.49 – 2.60	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.60) 93.6 (48.49-2.60)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.71 (at 2.61 Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.224 , 0.262 0.236 , 0.235	Depositor DCC
R_{free} test set	1996 reflections (5.02%)	DCC
Wilson B-factor (Å ²)	52.8	Xtriage
Anisotropy	0.525	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 66.6	EDS
Estimated twinning fraction	0.053 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 39759 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6015	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.29% 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: HTG, ZN, BMA, NAG, ACE, HTO, ID3, RET, PLM, HG, 4E6, 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	0.51	0/2831	0.58	1/3859 (0.0%)
1	B	0.49	0/2831	0.57	1/3859 (0.0%)
All	All	0.50	0/5662	0.57	2/7718 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	296	LYS	CD-CE-NZ	5.79	125.03	111.70
1	B	296	LYS	CD-CE-NZ	5.48	124.31	111.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2749	0	2706	183	0
1	B	2749	0	2708	215	0
2	A	39	0	34	1	0
3	A	20	0	27	1	0
3	B	20	0	27	0	0
4	A	34	0	62	0	0
4	B	34	0	62	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	28	0	25	0	0
5	B	28	0	25	0	0
6	A	3	0	0	0	0
6	B	3	0	0	1	0
7	A	4	0	0	0	0
7	B	3	0	0	0	0
8	A	16	0	27	1	0
8	B	16	0	27	0	0
9	A	38	0	52	1	0
9	B	38	0	52	3	0
10	A	14	0	20	5	0
10	B	14	0	20	9	0
11	B	50	0	43	2	0
12	B	10	0	16	1	0
13	A	57	0	0	2	0
13	B	48	0	0	3	0
All	All	6015	0	5933	397	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 34.

All (397) 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:A:65:HIS:HB3	1:A:337:VAL:HG22	1.28	1.15
1:B:346:ALA:H	1:B:347:PRO:HD3	1.02	1.07
1:A:345:VAL:HG12	1:A:347:PRO:HD3	1.32	1.06
1:A:67:LYS:HB2	1:A:337:VAL:HB	1.36	1.06
1:A:341:GLU:HG3	1:A:342:THR:H	1.23	1.00
1:B:338:SER:HB2	1:B:341:GLU:HG2	1.46	0.96
1:B:346:ALA:H	1:B:347:PRO:CD	1.82	0.93
1:A:284:GLY:H	10:A:6025:ID3:H17A	1.30	0.93
1:A:325:LYS:HG2	1:A:326:ASN:H	1.35	0.91
1:B:143:MET:HG2	1:B:146:PHE:HB2	1.51	0.90
1:B:59:LEU:HD12	1:B:77:LEU:HD11	1.52	0.90
1:B:346:ALA:N	1:B:347:PRO:HD3	1.87	0.88
1:B:239:GLU:HB3	1:B:244:GLN:HE22	1.39	0.88
1:A:341:GLU:HG3	1:A:342:THR:N	1.92	0.85
1:A:91:PHE:HA	1:A:94:THR:CG2	2.06	0.85
1:A:345:VAL:HG12	1:A:347:PRO:CD	2.07	0.84
1:B:237:GLN:H	1:B:237:GLN:NE2	1.76	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:245:LYS:HA	1:B:245:LYS:HE3	1.60	0.82
1:B:341:GLU:HG3	1:B:342:THR:N	1.92	0.81
1:B:143:MET:HG2	1:B:146:PHE:CB	2.11	0.81
1:B:230:VAL:HG23	1:B:248:LYS:HD3	1.63	0.81
1:A:183:MET:HE3	1:A:289:THR:HG21	1.64	0.80
1:B:239:GLU:HB3	1:B:244:GLN:NE2	1.96	0.80
1:B:67:LYS:HB3	1:B:337:VAL:CG2	2.12	0.79
1:B:64:GLN:HG2	1:B:339:LYS:HB2	1.63	0.79
1:B:332:GLU:HB2	1:B:336:THR:OG1	1.82	0.79
1:B:316:CYS:SG	1:B:337:VAL:HB	2.22	0.78
1:B:284:GLY:HA3	10:B:6026:ID3:H4A	1.64	0.78
1:A:325:LYS:HG2	1:A:326:ASN:N	1.98	0.78
1:A:311:LYS:HE3	1:A:315:ASN:HD21	1.48	0.78
1:A:59:LEU:HD12	1:A:77:LEU:HD11	1.66	0.78
1:A:65:HIS:CG	1:A:338:SER:HA	2.18	0.77
1:B:91:PHE:HA	1:B:94:THR:CG2	2.15	0.76
1:A:338:SER:CB	1:A:341:GLU:HG2	2.16	0.76
1:B:214:ILE:HB	1:B:215:PRO:HD3	1.68	0.76
1:B:284:GLY:CA	10:B:6026:ID3:H4A	2.16	0.75
1:B:91:PHE:HA	1:B:94:THR:HG23	1.68	0.75
1:A:331:ASP:O	1:A:332:GLU:HB2	1.86	0.74
1:A:67:LYS:HB2	1:A:337:VAL:CB	2.14	0.74
1:A:332:GLU:OE2	1:A:334:SER:HB2	1.87	0.74
1:B:238:GLN:HG2	1:B:239:GLU:H	1.52	0.74
1:B:341:GLU:HG3	1:B:342:THR:HG22	1.71	0.73
1:A:236:GLN:O	1:A:245:LYS:HD2	1.89	0.73
1:B:255:ILE:O	1:B:259:ILE:HG12	1.89	0.72
1:A:304:VAL:O	1:A:308:MET:HG2	1.90	0.72
1:B:332:GLU:HG3	1:B:336:THR:HA	1.71	0.71
1:B:238:GLN:HG2	1:B:239:GLU:N	2.06	0.71
1:B:67:LYS:HB3	1:B:337:VAL:CG1	2.20	0.70
1:A:195:HIS:HD1	1:A:198:THR:CG2	2.03	0.70
1:B:341:GLU:HG3	1:B:342:THR:H	1.56	0.70
1:A:245:LYS:HA	1:A:245:LYS:HZ1	1.57	0.70
1:B:222:CYS:O	1:B:226:LEU:HD13	1.92	0.70
1:A:238:GLN:O	1:A:239:GLU:HB2	1.92	0.69
1:A:66:LYS:N	1:A:66:LYS:HE2	2.07	0.69
1:A:316:CYS:SG	1:A:337:VAL:HG13	2.31	0.69
1:B:67:LYS:HB3	1:B:337:VAL:HG22	1.73	0.69
1:B:32:ALA:HB1	1:B:36:GLN:OE1	1.92	0.69
8:A:1410:4E6:H8	1:B:46:LEU:HD11	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:236:GLN:HB2	1:B:237:GLN:NE2	2.08	0.69
1:B:135:ARG:HA	1:B:135:ARG:NE	2.08	0.68
1:B:143:MET:HG3	1:B:144:SER:H	1.59	0.68
1:A:234:ALA:HB1	1:A:245:LYS:HE2	1.76	0.68
1:B:338:SER:HB2	1:B:341:GLU:CG	2.22	0.67
1:A:66:LYS:HE2	1:A:66:LYS:H	1.60	0.67
1:B:302:ASN:HB2	13:B:2016:HOH:O	1.93	0.67
1:A:161:TRP:O	1:A:165:LEU:HD23	1.94	0.67
1:B:239:GLU:HB2	1:B:245:LYS:HD2	1.76	0.67
1:A:237:GLN:NE2	1:A:237:GLN:H	1.93	0.67
1:B:222:CYS:SG	6:B:904:HG:HG	2.11	0.67
1:A:308:MET:HE1	1:B:41:ALA:HB1	1.75	0.67
1:A:67:LYS:H	1:A:337:VAL:HG23	1.59	0.66
1:B:65:HIS:CE1	1:B:338:SER:HA	2.30	0.66
1:B:239:GLU:CB	1:B:244:GLN:HE22	2.08	0.66
1:A:216:LEU:HD12	1:A:220:PHE:CE2	2.30	0.66
1:B:161:TRP:O	1:B:165:LEU:HD23	1.96	0.66
1:A:239:GLU:HB3	1:A:244:GLN:NE2	2.11	0.66
1:B:65:HIS:HB3	1:B:337:VAL:CG1	2.26	0.66
1:A:91:PHE:HA	1:A:94:THR:HG23	1.77	0.66
1:A:59:LEU:CD1	1:A:77:LEU:HD11	2.25	0.66
1:A:325:LYS:CG	1:A:326:ASN:H	2.03	0.66
1:A:75:ILE:HG13	1:A:131:LEU:HD13	1.77	0.66
1:B:325:LYS:HE3	1:B:340:THR:O	1.96	0.66
1:A:327:PRO:HB2	1:A:331:ASP:HA	1.77	0.66
1:A:346:ALA:N	1:A:347:PRO:HD3	2.12	0.65
1:B:336:THR:HB	1:B:342:THR:CG2	2.26	0.65
1:A:212:PHE:O	1:A:216:LEU:HD23	1.96	0.65
1:A:287:PHE:H	10:A:6025:ID3:H16	1.62	0.65
1:B:338:SER:CB	1:B:341:GLU:HG2	2.25	0.65
1:B:231:LYS:NZ	1:B:231:LYS:HB2	2.11	0.65
1:A:183:MET:CE	1:A:289:THR:HG21	2.27	0.64
1:B:96:TYR:O	1:B:100:HIS:HD2	1.80	0.64
1:B:65:HIS:CD2	1:B:338:SER:HA	2.33	0.64
1:A:341:GLU:OE1	1:A:342:THR:HG22	1.98	0.63
1:B:230:VAL:HG23	1:B:248:LYS:CD	2.27	0.63
1:A:65:HIS:HB3	1:A:337:VAL:CG2	2.19	0.63
1:B:230:VAL:HA	1:B:248:LYS:HE3	1.81	0.63
1:A:238:GLN:HG2	1:A:239:GLU:N	2.13	0.63
9:B:1506:HTG:H61	10:B:6026:ID3:H16B	1.80	0.63
1:A:195:HIS:HD1	1:A:198:THR:HG22	1.62	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:338:SER:HB2	1:A:341:GLU:HG2	1.80	0.62
1:B:143:MET:HG3	1:B:144:SER:N	2.13	0.62
1:A:308:MET:CE	1:B:99:LEU:HD21	2.29	0.62
1:B:182:GLY:HA2	13:B:2050:HOH:O	1.98	0.62
1:B:315:ASN:O	1:B:318:VAL:HG12	1.99	0.62
1:B:135:ARG:HA	1:B:135:ARG:HE	1.63	0.62
1:B:284:GLY:N	10:B:6026:ID3:H4A	2.15	0.62
1:B:287:PHE:HA	10:B:6026:ID3:H8	1.81	0.61
1:B:141:LYS:C	1:B:143:MET:H	2.03	0.61
1:B:225:GLN:C	1:B:226:LEU:HD12	2.21	0.61
1:A:33:GLU:HB2	1:A:36:GLN:HG3	1.83	0.60
1:A:338:SER:OG	1:A:341:GLU:HG2	2.01	0.60
1:A:75:ILE:O	1:A:79:LEU:HD22	2.02	0.60
1:A:70:THR:H	1:A:73:ASN:HD22	1.48	0.60
1:A:234:ALA:HB2	1:A:248:LYS:HD2	1.84	0.60
1:A:198:THR:HG23	1:A:200:ASN:OD1	2.02	0.60
1:A:64:GLN:O	1:A:339:LYS:HB2	2.02	0.60
1:A:239:GLU:HB3	1:A:244:GLN:HE22	1.65	0.59
1:A:341:GLU:CD	1:A:342:THR:HG22	2.22	0.59
1:B:316:CYS:SG	1:B:337:VAL:CB	2.90	0.59
1:B:135:ARG:O	1:B:139:VAL:HG23	2.01	0.59
1:A:220:PHE:HZ	1:A:262:LEU:HD11	1.66	0.59
1:A:126:TRP:CH2	1:A:215:PRO:HG3	2.38	0.59
1:B:341:GLU:CG	1:B:342:THR:H	2.15	0.59
1:B:195:HIS:HD1	1:B:198:THR:CG2	2.16	0.59
1:A:170:PRO:HB2	1:A:171:PRO:HD3	1.84	0.58
1:B:195:HIS:HD1	1:B:198:THR:HG22	1.68	0.58
1:B:59:LEU:CD1	1:B:77:LEU:HD11	2.28	0.58
1:A:227:VAL:HG13	1:A:228:PHE:N	2.17	0.58
1:B:250:VAL:O	1:B:254:VAL:HG23	2.03	0.58
1:A:302:ASN:HB2	1:A:303:PRO:HD3	1.85	0.57
1:A:6:GLY:HA3	1:A:9:PHE:CZ	2.39	0.57
1:A:259:ILE:O	1:A:263:ILE:HG13	2.04	0.57
1:B:248:LYS:O	1:B:252:ARG:HG3	2.03	0.57
1:B:311:LYS:HE3	9:B:1509:HTG:O3	2.05	0.57
1:A:137:VAL:HA	1:A:142:PRO:HD2	1.86	0.57
1:B:341:GLU:CG	1:B:342:THR:N	2.62	0.57
1:A:237:GLN:O	1:A:238:GLN:HB3	2.05	0.56
1:B:267:PRO:HG2	13:B:2019:HOH:O	2.04	0.56
1:A:284:GLY:HA3	10:A:6025:ID3:H2A	1.86	0.56
1:A:287:PHE:N	10:A:6025:ID3:H16	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:308:MET:HE1	1:B:99:LEU:HD21	1.85	0.56
1:B:331:ASP:O	1:B:332:GLU:HB2	2.06	0.56
1:A:216:LEU:HD12	1:A:220:PHE:HE2	1.68	0.56
1:A:64:GLN:HG3	1:A:339:LYS:HE2	1.87	0.56
1:B:208:PHE:O	1:B:213:ILE:HG13	2.05	0.56
1:B:67:LYS:HB3	1:B:337:VAL:HG13	1.85	0.56
1:B:75:ILE:HG13	1:B:131:LEU:CD1	2.36	0.56
1:B:132:ALA:O	1:B:222:CYS:SG	2.63	0.56
1:A:32:ALA:HB1	1:A:36:GLN:OE1	2.05	0.56
1:B:336:THR:HG22	1:B:337:VAL:H	1.71	0.56
1:A:88:PHE:HB3	4:B:1323:PLM:HB1	1.87	0.56
1:A:77:LEU:O	1:A:81:VAL:HG23	2.06	0.55
1:B:266:LEU:N	1:B:267:PRO:HD2	2.21	0.55
1:A:330:ASP:O	1:A:331:ASP:HB3	2.06	0.55
1:A:245:LYS:HA	1:A:245:LYS:NZ	2.21	0.55
1:A:90:GLY:O	1:A:94:THR:HG22	2.07	0.55
1:B:70:THR:H	1:B:73:ASN:HD22	1.54	0.55
1:B:167:CYS:HB2	1:B:211:HIS:CD2	2.42	0.55
1:A:298:SER:HA	1:A:301:TYR:CE2	2.42	0.55
1:B:75:ILE:HG21	1:B:131:LEU:CD1	2.36	0.55
1:B:226:LEU:HB3	1:B:230:VAL:CG1	2.36	0.55
1:B:75:ILE:HG13	1:B:131:LEU:HD12	1.88	0.55
1:B:156:GLY:O	1:B:160:THR:HG23	2.06	0.55
1:B:151:ASN:HD21	1:B:152:HIS:CE1	2.25	0.54
1:A:28:GLN:HB3	1:A:31:LEU:HD12	1.89	0.54
1:A:325:LYS:NZ	13:A:2007:HOH:O	2.39	0.54
1:B:87:VAL:O	1:B:91:PHE:HB2	2.08	0.54
1:B:75:ILE:HG21	1:B:131:LEU:HD11	1.89	0.54
1:B:175:TRP:O	1:B:176:SER:HB3	2.07	0.54
1:B:131:LEU:HD23	1:B:254:VAL:HG22	1.88	0.54
1:B:57:LEU:HD11	1:B:317:MET:HG3	1.89	0.54
1:A:213:ILE:O	1:A:217:ILE:HG13	2.07	0.53
1:B:332:GLU:O	1:B:333:ALA:HB3	2.08	0.53
9:B:1506:HTG:C6	10:B:6026:ID3:H16B	2.39	0.53
1:B:65:HIS:NE2	1:B:338:SER:HA	2.23	0.53
1:B:194:PRO:O	1:B:195:HIS:C	2.47	0.53
1:A:237:GLN:O	1:A:238:GLN:CB	2.57	0.53
1:A:240:SER:O	1:A:241:ALA:CB	2.56	0.52
1:A:325:LYS:HG2	1:A:327:PRO:HD3	1.90	0.52
1:B:158:ALA:O	1:B:162:VAL:HG23	2.09	0.52
1:A:137:VAL:O	1:A:141:LYS:HA	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:76:LEU:HD22	1:B:306:TYR:CG	2.43	0.52
1:B:65:HIS:CG	1:B:338:SER:HA	2.45	0.52
1:B:240:SER:O	1:B:241:ALA:HB2	2.08	0.52
1:B:212:PHE:O	1:B:216:LEU:HD23	2.09	0.52
1:A:67:LYS:H	1:A:337:VAL:CG2	2.22	0.52
1:A:338:SER:HB2	1:A:341:GLU:CG	2.40	0.51
1:A:33:GLU:HB3	1:A:35:TRP:CD1	2.44	0.51
1:A:327:PRO:HG3	1:A:331:ASP:OD2	2.11	0.51
1:A:227:VAL:CG1	1:A:228:PHE:N	2.72	0.51
1:A:319:THR:HG23	1:A:325:LYS:HA	1.91	0.51
1:A:250:VAL:O	1:A:254:VAL:HG23	2.09	0.51
1:A:284:GLY:C	10:A:6025:ID3:H16B	2.30	0.51
1:B:152:HIS:O	1:B:155:MET:HB2	2.11	0.51
1:B:234:ALA:HA	1:B:245:LYS:HZ1	1.75	0.51
1:A:323:CYS:O	1:A:324:GLY:C	2.49	0.51
1:A:42:ALA:HA	12:B:1401:HTO:H72	1.91	0.51
1:B:143:MET:CE	1:B:144:SER:H	2.23	0.51
1:B:141:LYS:N	1:B:142:PRO:HD3	2.26	0.51
1:B:210:VAL:HA	1:B:214:ILE:HD12	1.92	0.51
1:A:194:PRO:O	1:A:195:HIS:C	2.49	0.51
1:A:231:LYS:HZ2	1:A:233:ALA:HB3	1.75	0.51
1:A:342:THR:O	1:A:342:THR:HG23	2.09	0.50
1:B:197:GLU:HG2	1:B:197:GLU:O	2.12	0.50
1:A:152:HIS:O	1:A:155:MET:HB2	2.10	0.50
1:A:330:ASP:C	1:A:332:GLU:H	2.15	0.50
1:B:237:GLN:H	1:B:237:GLN:HE21	1.57	0.50
1:B:319:THR:HG21	1:B:338:SER:OG	2.12	0.50
1:B:249:GLU:HA	1:B:252:ARG:HG3	1.94	0.50
1:A:230:VAL:HG22	1:A:231:LYS:H	1.77	0.50
1:B:6:GLY:HA3	1:B:9:PHE:CZ	2.47	0.50
1:B:136:TYR:CE2	1:B:142:PRO:HG2	2.46	0.50
1:A:67:LYS:HB2	1:A:337:VAL:CG2	2.42	0.49
1:B:346:ALA:N	1:B:347:PRO:CD	2.58	0.49
1:B:226:LEU:HD23	1:B:230:VAL:HG11	1.93	0.49
1:B:241:ALA:HB1	1:B:243:THR:HG22	1.95	0.49
1:B:65:HIS:HB3	1:B:337:VAL:HG12	1.94	0.49
1:B:136:TYR:HE1	1:B:225:GLN:HB3	1.77	0.49
1:A:214:ILE:HB	1:A:215:PRO:HD3	1.94	0.49
1:B:129:VAL:HG13	1:B:218:VAL:HG11	1.93	0.49
1:A:225:GLN:C	1:A:227:VAL:H	2.16	0.49
1:B:315:ASN:HA	1:B:318:VAL:HG12	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:135:ARG:NH2	1:A:138:VAL:HG21	2.27	0.49
1:B:143:MET:HG2	1:B:146:PHE:HB3	1.93	0.49
1:A:135:ARG:NE	1:A:135:ARG:HA	2.28	0.49
1:B:65:HIS:HB2	1:B:68:LEU:HD12	1.95	0.49
1:A:230:VAL:HG22	1:A:231:LYS:N	2.26	0.49
1:A:267:PRO:HG2	13:A:964:HOH:O	2.11	0.49
1:A:341:GLU:CG	1:A:342:THR:N	2.67	0.49
1:A:308:MET:CE	1:B:41:ALA:HB1	2.41	0.49
1:B:332:GLU:HG3	1:B:336:THR:CA	2.42	0.48
1:A:176:SER:HA	1:A:200:ASN:OD1	2.13	0.48
1:A:342:THR:HG1	1:A:344:GLN:CD	2.16	0.48
1:A:198:THR:CG2	1:A:200:ASN:OD1	2.62	0.48
1:A:36:GLN:O	1:A:39:MET:HB2	2.14	0.48
1:A:189:ILE:HB	1:A:191:TYR:CE1	2.48	0.48
2:A:504:NAG:C7	2:A:505:NAG:H61	2.44	0.48
1:A:337:VAL:O	1:A:338:SER:OG	2.23	0.48
1:A:235:ALA:HB3	1:A:239:GLU:OE2	2.13	0.48
1:B:303:PRO:O	1:B:307:ILE:HG13	2.14	0.48
1:A:156:GLY:O	1:A:159:PHE:HB3	2.13	0.48
1:B:21:ARG:NH2	11:B:604:NAG:H61	2.28	0.48
1:A:97:THR:HG23	1:A:102:TYR:C	2.34	0.48
1:B:234:ALA:HA	1:B:245:LYS:NZ	2.28	0.48
1:A:234:ALA:CB	1:A:248:LYS:HD2	2.44	0.48
1:B:300:VAL:O	1:B:303:PRO:HD2	2.13	0.48
1:B:262:LEU:O	1:B:266:LEU:HB2	2.14	0.48
1:A:298:SER:HA	1:A:301:TYR:CD2	2.49	0.48
1:A:254:VAL:O	1:A:258:VAL:HG23	2.14	0.47
1:A:67:LYS:HE3	1:A:344:GLN:O	2.14	0.47
1:B:64:GLN:HG3	1:B:339:LYS:HE2	1.95	0.47
1:B:64:GLN:O	1:B:64:GLN:HG2	2.13	0.47
1:B:239:GLU:HB3	1:B:244:GLN:CD	2.33	0.47
1:A:88:PHE:HB2	4:B:1323:PLM:HF2	1.97	0.47
1:B:68:LEU:O	1:B:69:ARG:NH1	2.40	0.47
1:A:332:GLU:O	1:A:333:ALA:HB3	2.15	0.47
1:B:245:LYS:HA	1:B:245:LYS:CE	2.38	0.47
1:A:137:VAL:HA	1:A:142:PRO:CD	2.45	0.47
1:A:267:PRO:O	1:A:271:VAL:HG23	2.15	0.47
1:B:311:LYS:HE2	1:B:315:ASN:OD1	2.15	0.46
1:B:298:SER:HA	1:B:301:TYR:CD2	2.50	0.46
1:B:33:GLU:HB2	1:B:36:GLN:HG3	1.98	0.46
1:A:238:GLN:HG2	1:A:239:GLU:H	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:51:GLY:CA	1:B:300:VAL:HG12	2.45	0.46
1:B:51:GLY:HA2	1:B:300:VAL:HG12	1.97	0.46
1:B:137:VAL:O	1:B:137:VAL:HG12	2.15	0.46
1:A:129:VAL:O	1:A:133:ILE:HG12	2.14	0.46
1:B:237:GLN:O	1:B:238:GLN:HB3	2.16	0.46
1:B:290:ILE:HB	1:B:291:PRO:CD	2.46	0.46
1:B:216:LEU:HD11	1:B:262:LEU:HD21	1.98	0.46
1:A:195:HIS:ND1	1:A:198:THR:HG22	2.31	0.46
1:B:319:THR:HG23	1:B:325:LYS:HA	1.98	0.46
1:B:244:GLN:NE2	1:B:245:LYS:N	2.64	0.46
1:A:96:TYR:O	1:A:100:HIS:HD2	1.99	0.46
1:B:237:GLN:N	1:B:237:GLN:NE2	2.57	0.46
1:A:308:MET:CE	1:B:41:ALA:CB	2.94	0.46
1:B:330:ASP:O	1:B:331:ASP:CB	2.64	0.45
1:A:175:TRP:O	1:A:176:SER:HB3	2.16	0.45
1:A:240:SER:O	1:A:241:ALA:HB3	2.15	0.45
1:B:240:SER:O	1:B:241:ALA:CB	2.65	0.45
1:A:65:HIS:ND1	1:A:337:VAL:O	2.49	0.45
1:B:136:TYR:CE1	1:B:225:GLN:HB3	2.52	0.45
1:B:6:GLY:HA3	1:B:9:PHE:CE1	2.52	0.45
1:B:170:PRO:HB2	1:B:171:PRO:HD3	1.98	0.45
1:A:237:GLN:CD	1:A:237:GLN:H	2.19	0.45
1:B:332:GLU:C	1:B:334:SER:H	2.20	0.45
1:B:287:PHE:CA	10:B:6026:ID3:H8	2.46	0.45
1:A:234:ALA:HB1	1:A:245:LYS:CE	2.44	0.45
1:B:298:SER:HA	1:B:301:TYR:CE2	2.51	0.45
1:B:70:THR:H	1:B:73:ASN:ND2	2.13	0.45
1:B:183:MET:HE3	1:B:289:THR:HG21	1.97	0.45
1:A:337:VAL:CG2	1:A:338:SER:N	2.80	0.45
1:A:315:ASN:ND2	1:A:332:GLU:HA	2.32	0.45
1:B:131:LEU:HD23	1:B:254:VAL:HG13	1.98	0.45
1:B:332:GLU:OE1	1:B:332:GLU:O	2.34	0.45
1:B:67:LYS:CB	1:B:337:VAL:HG13	2.47	0.45
1:A:326:ASN:O	1:A:328:LEU:HD22	2.17	0.45
1:A:85:PHE:O	1:A:89:GLY:N	2.49	0.45
1:A:87:VAL:O	1:A:91:PHE:HB2	2.17	0.44
1:B:231:LYS:HZ3	1:B:231:LYS:HB2	1.79	0.44
1:B:27:PRO:HB3	1:B:29:TYR:CE2	2.52	0.44
1:B:210:VAL:O	1:B:215:PRO:HD3	2.17	0.44
1:B:129:VAL:O	1:B:133:ILE:HG12	2.17	0.44
1:B:19:VAL:O	1:B:19:VAL:HG22	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:67:LYS:N	1:A:337:VAL:CG2	2.81	0.44
1:B:226:LEU:HB3	1:B:230:VAL:HG12	2.00	0.44
1:B:239:GLU:HG2	1:B:245:LYS:HZ2	1.83	0.44
1:B:119:LEU:HD13	1:B:123:ILE:HD12	1.99	0.44
1:B:336:THR:HB	1:B:342:THR:HG23	1.98	0.44
1:A:228:PHE:O	1:A:229:THR:C	2.55	0.44
1:B:67:LYS:CB	1:B:337:VAL:HG22	2.43	0.44
1:A:96:TYR:O	1:A:100:HIS:CD2	2.70	0.44
1:A:256:ILE:HG13	9:A:1508:HTG:H1'1	2.00	0.44
1:B:254:VAL:O	1:B:258:VAL:HG23	2.17	0.44
1:A:150:GLU:O	1:A:154:ILE:HG13	2.17	0.44
1:A:8:ASN:HA	1:A:8:ASN:HD22	1.53	0.44
1:A:247:GLU:HA	1:A:247:GLU:OE1	2.18	0.44
1:B:146:PHE:HZ	1:B:152:HIS:CD2	2.35	0.44
1:A:300:VAL:O	1:A:304:VAL:HG23	2.17	0.44
1:B:195:HIS:HB3	1:B:200:ASN:ND2	2.33	0.44
1:B:135:ARG:NH2	1:B:138:VAL:HG21	2.33	0.44
1:A:238:GLN:CG	1:A:239:GLU:N	2.78	0.43
1:B:336:THR:HB	1:B:342:THR:HG21	2.00	0.43
1:A:303:PRO:O	1:A:307:ILE:HG13	2.18	0.43
11:B:602:MAN:H61	11:B:603:BMA:O4	2.18	0.43
1:B:8:ASN:HA	1:B:8:ASN:HD22	1.53	0.43
1:B:9:PHE:HA	1:B:179:ILE:HD11	2.00	0.43
1:B:139:VAL:HG11	1:B:230:VAL:HG12	2.01	0.43
1:B:126:TRP:CH2	1:B:215:PRO:HG3	2.53	0.43
1:A:134:GLU:HA	1:A:148:PHE:CE2	2.53	0.43
1:A:321:LEU:C	1:A:323:CYS:H	2.21	0.43
1:A:248:LYS:HE3	1:A:248:LYS:HB2	1.83	0.43
1:A:66:LYS:CE	1:A:66:LYS:H	2.31	0.43
1:A:9:PHE:HA	1:A:179:ILE:HD11	2.00	0.43
1:B:141:LYS:C	1:B:143:MET:N	2.71	0.43
1:B:284:GLY:N	10:B:6026:ID3:H3A	2.34	0.43
1:B:161:TRP:O	1:B:165:LEU:CD2	2.67	0.43
1:B:293:PHE:HA	1:B:296:LYS:HD2	2.01	0.43
1:B:324:GLY:O	1:B:325:LYS:HG3	2.19	0.42
1:B:59:LEU:HD12	1:B:77:LEU:CD1	2.36	0.42
1:A:262:LEU:HB3	1:A:266:LEU:HD22	2.01	0.42
1:A:323:CYS:O	1:A:325:LYS:N	2.52	0.42
1:A:326:ASN:OD1	1:A:328:LEU:HD22	2.20	0.42
1:A:308:MET:HE3	1:B:99:LEU:HD21	2.01	0.42
1:B:67:LYS:H	1:B:337:VAL:CG1	2.32	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:340:THR:O	1:B:340:THR:HG23	2.19	0.42
1:A:238:GLN:HA	1:A:241:ALA:C	2.40	0.42
1:A:169:ALA:O	1:A:170:PRO:C	2.58	0.42
1:B:143:MET:CG	1:B:144:SER:H	2.30	0.42
1:A:182:GLY:HA2	1:A:285:PRO:O	2.19	0.42
1:B:325:LYS:O	1:B:326:ASN:C	2.58	0.42
1:A:68:LEU:N	1:A:337:VAL:HG21	2.34	0.42
1:B:77:LEU:O	1:B:81:VAL:HG23	2.19	0.42
1:A:96:TYR:HE2	1:A:104:VAL:CG2	2.32	0.42
1:B:135:ARG:CA	1:B:135:ARG:HE	2.30	0.42
1:B:141:LYS:O	1:B:143:MET:N	2.52	0.42
1:B:147:ARG:O	1:B:149:GLY:N	2.52	0.42
1:B:345:VAL:O	1:B:346:ALA:HB2	2.20	0.42
1:A:11:VAL:CG1	1:A:31:LEU:HD21	2.49	0.42
1:B:224:GLY:O	1:B:227:VAL:HG12	2.20	0.42
1:B:20:VAL:HA	1:B:30:TYR:CZ	2.54	0.42
1:A:332:GLU:O	1:A:332:GLU:OE1	2.38	0.42
1:B:131:LEU:O	1:B:135:ARG:HB2	2.20	0.42
1:B:90:GLY:O	1:B:94:THR:HG22	2.20	0.42
1:A:271:VAL:HG21	1:A:291:PRO:HG3	2.03	0.41
1:B:51:GLY:O	1:B:55:ASN:HB2	2.21	0.41
1:A:66:LYS:HD2	1:A:339:LYS:HA	2.01	0.41
1:B:266:LEU:N	1:B:267:PRO:CD	2.83	0.41
1:B:102:TYR:CE2	1:B:104:VAL:HA	2.55	0.41
1:A:255:ILE:O	1:A:259:ILE:HG12	2.20	0.41
1:A:101:GLY:O	1:A:102:TYR:HB3	2.21	0.41
1:B:239:GLU:HB3	1:B:244:GLN:OE1	2.21	0.41
1:B:183:MET:CE	1:B:289:THR:HG21	2.51	0.41
1:A:226:LEU:HD12	1:A:226:LEU:N	2.36	0.41
1:B:322:CYS:O	1:B:324:GLY:N	2.54	0.41
1:B:64:GLN:OE1	1:B:320:THR:HG23	2.21	0.41
1:B:135:ARG:HD3	1:B:251:THR:OG1	2.20	0.41
1:A:308:MET:HE2	1:B:41:ALA:HB3	2.02	0.41
1:A:195:HIS:HD1	1:A:198:THR:HG21	1.84	0.41
1:B:70:THR:HB	1:B:71:PRO:CD	2.51	0.41
1:B:57:LEU:HD21	1:B:321:LEU:HD21	2.03	0.41
1:B:67:LYS:HG2	1:B:337:VAL:HG22	2.04	0.40
1:B:238:GLN:O	1:B:245:LYS:HD2	2.21	0.40
10:B:6026:ID3:H7	10:B:6026:ID3:H19	1.82	0.40
1:A:66:LYS:CD	1:A:339:LYS:HA	2.52	0.40
1:A:57:LEU:O	1:A:57:LEU:HD23	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:44:MET:O	1:A:48:ILE:HG13	2.21	0.40
1:A:52:PHE:HB3	1:A:53:PRO:CD	2.51	0.40
1:A:262:LEU:O	1:A:266:LEU:HB2	2.22	0.40
1:B:146:PHE:CG	1:B:147:ARG:N	2.89	0.40
1:B:249:GLU:HG3	1:B:250:VAL:N	2.36	0.40
1:B:33:GLU:HB3	1:B:35:TRP:CD1	2.56	0.40
1:A:96:TYR:HE2	1:A:104:VAL:HG21	1.87	0.40
1:B:125:LEU:HB2	1:B:261:PHE:CZ	2.57	0.40
3:A:1296:RET:H8	3:A:1296:RET:H181	2.03	0.40
1:A:20:VAL:HG13	1:A:30:TYR:OH	2.22	0.40
1:A:68:LEU:O	1:A:69:ARG:HD3	2.21	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	347/349 (99%)	302 (87%)	34 (10%)	11 (3%)	5	8
1	B	347/349 (99%)	300 (86%)	32 (9%)	15 (4%)	3	4
All	All	694/698 (99%)	602 (87%)	66 (10%)	26 (4%)	4	5

All (26) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	229	THR
1	A	238	GLN
1	A	241	ALA
1	A	325	LYS
1	B	240	SER
1	B	241	ALA
1	B	332	GLU

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Mol	Chain	Res	Type
1	B	346	ALA
1	A	195	HIS
1	A	324	GLY
1	A	329	GLY
1	A	332	GLU
1	A	347	PRO
1	B	195	HIS
1	B	229	THR
1	B	239	GLU
1	B	323	CYS
1	B	324	GLY
1	B	329	GLY
1	B	340	THR
1	A	240	SER
1	B	236	GLN
1	B	235	ALA
1	B	331	ASP
1	A	338	SER
1	B	347	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	296/296 (100%)	276 (93%)	20 (7%)	20	39
1	B	296/296 (100%)	282 (95%)	14 (5%)	32	59
All	All	592/592 (100%)	558 (94%)	34 (6%)	25	49

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	ASN
1	A	66	LYS
1	A	76	LEU
1	A	79	LEU

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Mol	Chain	Res	Type
1	A	94	THR
1	A	104	VAL
1	A	119	LEU
1	A	131	LEU
1	A	135	ARG
1	A	143	MET
1	A	237	GLN
1	A	239	GLU
1	A	245	LYS
1	A	252	ARG
1	A	266	LEU
1	A	300	VAL
1	A	332	GLU
1	A	336	THR
1	A	341	GLU
1	A	344	GLN
1	B	8	ASN
1	B	50	LEU
1	B	79	LEU
1	B	94	THR
1	B	104	VAL
1	B	134	GLU
1	B	135	ARG
1	B	236	GLN
1	B	237	GLN
1	B	244	GLN
1	B	245	LYS
1	B	264	CYS
1	B	266	LEU
1	B	332	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	ASN
1	A	64	GLN
1	A	73	ASN
1	A	100	HIS
1	A	236	GLN
1	A	237	GLN
1	A	302	ASN
1	A	315	ASN

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Mol	Chain	Res	Type
1	B	8	ASN
1	B	73	ASN
1	B	100	HIS
1	B	151	ASN
1	B	237	GLN
1	B	244	GLN
1	B	279	GLN
1	B	302	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

11 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	BMA	A	503	2	11,11,12	0.49	0	14,15,17	0.47	0
2	NAG	A	504	2	14,14,15	0.61	0	15,19,21	0.82	0
2	NAG	A	505	1,2	14,14,15	0.58	0	15,19,21	0.74	0
5	NAG	A	704	5	14,14,15	0.47	0	15,19,21	0.78	1 (6%)
5	NAG	A	705	1,5	14,14,15	0.52	0	15,19,21	0.75	0
11	MAN	B	602	11	11,11,12	0.66	0	14,15,17	0.70	1 (7%)
11	BMA	B	603	11	11,11,12	0.61	0	14,15,17	0.50	0
11	NAG	B	604	11	14,14,15	0.54	0	15,19,21	0.77	1 (6%)
11	NAG	B	605	11,1	14,14,15	0.65	0	15,19,21	0.67	0
5	NAG	B	804	5	14,14,15	0.58	0	15,19,21	0.82	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	B	805	1,5	14,14,15	0.54	0	15,19,21	0.58	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
2	BMA	A	503	2	-	0/2/19/22	0/1/1/1
2	NAG	A	504	2	-	0/6/23/26	0/1/1/1
2	NAG	A	505	1,2	-	0/6/23/26	0/1/1/1
5	NAG	A	704	5	-	0/6/23/26	0/1/1/1
5	NAG	A	705	1,5	-	0/6/23/26	0/1/1/1
11	MAN	B	602	11	-	0/2/19/22	0/1/1/1
11	BMA	B	603	11	-	0/2/19/22	0/1/1/1
11	NAG	B	604	11	-	0/6/23/26	0/1/1/1
11	NAG	B	605	11,1	-	0/6/23/26	0/1/1/1
5	NAG	B	804	5	-	0/6/23/26	0/1/1/1
5	NAG	B	805	1,5	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	B	604	NAG	C2-N2-C7	-2.49	119.84	123.04
5	A	704	NAG	C2-N2-C7	-2.47	119.86	123.04
5	B	804	NAG	C2-N2-C7	-2.46	119.88	123.04
11	B	602	MAN	C1-O5-C5	2.09	114.90	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	504	NAG	1	0
2	A	505	NAG	1	0
11	B	602	MAN	1	0
11	B	603	BMA	1	0
11	B	604	NAG	1	0

5.6 Ligand geometry

Of 28 ligands modelled in this entry, 13 are monoatomic - leaving 15 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$
3	RET	A	1296	1	19,20,21	1.95	3 (15%)	27,27,28	1.66	8 (29%)
4	PLM	A	1322	1	16,16,17	0.40	0	14,15,17	0.52	0
4	PLM	A	1323	1	16,16,17	0.47	0	14,15,17	0.51	0
8	4E6	A	1410	-	15,15,15	2.01	1 (6%)	12,14,14	3.61	6 (50%)
9	HTG	A	1507	-	19,19,19	2.66	7 (36%)	22,24,24	2.56	1 (4%)
9	HTG	A	1508	-	19,19,19	2.31	7 (36%)	22,24,24	2.63	1 (4%)
10	ID3	A	6025	-	14,14,14	2.65	5 (35%)	20,20,20	1.76	4 (20%)
3	RET	B	1296	1	19,20,21	2.02	2 (10%)	27,27,28	1.68	9 (33%)
4	PLM	B	1322	1	16,16,17	0.44	0	14,15,17	0.44	0
4	PLM	B	1323	1	16,16,17	0.55	0	14,15,17	0.49	0
12	HTO	B	1401	-	9,9,9	1.72	1 (11%)	8,10,10	0.97	1 (12%)
8	4E6	B	1407	-	15,15,15	1.95	1 (6%)	12,14,14	3.49	5 (41%)
9	HTG	B	1506	-	19,19,19	2.53	7 (36%)	22,24,24	3.27	3 (13%)
9	HTG	B	1509	-	19,19,19	2.61	7 (36%)	22,24,24	2.94	2 (9%)
10	ID3	B	6026	-	14,14,14	2.32	3 (21%)	20,20,20	1.52	4 (20%)

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
3	RET	A	1296	1	-	0/13/30/31	0/1/1/1
4	PLM	A	1322	1	-	0/13/14/15	0/0/0/0
4	PLM	A	1323	1	-	0/13/14/15	0/0/0/0
8	4E6	A	1410	-	-	0/13/13/13	0/0/0/0
9	HTG	A	1507	-	-	0/10/30/30	0/1/1/1
9	HTG	A	1508	-	-	0/10/30/30	0/1/1/1
10	ID3	A	6025	-	-	0/5/22/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	RET	B	1296	1	-	0/13/30/31	0/1/1/1
4	PLM	B	1322	1	-	0/13/14/15	0/0/0/0
4	PLM	B	1323	1	-	0/13/14/15	0/0/0/0
12	HTO	B	1401	-	-	0/10/10/10	0/0/0/0
8	4E6	B	1407	-	-	0/13/13/13	0/0/0/0
9	HTG	B	1506	-	-	0/10/30/30	0/1/1/1
9	HTG	B	1509	-	-	0/10/30/30	0/1/1/1
10	ID3	B	6026	-	-	0/5/22/22	0/1/1/1

All (44) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1410	4E6	C12-C11	-6.93	1.23	1.44
8	B	1407	4E6	C12-C11	-6.80	1.24	1.44
3	A	1296	RET	C10-C9	2.05	1.38	1.35
10	B	6026	ID3	C5-C6	2.40	1.38	1.34
9	A	1508	HTG	C1-S1	2.63	1.84	1.80
9	B	1506	HTG	C4-C3	2.63	1.59	1.52
10	A	6025	ID3	C7-C6	2.74	1.55	1.45
9	A	1508	HTG	C4-C3	2.83	1.59	1.52
9	A	1508	HTG	O5-C5	2.93	1.51	1.44
10	A	6025	ID3	C8-C7	2.95	1.41	1.33
9	A	1508	HTG	C3-C2	2.96	1.60	1.52
9	B	1509	HTG	C4-C3	3.00	1.60	1.52
9	B	1506	HTG	C3-C2	3.04	1.60	1.52
10	B	6026	ID3	C7-C6	3.04	1.56	1.45
9	B	1509	HTG	C3-C2	3.04	1.60	1.52
9	A	1507	HTG	C4-C3	3.15	1.60	1.52
9	A	1507	HTG	O5-C5	3.16	1.52	1.44
9	A	1507	HTG	C1-C2	3.19	1.59	1.53
9	B	1506	HTG	C1-C2	3.23	1.59	1.53
9	A	1508	HTG	C1-C2	3.28	1.59	1.53
9	A	1507	HTG	C3-C2	3.28	1.61	1.52
9	B	1509	HTG	C1-S1	3.29	1.85	1.80
9	A	1508	HTG	C4-C5	3.44	1.60	1.53
9	B	1509	HTG	O5-C5	3.46	1.53	1.44
9	B	1506	HTG	C1-S1	3.47	1.86	1.80
9	B	1506	HTG	O5-C5	3.47	1.53	1.44
9	B	1509	HTG	C1-C2	3.60	1.60	1.53
10	A	6025	ID3	C18-C5	3.65	1.57	1.51
9	B	1506	HTG	C4-C5	3.67	1.60	1.53
9	A	1507	HTG	C1-S1	3.75	1.86	1.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	1507	HTG	C4-C5	3.97	1.61	1.53
9	B	1509	HTG	C4-C5	4.15	1.61	1.53
12	B	1401	HTO	C3-C2	4.18	1.64	1.52
10	A	6025	ID3	C5-C6	4.41	1.41	1.34
3	A	1296	RET	C1-C6	4.58	1.60	1.53
3	B	1296	RET	C1-C6	5.01	1.60	1.53
3	A	1296	RET	C5-C6	5.41	1.43	1.34
3	B	1296	RET	C5-C6	5.45	1.43	1.34
10	A	6025	ID3	O1-C9	6.11	1.40	1.24
10	B	6026	ID3	O1-C9	6.31	1.40	1.24
9	A	1508	HTG	O5-C1	6.45	1.53	1.42
9	B	1506	HTG	O5-C1	7.25	1.54	1.42
9	B	1509	HTG	O5-C1	7.29	1.54	1.42
9	A	1507	HTG	O5-C1	7.41	1.55	1.42

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	A	6025	ID3	C17-C1-C6	-5.74	101.30	110.30
8	A	1410	4E6	C13-C14-C15	-5.29	94.41	112.00
8	B	1407	4E6	C13-C14-C15	-4.99	95.40	112.00
10	B	6026	ID3	C17-C1-C6	-4.21	103.70	110.30
8	A	1410	4E6	C9-C10-C11	-2.90	109.71	126.01
10	A	6025	ID3	C18-C5-C6	-2.72	121.94	124.61
3	B	1296	RET	C8-C9-C10	-2.17	115.49	118.98
3	A	1296	RET	C8-C9-C10	-2.16	115.50	118.98
9	B	1506	HTG	O5-C1-C2	-2.16	107.25	110.19
10	B	6026	ID3	C17-C1-C2	-2.11	101.24	108.79
12	B	1401	HTO	O3-C3-C4	-2.08	104.72	109.35
3	B	1296	RET	C12-C13-C14	-2.08	112.15	118.92
3	B	1296	RET	C1-C6-C5	-2.08	119.61	122.66
3	B	1296	RET	C11-C10-C9	-2.07	124.21	127.20
3	A	1296	RET	C12-C13-C14	-2.04	112.29	118.92
3	A	1296	RET	C1-C6-C5	-2.01	119.71	122.66
9	B	1509	HTG	O5-C5-C6	2.03	111.49	106.36
8	B	1407	4E6	C5-C4-C3	2.06	125.17	114.53
10	B	6026	ID3	C2-C1-C6	2.07	113.64	110.36
10	A	6025	ID3	C17-C1-C16	2.14	115.24	108.37
9	B	1506	HTG	O5-C5-C6	2.15	111.80	106.36
3	B	1296	RET	C2-C1-C6	2.19	113.83	110.36
8	A	1410	4E6	C12-C11-C10	2.22	134.75	124.44
10	B	6026	ID3	C3-C4-C5	2.34	117.58	113.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1296	RET	C19-C9-C10	2.44	126.50	122.90
8	A	1410	4E6	C5-C4-C3	2.46	127.26	114.53
3	A	1296	RET	C2-C1-C6	2.54	114.38	110.36
10	A	6025	ID3	C16-C1-C6	2.54	114.28	110.30
3	A	1296	RET	C7-C8-C9	2.59	130.16	126.22
8	B	1407	4E6	C7-C8-C9	2.66	124.23	113.86
3	A	1296	RET	C19-C9-C10	2.73	126.93	122.90
3	B	1296	RET	C7-C8-C9	2.78	130.46	126.22
3	A	1296	RET	C20-C13-C12	3.14	123.32	118.10
3	B	1296	RET	C20-C13-C12	3.23	123.47	118.10
3	A	1296	RET	C18-C5-C6	3.54	128.08	124.61
3	B	1296	RET	C18-C5-C6	3.61	128.15	124.61
8	A	1410	4E6	C11-C12-C13	6.01	152.31	124.44
8	B	1407	4E6	C11-C12-C13	6.93	156.59	124.44
8	B	1407	4E6	C8-C9-C10	7.27	150.61	112.45
8	A	1410	4E6	C8-C9-C10	8.17	155.32	112.45
9	A	1507	HTG	C1'-S1-C1	11.37	115.98	100.30
9	A	1508	HTG	C1'-S1-C1	11.79	116.56	100.30
9	B	1509	HTG	C1'-S1-C1	13.27	118.59	100.30
9	B	1506	HTG	C1'-S1-C1	14.71	120.58	100.30

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1296	RET	1	0
8	A	1410	4E6	1	0
9	A	1508	HTG	1	0
10	A	6025	ID3	5	0
4	B	1323	PLM	2	0
12	B	1401	HTO	1	0
9	B	1506	HTG	2	0
9	B	1509	HTG	1	0
10	B	6026	ID3	9	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	348/349 (99%)	0.31	36 (10%) 9 5	42, 56, 138, 155	0
1	B	348/349 (99%)	0.68	49 (14%) 4 2	41, 62, 156, 161	0
All	All	696/698 (99%)	0.49	85 (12%) 5 3	41, 58, 151, 161	0

All (85) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	236	GLN	14.6
1	B	348	ALA	12.5
1	A	237	GLN	11.3
1	A	235	ALA	11.2
1	B	344	GLN	10.9
1	B	343	SER	10.9
1	B	346	ALA	10.4
1	B	141	LYS	10.2
1	B	234	ALA	9.9
1	B	230	VAL	9.5
1	B	233	ALA	9.3
1	B	235	ALA	9.2
1	B	345	VAL	8.7
1	B	142	PRO	8.7
1	B	229	THR	8.6
1	A	234	ALA	7.7
1	B	228	PHE	7.3
1	B	148	PHE	7.0
1	B	240	SER	6.5
1	B	333	ALA	6.4
1	B	146	PHE	6.3
1	A	240	SER	6.3
1	B	144	SER	6.3
1	B	347	PRO	6.2

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Mol	Chain	Res	Type	RSRZ
1	A	348	ALA	6.0
1	A	230	VAL	5.8
1	B	334	SER	5.8
1	A	146	PHE	5.8
1	A	144	SER	5.8
1	B	145	ASN	5.6
1	A	239	GLU	5.5
1	B	140	CYS	5.4
1	B	329	GLY	5.3
1	B	340	THR	5.2
1	B	237	GLN	5.1
1	A	143	MET	5.0
1	B	143	MET	4.9
1	B	335	THR	4.8
1	B	238	GLN	4.8
1	B	339	LYS	4.7
1	A	142	PRO	4.7
1	B	232	GLU	4.6
1	B	147	ARG	4.6
1	B	137	VAL	4.6
1	A	145	ASN	4.5
1	B	239	GLU	4.4
1	B	231	LYS	4.4
1	A	147	ARG	4.3
1	B	227	VAL	4.2
1	A	228	PHE	4.1
1	B	139	VAL	4.0
1	A	141	LYS	4.0
1	A	238	GLN	3.9
1	A	139	VAL	3.4
1	A	331	ASP	3.4
1	A	233	ALA	3.4
1	B	242	THR	3.4
1	A	340	THR	3.2
1	A	229	THR	3.1
1	B	236	GLN	3.1
1	B	337	VAL	3.1
1	A	245	LYS	3.0
1	A	332	GLU	2.9
1	A	333	ALA	2.8
1	B	217	ILE	2.8
1	B	66	LYS	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	338	SER	2.7
1	A	148	PHE	2.7
1	B	221	PHE	2.7
1	B	330	ASP	2.7
1	A	242	THR	2.6
1	B	133	ILE	2.5
1	A	244	GLN	2.5
1	A	227	VAL	2.5
1	A	339	LYS	2.4
1	B	342	THR	2.4
1	A	337	VAL	2.4
1	A	232	GLU	2.3
1	A	152	HIS	2.3
1	B	151	ASN	2.2
1	B	248	LYS	2.2
1	A	128	LEU	2.1
1	B	226	LEU	2.1
1	B	225	GLN	2.1
1	A	252	ARG	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	NAG	A	505	14/15	0.96	0.15	0.40	59,62,67,70	0
5	NAG	B	805	14/15	0.94	0.15	0.04	63,66,69,75	0
5	NAG	A	705	14/15	0.95	0.14	-0.41	63,68,72,78	0
11	NAG	B	605	14/15	0.96	0.12	-0.63	59,63,65,68	0
11	NAG	B	604	14/15	0.94	0.12	-0.67	72,78,84,92	0
2	NAG	A	504	14/15	0.94	0.13	-	76,80,86,92	0
5	NAG	B	804	14/15	0.90	0.23	-	81,86,87,88	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
11	MAN	B	602	11/12	0.83	0.18	-	111,113,113,114	0
11	BMA	B	603	11/12	0.81	0.19	-	99,105,106,109	0
2	BMA	A	503	11/12	0.85	0.19	-	99,103,106,106	0
5	NAG	A	704	14/15	0.85	0.34	-	85,91,95,96	0

6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	PLM	B	1323	17/18	0.52	0.77	21.21	115,121,122,122	0
10	ID3	B	6026	14/14	0.62	0.42	20.44	69,75,76,78	0
4	PLM	A	1322	17/18	0.80	0.49	12.98	88,92,102,103	0
9	HTG	B	1506	19/19	0.76	0.42	10.45	97,104,107,107	0
8	4E6	B	1407	16/16	0.69	0.43	9.86	83,91,97,97	0
12	HTO	B	1401	10/10	0.86	0.36	8.60	63,67,68,72	0
8	4E6	A	1410	16/16	0.68	0.40	8.22	81,83,85,85	0
4	PLM	A	1323	17/18	0.75	0.38	7.89	100,108,113,113	0
9	HTG	A	1507	19/19	0.82	0.35	7.00	95,102,105,105	0
4	PLM	B	1322	17/18	0.79	0.41	6.37	102,104,106,106	0
10	ID3	A	6025	14/14	0.71	0.26	5.23	64,70,72,72	0
7	ZN	A	962	1/1	0.97	0.22	2.97	120,120,120,120	1
3	RET	B	1296	20/21	0.95	0.22	2.55	43,49,51,51	0
3	RET	A	1296	20/21	0.96	0.19	1.58	43,45,48,49	0
9	HTG	A	1508	19/19	0.89	0.24	1.09	61,76,81,84	0
7	ZN	B	963	1/1	0.89	0.16	0.93	136,136,136,136	1
6	HG	A	901	1/1	0.99	0.17	0.77	73,73,73,73	1
6	HG	B	902	1/1	0.99	0.15	0.47	79,79,79,79	1
9	HTG	B	1509	19/19	0.82	0.28	0.46	101,102,105,105	0
6	HG	B	904	1/1	0.97	0.12	-0.88	98,98,98,98	1
6	HG	A	903	1/1	0.99	0.12	-0.95	82,82,82,82	1
6	HG	A	905	1/1	0.98	0.14	-0.99	81,81,81,81	1
6	HG	B	906	1/1	0.94	0.10	-1.58	121,121,121,121	1
7	ZN	A	957	1/1	0.96	0.18	-	53,53,53,53	1
7	ZN	A	2011	1/1	0.90	0.20	-	59,59,59,59	1
7	ZN	A	959	1/1	0.95	0.25	-	96,96,96,96	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
7	ZN	B	956	1/1	0.97	0.29	-	70,70,70,70	1
7	ZN	B	958	1/1	0.94	0.16	-	41,41,41,41	1

6.5 Other polymers [i](#)

There are no such residues in this entry.