



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 13, 2020 – 06:18 pm BST

PDB ID : 2Z87  
Title : Crystal structure of chondroitin polymerase from Escherichia coli strain K4 (K4CP) complexed with UDP-GalNAc and UDP  
Authors : Osawa, T.; Sugiura, N.; Shimada, H.; Hirooka, R.; Tsuji, A.; Kimura, M.; Kimata, K.; Kakuta, Y.  
Deposited on : 2007-09-03  
Resolution : 3.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

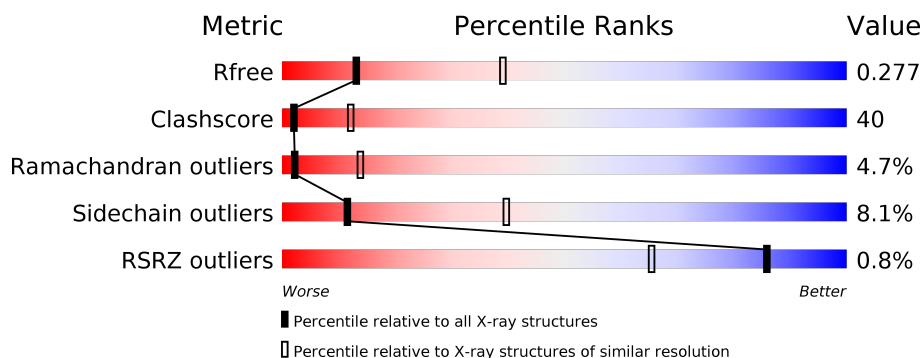
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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))
$R_{free}$	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. 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	624	<div> <div>%</div> <div> <div></div> <div>43%</div> <div>46%</div> <div>6%</div> <div>• •</div> </div> </div>
1	B	624	<div> <div>%</div> <div> <div></div> <div>36%</div> <div>50%</div> <div>8%</div> <div>5%</div> </div> </div>

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	UDP	A	684	-	-	X	-

## 2 Entry composition [i](#)

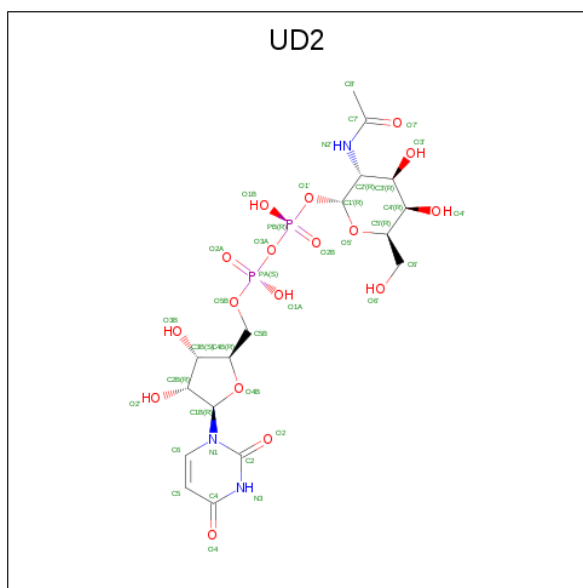
There are 5 unique types of molecules in this entry. The entry contains 9983 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Chondroitin synthase.

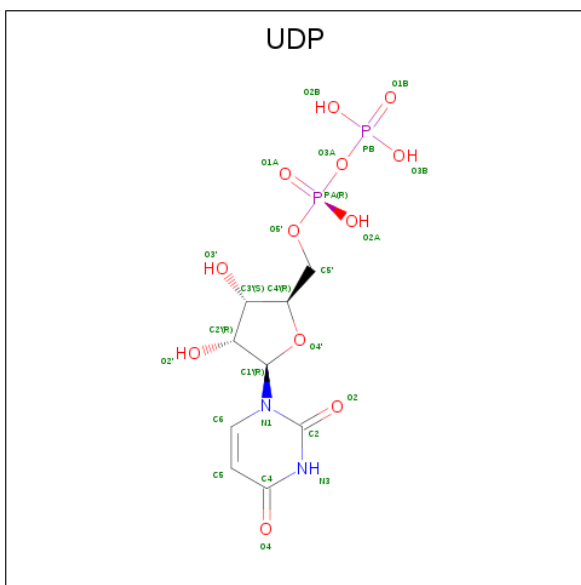
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	601	Total	C	N	O	S	25	0	0
			4894	3119	835	916	24			
1	B	591	Total	C	N	O	S	25	0	0
			4816	3071	822	899	24			

- Molecule 2 is URIDINE-DIPHOSPHATE-N-ACETYL GALACTOSAMINE (three-letter code: UD2) (formula:  $C_{17}H_{27}N_3O_{17}P_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			39	17	3	17	2		
2	B	1	Total	C	N	O	P	0	0
			39	17	3	17	2		

- Molecule 3 is URIDINE-5'-DIPHOSPHATE (three-letter code: UDP) (formula:  $C_9H_{14}N_2O_{12}P_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			25	9	2	12	2		
3	B	1	Total	C	N	O	P	0	0
			25	9	2	12	2		

- Molecule 4 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	2	Total	Mn	0	0
			2	2		
4	A	2	Total	Mn	0	0
			2	2		

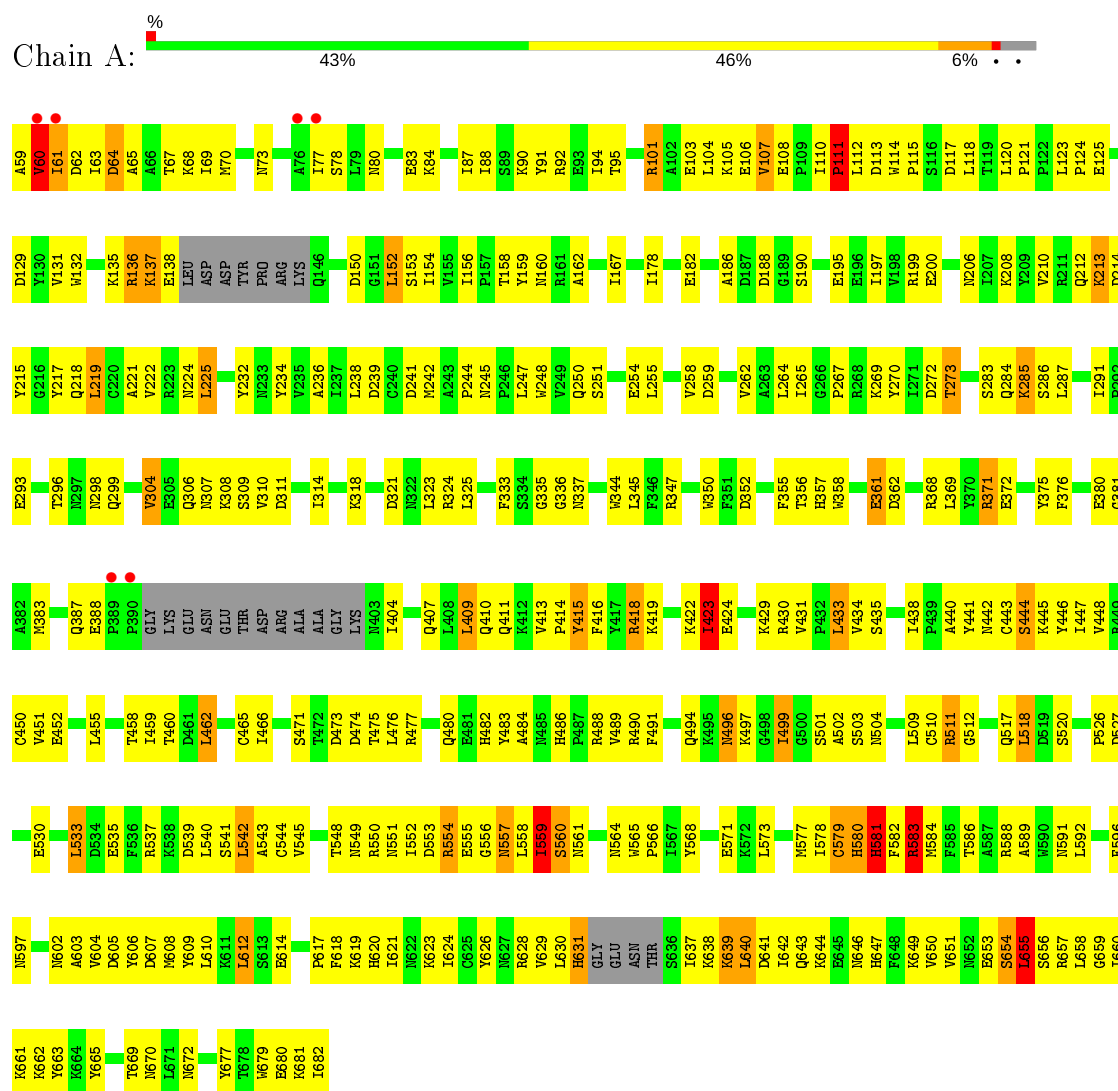
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	78	Total	O	0	0
			78	78		
5	B	63	Total	O	0	0
			63	63		

### 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 the various outlier classes 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: Chondroitin synthase



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Q643	RG44	BE45	RG46	RG47	RG48	RG49	RG50	RG51	RG52	RG53	RG54	RG55	RG56	RG57	RG58	RG59	RG60	RG61	RG62	RG63	RG64	RG65
S569	RG70	RG71	RG72	RG73	RG74	RG75	RG76	RG77	RG78	RG79	RG80	RG81	RG82	RG83	RG84	RG85	RG86	RG87	RG88	RG89	RG90	RG91
S503	RG94	RG95	RG96	RG97	RG98	RG99	RG100	RG101	RG102	RG103	RG104	RG105	RG106	RG107	RG108	RG109	RG110	RG111	RG112	RG113	RG114	RG115
R430	R431	R432	R433	R434	R435	R436	R437	R438	R439	R440	R441	R442	R443	R444	R445	R446	R447	R448	R449	R450	R451	R452
R504	R505	R506	R507	R508	R509	R510	R511	R512	R513	R514	R515	R516	R517	R518	R519	R520	R521	R522	R523	R524	R525	R526
S601	S602	S603	S604	S605	S606	S607	S608	S609	S610	S611	S612	S613	S614	S615	S616	S617	S618	S619	S620	S621	S622	S623
G616	G617	G618	G619	G620	G621	G622	G623	G624	G625	G626	G627	G628	G629	G630	G631	G632	G633	G634	G635	G636	G637	G638
L104	L105	L106	L107	L108	L109	L110	L111	L112	L113	L114	L115	L116	L117	L118	L119	L120	L121	L122	L123	L124	L125	L126
D129	D130	D131	D132	D133	D134	D135	D136	D137	D138	D139	D140	D141	D142	D143	D144	D145	D146	D147	D148	D149	D150	D151
Y209	Y210	Y211	Y212	Y213	Y214	Y215	Y216	Y217	Y218	Y219	Y220	Y221	Y222	Y223	Y224	Y225	Y226	Y227	Y228	Y229	Y230	Y231
L294	L295	L296	L297	L298	L299	L300	L301	L302	L303	L304	L305	L306	L307	L308	L309	L310	L311	L312	L313	L314	L315	L316
R363	R364	R365	R366	R367	R368	R369	R370	R371	R372	R373	R374	R375	R376	R377	R378	R379	R380	R381	R382	R383	R384	R385
R386	R387	R388	R389	R390	R391	R392	R393	R394	R395	R396	R397	R398	R399	R400	R401	R402	R403	R404	R405	R406	R407	R408
R480	R481	R482	R483	R484	R485	R486	R487	R488	R489	R490	R491	R492	R493	R494	R495	R496	R497	R498	R499	R500	R501	R502
S549	S550	S551	S552	S553	S554	S555	S556	S557	S558	S559	S560	S561	S562	S563	S564	S565	S566	S567	S568	S569	S570	S571
G616	G617	G618	G619	G620	G621	G622	G623	G624	G625	G626	G627	G628	G629	G630	G631	G632	G633	G634	G635	G636	G637	G638
L104	L105	L106	L107	L108	L109	L110	L111	L112	L113	L114	L115	L116	L117	L118	L119	L120	L121	L122	L123	L124	L125	L126

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	82.37Å 109.28Å 85.58Å 90.00° 103.47° 90.00°	Depositor
Resolution (Å)	19.96 – 3.00 46.94 – 2.76	Depositor EDS
% Data completeness (in resolution range)	93.3 (19.96-3.00) 80.8 (46.94-2.76)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.73 (at 2.77Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.199 , 0.283 0.198 , 0.277	Depositor DCC
$R_{free}$ test set	1440 reflections (4.39%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	47.3	Xtriage
Anisotropy	0.565	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 61.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.026 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	9983	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.65% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

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

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: UD2, UDP, MN

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	0.74	15/4998 (0.3%)	0.73	5/6761 (0.1%)
1	B	0.72	15/4919 (0.3%)	0.69	4/6651 (0.1%)
All	All	0.73	30/9917 (0.3%)	0.71	9/13412 (0.1%)

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
1	A	0	1
1	B	0	2
All	All	0	3

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	582	PHE	CE1-CZ	-15.79	1.07	1.37
1	A	583	ARG	CZ-NH1	-14.93	1.13	1.33
1	A	582	PHE	CE1-CZ	-14.83	1.09	1.37
1	A	582	PHE	CE2-CZ	-14.67	1.09	1.37
1	B	582	PHE	CE2-CZ	-14.01	1.10	1.37
1	B	581	HIS	C-O	-12.98	0.98	1.23
1	B	583	ARG	CZ-NH1	-12.93	1.16	1.33
1	B	582	PHE	CG-CD2	-12.85	1.19	1.38
1	A	581	HIS	C-O	-12.63	0.99	1.23
1	A	582	PHE	CG-CD2	-12.31	1.20	1.38
1	A	582	PHE	CD2-CE2	-12.24	1.14	1.39
1	A	582	PHE	CD1-CE1	-11.79	1.15	1.39
1	A	583	ARG	C-O	-11.07	1.02	1.23
1	B	582	PHE	CD2-CE2	-10.81	1.17	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	582	PHE	CG-CD1	-10.66	1.22	1.38
1	B	583	ARG	C-O	-9.85	1.04	1.23
1	A	582	PHE	C-O	-9.80	1.04	1.23
1	B	583	ARG	CZ-NH2	-9.33	1.21	1.33
1	A	583	ARG	CZ-NH2	-9.16	1.21	1.33
1	A	582	PHE	CG-CD1	-8.93	1.25	1.38
1	B	582	PHE	C-O	-8.43	1.07	1.23
1	A	581	HIS	CA-C	-7.36	1.33	1.52
1	B	582	PHE	CD1-CE1	-7.08	1.25	1.39
1	A	582	PHE	CA-C	-6.89	1.35	1.52
1	B	581	HIS	CA-C	-6.85	1.35	1.52
1	A	581	HIS	CA-CB	-6.66	1.39	1.53
1	B	583	ARG	CA-C	-6.25	1.36	1.52
1	B	583	ARG	NE-CZ	-5.74	1.25	1.33
1	A	583	ARG	NE-CZ	-5.68	1.25	1.33
1	B	581	HIS	CA-CB	-5.06	1.42	1.53

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	583	ARG	NE-CZ-NH2	15.13	127.86	120.30
1	A	583	ARG	NE-CZ-NH1	-9.31	115.64	120.30
1	B	583	ARG	NE-CZ-NH1	-6.25	117.17	120.30
1	A	582	PHE	N-CA-C	-5.64	95.78	111.00
1	A	581	HIS	CA-C-N	5.42	129.11	117.20
1	B	238	LEU	CA-CB-CG	5.32	127.53	115.30
1	A	581	HIS	C-N-CA	5.09	134.44	121.70
1	B	582	PHE	N-CA-C	-5.04	97.38	111.00
1	B	583	ARG	N-CA-C	-5.01	97.48	111.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	581	HIS	Peptide
1	B	581	HIS	Peptide
1	B	582	PHE	Peptide

## 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	4894	0	4853	361	0
1	B	4816	0	4775	422	0
2	A	39	0	25	0	0
2	B	39	0	25	1	0
3	A	25	0	11	8	0
3	B	25	0	11	1	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
5	A	78	0	0	47	0
5	B	63	0	0	26	0
All	All	9983	0	9700	782	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 40.

All (782) 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:539:ASP:HB3	1:A:542:LEU:HD22	1.20	1.18
1:A:273:THR:HG21	1:A:387:GLN:HE21	0.99	1.07
3:A:684:UDP:H5'1	3:A:684:UDP:O1B	1.54	1.05
1:B:423:ILE:HD12	1:B:423:ILE:H	1.20	1.04
1:B:466:ILE:HA	5:B:709:HOH:O	1.59	1.01
1:B:549:ASN:HB3	1:B:626:TYR:HB3	1.42	0.98
1:B:107:VAL:HG12	1:B:108:GLU:H	1.27	0.98
1:B:90:LYS:HE3	1:B:94:ILE:HD12	1.47	0.96
1:A:418:ARG:HH11	1:A:418:ARG:HB2	1.27	0.96
1:A:411:GLN:HE22	1:A:430:ARG:H	1.05	0.95
1:A:273:THR:HG21	1:A:387:GLN:NE2	1.81	0.94
1:B:107:VAL:HG11	1:B:565:TRP:CH2	2.01	0.94
1:B:555:GLU:HB3	5:B:718:HOH:O	1.67	0.94
1:A:605:ASP:HB3	5:A:711:HOH:O	1.67	0.93
1:B:186:ALA:HB1	1:B:222:VAL:HG22	1.51	0.93
1:A:649:LYS:HD3	5:A:757:HOH:O	1.67	0.93
1:A:423:ILE:HD12	1:A:423:ILE:H	1.34	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:433:LEU:HD13	1:B:434:VAL:HG23	1.48	0.91
1:A:586:THR:HG22	1:A:589:ALA:H	1.32	0.91
1:B:273:THR:HG22	5:B:742:HOH:O	1.72	0.89
1:B:646:ASN:O	1:B:650:VAL:HG23	1.73	0.88
1:B:420:LYS:HE3	1:B:537:ARG:HH22	1.37	0.88
1:A:557:ASN:HD22	1:A:557:ASN:N	1.72	0.87
1:B:453:SER:HB3	5:B:731:HOH:O	1.75	0.87
1:A:554:ARG:HD3	1:A:554:ARG:H	1.40	0.85
1:A:206:ASN:HB3	5:A:706:HOH:O	1.74	0.85
1:B:120:LEU:HD12	5:B:738:HOH:O	1.76	0.84
1:B:411:GLN:NE2	1:B:430:ARG:H	1.75	0.84
1:B:104:LEU:HA	5:B:705:HOH:O	1.78	0.84
1:B:605:ASP:HB3	5:B:693:HOH:O	1.77	0.84
1:A:267:PRO:HG2	1:A:383:MET:HE2	1.59	0.83
1:B:414:PRO:HB2	1:B:433:LEU:HD23	1.59	0.83
1:A:411:GLN:NE2	1:A:430:ARG:H	1.78	0.82
1:B:177:THR:HA	1:B:250:GLN:HE21	1.45	0.81
1:A:643:GLN:HG3	1:A:644:LYS:N	1.94	0.81
1:A:639:LYS:HD3	1:B:639:LYS:HZ2	1.46	0.81
1:B:660:ILE:HD11	5:B:738:HOH:O	1.81	0.81
1:B:161:ARG:HH21	1:B:392:LYS:HE2	1.45	0.80
1:A:549:ASN:HB3	1:A:626:TYR:HB3	1.63	0.80
3:A:684:UDP:C5'	3:A:684:UDP:PB	2.68	0.80
1:A:433:LEU:HD13	1:A:434:VAL:HG23	1.63	0.79
1:B:411:GLN:HE22	1:B:430:ARG:H	1.29	0.79
1:B:414:PRO:HA	1:B:418:ARG:HB2	1.64	0.79
1:B:107:VAL:HG12	1:B:108:GLU:N	1.96	0.79
1:A:640:LEU:O	1:A:643:GLN:HG2	1.83	0.78
1:A:208:LYS:HE3	1:B:212:GLN:HB3	1.64	0.78
3:A:684:UDP:C5'	3:A:684:UDP:O1B	2.30	0.78
1:A:264:LEU:HD21	5:A:691:HOH:O	1.81	0.78
1:B:120:LEU:HA	5:B:738:HOH:O	1.84	0.78
1:B:130:TYR:CE2	1:B:377:ARG:HD2	2.18	0.78
1:A:375:TYR:HA	5:A:748:HOH:O	1.83	0.77
1:A:539:ASP:HB3	1:A:542:LEU:CD2	2.08	0.76
1:A:105:LYS:HB2	1:A:566:PRO:HG2	1.67	0.76
1:B:219:LEU:O	1:B:222:VAL:HG12	1.86	0.76
1:B:559:ILE:HG22	1:B:560:SER:N	2.01	0.75
1:A:245:ASN:ND2	1:A:247:LEU:H	1.83	0.75
1:A:418:ARG:HH21	1:A:429:LYS:HB3	1.52	0.75
1:B:606:TYR:O	1:B:610:LEU:HB2	1.86	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:438:ILE:HG23	1:A:518:LEU:O	1.86	0.75
1:A:59:ALA:O	1:A:60:VAL:HG13	1.87	0.75
1:B:653:GLU:OE2	1:B:665:TYR:HB3	1.87	0.75
1:B:497:LYS:NZ	1:B:497:LYS:HB2	2.02	0.74
1:A:517:GLN:HE22	1:A:583:ARG:HH11	1.35	0.74
1:A:323:LEU:HD12	5:A:742:HOH:O	1.87	0.74
1:A:443:CYS:CB	1:A:520:SER:HB2	2.18	0.74
1:B:294:ILE:HD12	1:B:295:ILE:N	2.02	0.74
1:B:418:ARG:HE	1:B:429:LYS:HG3	1.52	0.74
1:A:612:LEU:HB3	1:A:618:PHE:HZ	1.53	0.74
1:B:152:LEU:HG	1:B:253:MET:SD	2.27	0.73
1:B:410:GLN:NE2	1:B:418:ARG:HA	2.03	0.73
1:A:612:LEU:HG	5:A:737:HOH:O	1.87	0.73
1:A:91:TYR:CE2	1:A:423:ILE:HG12	2.22	0.73
1:A:662:LYS:HG3	1:A:663:TYR:HD1	1.54	0.73
1:A:352:ASP:HB3	1:A:355:PHE:CD2	2.24	0.72
1:A:423:ILE:N	1:A:423:ILE:HD12	2.03	0.72
1:B:111:PRO:HG3	1:B:572:LYS:HD2	1.70	0.72
1:B:79:LEU:HD21	1:B:83:GLU:HB3	1.70	0.72
1:A:418:ARG:HE	1:A:429:LYS:HG3	1.54	0.71
1:B:115:PRO:HB2	1:B:118:LEU:HB2	1.72	0.71
1:B:61:ILE:HD13	1:B:62:ASP:N	2.04	0.71
1:B:656:SER:HA	5:B:685:HOH:O	1.91	0.71
1:A:610:LEU:HD22	5:A:732:HOH:O	1.89	0.70
1:B:529:VAL:O	1:B:533:LEU:HB2	1.92	0.70
1:A:649:LYS:O	1:A:653:GLU:HG2	1.91	0.70
1:A:557:ASN:ND2	1:A:557:ASN:N	2.39	0.70
1:A:418:ARG:CZ	5:A:738:HOH:O	2.39	0.70
1:B:655:LEU:CD2	1:B:658:LEU:HG	2.22	0.70
1:A:152:LEU:HD21	1:A:236:ALA:HB2	1.74	0.70
3:A:684:UDP:C5'	3:A:684:UDP:O2B	2.39	0.70
1:B:288:ILE:HG13	1:B:385:TYR:CD2	2.27	0.70
1:B:433:LEU:CD1	1:B:434:VAL:HG23	2.21	0.70
1:B:649:LYS:HG3	5:B:706:HOH:O	1.91	0.70
1:B:255:LEU:O	1:B:258:VAL:HG22	1.92	0.70
1:B:360:GLY:HA2	1:B:409:LEU:HD11	1.74	0.69
1:A:643:GLN:HG3	1:A:644:LYS:H	1.56	0.69
1:B:517:GLN:HE22	1:B:583:ARG:HH11	1.37	0.69
1:B:499:ILE:HD11	1:B:604:VAL:CB	2.23	0.69
1:A:656:SER:HA	5:A:722:HOH:O	1.92	0.69
1:B:136:ARG:O	1:B:137:LYS:HG2	1.93	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:404:ILE:HD12	1:A:407:GLN:NE2	2.08	0.69
1:A:309:SER:HB2	5:A:753:HOH:O	1.92	0.68
1:A:559:ILE:O	1:A:559:ILE:HG13	1.93	0.68
1:B:607:ASP:O	1:B:611:LYS:HG3	1.93	0.68
1:A:612:LEU:HB3	1:A:618:PHE:CZ	2.28	0.68
1:B:360:GLY:CA	1:B:409:LEU:HD11	2.24	0.68
1:A:323:LEU:HB2	5:A:742:HOH:O	1.92	0.68
1:A:414:PRO:HA	1:A:418:ARG:NH1	2.09	0.68
1:A:78:SER:HA	5:A:751:HOH:O	1.94	0.68
1:A:162:ALA:HB1	1:A:197:ILE:HG13	1.75	0.68
1:A:490:ARG:HH12	1:A:509:LEU:HD22	1.59	0.68
1:A:573:LEU:HD12	5:A:715:HOH:O	1.94	0.68
1:B:572:LYS:CG	1:B:578:ILE:HD13	2.24	0.68
1:B:669:THR:HG23	1:B:671:LEU:H	1.57	0.68
1:A:610:LEU:HB2	5:A:732:HOH:O	1.93	0.68
1:A:443:CYS:SG	1:A:520:SER:HB2	2.34	0.67
1:B:504:ASN:ND2	1:B:596:PHE:HB2	2.10	0.67
1:A:61:ILE:HD13	1:A:62:ASP:N	2.10	0.67
1:A:643:GLN:O	1:A:646:ASN:HB3	1.93	0.66
3:A:684:UDP:H5'1	3:A:684:UDP:PB	2.34	0.66
1:B:550:ARG:HA	1:B:562:GLY:H	1.60	0.66
1:A:137:LYS:HG3	1:A:138:GLU:H	1.59	0.66
1:A:154:ILE:HD13	1:A:248:TRP:HZ3	1.60	0.66
1:B:217:TYR:CD2	1:B:357:HIS:HA	2.31	0.66
1:A:553:ASP:HB3	1:A:557:ASN:N	2.11	0.66
1:B:357:HIS:ND1	1:B:357:HIS:O	2.27	0.66
1:B:669:THR:HG23	1:B:671:LEU:HG	1.77	0.66
1:A:84:LYS:O	1:A:88:ILE:HG13	1.96	0.65
1:B:536:PHE:CE1	1:B:545:VAL:HG22	2.31	0.65
1:B:161:ARG:HE	1:B:392:LYS:HE2	1.61	0.65
1:B:69:ILE:HG22	1:B:73:ASN:HD21	1.61	0.65
1:B:552:ILE:HD13	1:B:558:LEU:HA	1.77	0.65
1:A:434:VAL:HB	1:A:462:LEU:HB2	1.79	0.65
1:A:553:ASP:HB3	1:A:557:ASN:H	1.61	0.65
1:A:69:ILE:HD11	1:A:88:ILE:HA	1.79	0.65
1:A:123:LEU:HB3	1:A:124:PRO:HD2	1.79	0.65
1:B:462:LEU:HD12	1:B:529:VAL:HG11	1.79	0.64
1:B:91:TYR:HA	1:B:94:ILE:HG22	1.77	0.64
1:A:238:LEU:HD13	1:A:248:TRP:CZ2	2.33	0.64
1:A:682:ILE:HD11	5:A:710:HOH:O	1.96	0.64
1:B:504:ASN:O	1:B:508:ARG:HB2	1.96	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:458:THR:OG1	1:A:530:GLU:HB2	1.96	0.64
1:A:131:VAL:HG23	1:A:324:ARG:HD2	1.78	0.64
1:A:414:PRO:HB3	5:A:738:HOH:O	1.97	0.64
1:B:476:LEU:O	1:B:480:GLN:HG3	1.98	0.64
1:A:121:PRO:HD2	1:A:658:LEU:HD22	1.79	0.64
1:A:416:PHE:N	5:A:736:HOH:O	2.31	0.64
1:A:527:ASP:HA	5:A:761:HOH:O	1.98	0.64
1:B:286:SER:C	5:B:729:HOH:O	2.36	0.64
1:B:358:TRP:O	1:B:359:GLY:O	2.16	0.64
1:A:620:HIS:CD2	1:A:621:ILE:O	2.50	0.64
1:A:105:LYS:HB2	1:A:566:PRO:CG	2.28	0.63
1:A:376:PHE:HD2	5:A:748:HOH:O	1.80	0.63
1:B:499:ILE:HD11	1:B:604:VAL:HB	1.79	0.63
1:B:565:TRP:NE1	1:B:572:LYS:HG2	2.14	0.63
1:B:549:ASN:HA	1:B:624:ILE:HG23	1.81	0.63
1:B:669:THR:CG2	1:B:671:LEU:H	2.11	0.63
1:B:410:GLN:HE22	1:B:418:ARG:HA	1.63	0.63
1:A:411:GLN:HB2	5:A:747:HOH:O	1.98	0.62
1:A:273:THR:HB	1:A:387:GLN:HG2	1.80	0.62
1:A:218:GLN:HB3	1:A:221:ALA:HB3	1.80	0.62
1:A:551:ASN:O	1:A:552:ILE:HD13	2.00	0.62
1:A:551:ASN:HB2	1:A:560:SER:HB3	1.82	0.62
1:A:352:ASP:HB3	1:A:355:PHE:HD2	1.65	0.62
1:A:483:TYR:CD1	1:A:489:VAL:HG21	2.34	0.62
1:B:586:THR:HG22	1:B:588:ARG:N	2.15	0.62
1:B:107:VAL:CG1	1:B:108:GLU:H	2.09	0.61
1:B:266:GLY:HA3	1:B:337:ASN:ND2	2.15	0.61
1:B:410:GLN:HE21	1:B:418:ARG:HD3	1.63	0.61
1:B:528:ALA:HB2	1:B:625:CYS:HB3	1.82	0.61
1:A:69:ILE:HG22	1:A:73:ASN:HD21	1.65	0.61
1:A:435:SER:CB	1:A:510:CYS:HB3	2.31	0.61
1:B:423:ILE:H	1:B:423:ILE:CD1	1.95	0.61
1:B:90:LYS:O	1:B:94:ILE:HB	2.01	0.61
1:B:191:LYS:HE2	5:B:708:HOH:O	2.00	0.61
1:B:215:TYR:CE2	1:B:218:GLN:HG3	2.35	0.61
1:A:628:ARG:HG2	1:A:629:VAL:O	2.01	0.61
1:A:92:ARG:HH11	1:A:92:ARG:HG3	1.66	0.61
1:B:416:PHE:HD2	1:B:417:TYR:CE1	2.18	0.61
1:B:418:ARG:HB2	1:B:418:ARG:HH11	1.64	0.60
1:B:494:GLN:NE2	1:B:497:LYS:NZ	2.49	0.60
3:A:684:UDP:H5'2	3:A:684:UDP:O2B	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:361:GLU:OE2	1:A:362:ASP:N	2.35	0.60
1:B:161:ARG:NH2	1:B:392:LYS:HE2	2.15	0.60
1:A:418:ARG:NH2	5:A:738:HOH:O	2.34	0.60
1:A:418:ARG:HH21	1:A:429:LYS:CB	2.14	0.60
1:A:550:ARG:CD	1:A:552:ILE:HD11	2.32	0.60
1:B:499:ILE:HD11	1:B:604:VAL:HG11	1.84	0.60
1:B:458:THR:OG1	1:B:530:GLU:HB2	2.02	0.59
1:B:79:LEU:HD22	1:B:84:LYS:HB2	1.83	0.59
1:B:577:MET:CE	1:B:579:CYS:HB3	2.32	0.59
1:A:418:ARG:HH11	1:A:418:ARG:CB	2.10	0.59
1:B:91:TYR:O	1:B:94:ILE:HG22	2.03	0.59
1:A:224:ASN:OD1	1:A:350:TRP:HB3	2.02	0.59
1:A:60:VAL:HG23	1:A:61:ILE:H	1.66	0.59
1:A:548:THR:HG22	1:A:623:LYS:O	2.01	0.59
1:A:646:ASN:O	1:A:650:VAL:HG23	2.01	0.59
1:A:91:TYR:HE2	1:A:423:ILE:HG12	1.66	0.59
1:B:539:ASP:HB3	1:B:542:LEU:HD22	1.83	0.59
1:B:167:ILE:HG21	1:B:387:GLN:NE2	2.18	0.59
1:A:304:VAL:HB	5:A:762:HOH:O	2.03	0.59
1:A:368:ARG:O	1:A:372:GLU:HG2	2.02	0.59
1:A:64:ASP:O	1:A:67:THR:HG22	2.01	0.59
1:B:655:LEU:HD21	1:B:658:LEU:HG	1.83	0.59
1:A:308:LYS:O	1:A:310:VAL:HG13	2.03	0.59
1:A:578:ILE:HB	5:A:724:HOH:O	2.01	0.59
1:B:294:ILE:HD12	1:B:295:ILE:C	2.23	0.59
1:A:558:LEU:HD12	1:A:559:ILE:H	1.67	0.58
1:B:549:ASN:CB	1:B:626:TYR:HB3	2.24	0.58
1:B:371:ARG:NH2	1:B:512:GLY:O	2.36	0.58
1:A:131:VAL:CG2	1:A:324:ARG:HD2	2.34	0.58
1:A:554:ARG:HA	1:A:629:VAL:HG13	1.85	0.58
1:B:289:ASN:HB2	5:B:729:HOH:O	2.03	0.58
1:B:576:ALA:O	1:B:578:ILE:HG23	2.03	0.58
1:A:114:TRP:CZ2	1:A:571:GLU:HG3	2.39	0.58
1:B:511:ARG:HH11	1:B:511:ARG:HG3	1.69	0.58
1:B:542:LEU:HA	1:B:617:PRO:HG2	1.84	0.58
1:A:299:GLN:HE21	1:A:304:VAL:HG22	1.69	0.58
1:A:409:LEU:O	1:A:411:GLN:N	2.36	0.58
1:A:517:GLN:HE22	1:A:583:ARG:NH1	2.01	0.58
1:B:65:ALA:O	1:B:68:LYS:N	2.37	0.58
1:A:124:PRO:HD3	1:A:132:TRP:CE2	2.38	0.58
1:B:63:ILE:HG13	1:B:64:ASP:N	2.17	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:494:GLN:NE2	1:B:497:LYS:HZ2	2.01	0.58
1:B:358:TRP:CD1	2:B:683:UD2:H6'1	2.39	0.58
1:A:423:ILE:CD1	1:A:423:ILE:H	2.05	0.57
1:A:577:MET:HA	5:A:715:HOH:O	2.03	0.57
1:B:466:ILE:N	1:B:466:ILE:HD12	2.19	0.57
1:B:160:ASN:HB3	1:B:192:GLU:OE2	2.04	0.57
1:A:639:LYS:HD3	1:B:639:LYS:NZ	2.17	0.57
1:A:69:ILE:HG22	1:A:73:ASN:ND2	2.19	0.57
1:B:509:LEU:HD23	1:B:509:LEU:O	2.04	0.57
1:B:245:ASN:ND2	1:B:247:LEU:H	2.02	0.57
1:A:559:ILE:O	1:A:560:SER:HB2	2.03	0.57
1:B:328:THR:O	1:B:331:ARG:HG3	2.04	0.57
1:A:269:LYS:HG3	1:A:383:MET:SD	2.45	0.57
1:B:499:ILE:HD11	1:B:604:VAL:CG1	2.35	0.57
1:A:642:ILE:O	1:A:646:ASN:HB2	2.05	0.57
1:B:265:ILE:HD13	1:B:332:PHE:O	2.04	0.57
1:B:363:ASN:HD22	1:B:409:LEU:HD23	1.70	0.57
1:B:67:THR:HG23	1:B:68:LYS:N	2.20	0.57
1:A:458:THR:HG1	1:A:530:GLU:HB2	1.68	0.57
1:A:68:LYS:HG2	1:A:87:ILE:HD13	1.85	0.57
1:A:371:ARG:NH2	1:A:512:GLY:O	2.38	0.57
1:B:611:LYS:HG2	1:B:657:ARG:NH1	2.19	0.57
1:B:224:ASN:OD1	1:B:350:TRP:HB3	2.05	0.56
1:B:552:ILE:HG22	1:B:553:ASP:N	2.19	0.56
1:A:267:PRO:HG2	1:A:383:MET:CE	2.34	0.56
1:A:186:ALA:HB1	1:A:222:VAL:HG22	1.86	0.56
1:A:637:ILE:O	1:A:640:LEU:HD13	2.05	0.56
1:B:492:ILE:HG12	1:B:493:SER:N	2.20	0.56
1:A:137:LYS:O	1:A:138:GLU:HB3	2.04	0.56
1:A:565:TRP:N	1:A:580:HIS:NE2	2.52	0.56
1:B:159:TYR:O	1:B:160:ASN:HB2	2.05	0.56
1:B:388:GLU:OE2	1:B:389:PRO:HD2	2.06	0.56
1:B:87:ILE:O	1:B:90:LYS:HB3	2.04	0.56
1:A:212:GLN:NE2	5:A:744:HOH:O	2.38	0.56
1:A:273:THR:CG2	1:A:387:GLN:HE21	1.94	0.56
1:A:443:CYS:HB3	1:A:520:SER:HB2	1.87	0.56
1:A:662:LYS:HG3	1:A:663:TYR:CD1	2.38	0.56
1:B:177:THR:HA	1:B:250:GLN:NE2	2.18	0.56
1:B:638:LYS:O	1:B:642:ILE:HG12	2.06	0.56
1:A:649:LYS:HD2	1:A:665:TYR:HE1	1.70	0.56
1:B:420:LYS:CE	1:B:537:ARG:HH22	2.15	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:620:HIS:HD2	1:A:621:ILE:N	2.03	0.56
1:A:639:LYS:O	1:A:639:LYS:HE2	2.05	0.56
1:B:411:GLN:HE22	1:B:430:ARG:N	2.02	0.56
1:B:544:CYS:HB3	1:B:618:PHE:CE1	2.41	0.56
1:B:586:THR:HG22	1:B:588:ARG:H	1.70	0.56
1:B:69:ILE:HG22	1:B:73:ASN:ND2	2.21	0.56
1:B:131:VAL:CG2	1:B:324:ARG:HD2	2.36	0.56
1:B:215:TYR:CZ	1:B:218:GLN:HG3	2.40	0.56
1:B:167:ILE:HB	1:B:387:GLN:HE22	1.70	0.56
1:A:654:SER:C	1:A:656:SER:H	2.09	0.55
1:B:668:LEU:HG	1:B:668:LEU:O	2.05	0.55
1:A:568:TYR:CD2	1:A:618:PHE:HB2	2.41	0.55
1:B:185:VAL:HG21	1:B:198:VAL:HG22	1.88	0.55
1:A:213:LYS:HE3	1:B:202:GLU:O	2.07	0.55
1:B:218:GLN:HB3	1:B:221:ALA:HB3	1.89	0.55
1:B:255:LEU:CD1	1:B:379:VAL:HG22	2.36	0.55
1:B:390:PRO:O	1:B:392:LYS:N	2.39	0.55
1:A:217:TYR:CE2	1:A:357:HIS:HA	2.42	0.55
1:A:558:LEU:HD12	1:A:559:ILE:N	2.22	0.55
1:A:620:HIS:CD2	1:A:621:ILE:N	2.75	0.55
1:B:114:TRP:CZ2	1:B:118:LEU:HD13	2.41	0.55
1:A:415:TYR:CG	1:A:416:PHE:N	2.75	0.55
1:A:497:LYS:NZ	1:A:497:LYS:HB2	2.22	0.55
1:A:596:PHE:HA	1:A:608:MET:CE	2.36	0.55
1:B:418:ARG:NH2	1:B:431:VAL:O	2.40	0.55
1:B:64:ASP:OD1	1:B:67:THR:HG21	2.07	0.55
1:A:135:LYS:O	1:A:137:LYS:N	2.40	0.55
1:B:318:LYS:HB2	1:B:318:LYS:NZ	2.22	0.55
1:A:311:ASP:HB3	1:A:314:ILE:HG13	1.89	0.54
1:A:550:ARG:CZ	1:A:624:ILE:HG21	2.37	0.54
1:B:123:LEU:HB3	1:B:124:PRO:HD2	1.88	0.54
1:B:653:GLU:OE2	1:B:665:TYR:N	2.39	0.54
1:B:80:ASN:HD21	1:B:83:GLU:HB2	1.71	0.54
1:A:208:LYS:HE3	1:B:212:GLN:CB	2.35	0.54
1:A:543:ALA:HB2	5:A:739:HOH:O	2.07	0.54
1:B:198:VAL:HG11	1:B:209:TYR:HB2	1.89	0.54
1:B:333:PHE:O	1:B:362:ASP:HB3	2.06	0.54
1:A:553:ASP:OD1	1:A:555:GLU:HB3	2.08	0.54
1:A:597:ASN:HB2	1:A:607:ASP:OD2	2.07	0.54
1:B:92:ARG:O	1:B:96:ALA:N	2.41	0.54
1:B:114:TRP:CZ2	1:B:120:LEU:HD13	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:287:LEU:O	1:B:291:ILE:HG13	2.07	0.54
1:B:568:TYR:CE2	1:B:618:PHE:HB2	2.42	0.54
1:B:72:SER:O	1:B:74:ALA:N	2.40	0.54
1:A:137:LYS:O	1:A:138:GLU:CB	2.56	0.54
1:A:255:LEU:O	1:A:258:VAL:HG22	2.08	0.54
1:A:550:ARG:HG3	1:A:552:ILE:HD11	1.90	0.54
1:B:178:ILE:H	1:B:250:GLN:HE22	1.54	0.54
1:B:577:MET:HE1	1:B:579:CYS:HB3	1.89	0.54
1:B:638:LYS:NZ	1:B:639:LYS:HD2	2.23	0.54
1:A:462:LEU:CD2	1:A:488:ARG:HH21	2.20	0.54
1:B:525:GLU:HG3	1:B:625:CYS:HA	1.89	0.54
1:B:72:SER:C	1:B:74:ALA:N	2.60	0.54
1:B:513:PHE:CZ	1:B:586:THR:HG23	2.42	0.54
1:B:470:GLY:N	1:B:494:GLN:O	2.41	0.54
1:A:480:GLN:C	1:A:482:HIS:H	2.09	0.54
1:B:311:ASP:HB3	1:B:314:ILE:HG13	1.90	0.54
1:B:495:LYS:O	1:B:497:LYS:HG3	2.07	0.54
1:A:124:PRO:HB3	1:A:132:TRP:CD2	2.43	0.54
1:B:497:LYS:HZ3	1:B:497:LYS:HB2	1.72	0.54
1:B:84:LYS:HG2	1:B:88:ILE:HD11	1.90	0.53
1:B:412:LYS:HA	1:B:431:VAL:HB	1.91	0.53
1:B:434:VAL:HG22	1:B:514:TYR:HB2	1.90	0.53
1:A:245:ASN:HD21	1:A:247:LEU:HB2	1.73	0.53
1:A:80:ASN:OD1	1:A:83:GLU:HB2	2.08	0.53
1:A:80:ASN:OD1	1:A:83:GLU:OE1	2.26	0.53
1:A:106:GLU:O	1:A:107:VAL:HG13	2.06	0.53
1:A:345:LEU:HD13	1:A:350:TRP:CZ3	2.43	0.53
1:B:423:ILE:HA	1:B:426:ALA:HB2	1.90	0.53
1:B:559:ILE:HG22	1:B:560:SER:H	1.71	0.53
1:A:444:SER:O	1:A:447:ILE:HG22	2.08	0.53
1:A:497:LYS:HZ2	1:A:497:LYS:HB2	1.74	0.53
1:B:568:TYR:CG	1:B:569:SER:N	2.76	0.53
1:B:653:GLU:OE1	1:B:664:LYS:HG3	2.07	0.53
1:A:423:ILE:HG13	5:A:714:HOH:O	2.08	0.53
1:B:341:ALA:HB3	1:B:344:TRP:CD1	2.43	0.53
1:B:527:ASP:O	1:B:531:LEU:HG	2.09	0.53
1:A:296:THR:O	1:A:306:GLN:HA	2.09	0.53
1:B:130:TYR:CZ	1:B:324:ARG:HB2	2.44	0.53
1:B:328:THR:N	1:B:329:PRO:CD	2.70	0.53
1:B:392:LYS:HB2	1:B:392:LYS:NZ	2.23	0.53
1:B:186:ALA:HA	1:B:210:VAL:HG23	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:554:ARG:CD	1:A:554:ARG:H	2.16	0.52
1:B:295:ILE:HG12	1:B:308:LYS:HA	1.89	0.52
1:B:503:SER:O	1:B:505:THR:N	2.42	0.52
1:A:450:CYS:SG	1:A:518:LEU:HD22	2.49	0.52
1:B:105:LYS:HB3	1:B:566:PRO:HG3	1.92	0.52
1:B:238:LEU:HD13	1:B:248:TRP:CZ2	2.44	0.52
1:B:654:SER:C	1:B:656:SER:H	2.13	0.52
1:A:199:ARG:HH21	1:B:211:ARG:HH21	1.57	0.52
1:B:411:GLN:NE2	1:B:430:ARG:HB2	2.25	0.52
1:A:114:TRP:CE2	1:A:571:GLU:HG3	2.45	0.52
1:A:442:ASN:HA	1:A:473:ASP:OD2	2.10	0.52
1:B:71:CYS:O	1:B:75:LYS:HG3	2.09	0.52
1:A:605:ASP:CG	1:A:606:TYR:N	2.62	0.52
1:A:649:LYS:HB2	5:A:757:HOH:O	2.09	0.52
1:A:91:TYR:O	1:A:94:ILE:HG22	2.09	0.52
1:B:602:ASN:O	1:B:603:ALA:HB3	2.10	0.52
1:A:565:TRP:H	1:A:580:HIS:CE1	2.27	0.52
1:B:545:VAL:HG12	1:B:619:LYS:HB3	1.91	0.52
1:B:557:ASN:N	1:B:557:ASN:HD22	2.08	0.52
1:A:296:THR:HB	1:A:309:SER:OG	2.09	0.52
1:A:499:ILE:O	1:A:499:ILE:HD12	2.10	0.52
1:B:490:ARG:HH12	1:B:511:ARG:NH1	2.08	0.52
1:A:490:ARG:NH2	1:A:511:ARG:HD3	2.25	0.51
1:A:552:ILE:HG22	1:A:553:ASP:O	2.11	0.51
1:B:474:ASP:O	1:B:475:THR:C	2.46	0.51
1:A:418:ARG:HH21	1:A:429:LYS:CG	2.23	0.51
1:A:517:GLN:NE2	1:A:583:ARG:HH11	2.05	0.51
1:A:64:ASP:OD2	1:A:67:THR:HB	2.10	0.51
1:B:131:VAL:HG23	1:B:324:ARG:HD2	1.92	0.51
1:A:132:TRP:CH2	1:A:136:ARG:HD2	2.46	0.51
1:A:647:HIS:O	1:A:651:VAL:HG23	2.10	0.51
1:A:535:GLU:O	1:A:542:LEU:HD23	2.10	0.51
1:A:559:ILE:O	1:A:560:SER:CB	2.58	0.51
1:B:287:LEU:N	5:B:729:HOH:O	2.43	0.51
1:B:466:ILE:HD12	1:B:466:ILE:H	1.75	0.51
1:B:499:ILE:HD12	1:B:499:ILE:C	2.31	0.51
1:B:649:LYS:N	1:B:649:LYS:HD2	2.26	0.51
1:A:462:LEU:HD23	1:A:488:ARG:HH21	1.76	0.51
1:B:107:VAL:HG11	1:B:565:TRP:CZ2	2.43	0.51
1:B:541:SER:HB2	5:B:703:HOH:O	2.11	0.51
1:A:596:PHE:N	1:A:608:MET:HE1	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:450:CYS:SG	1:B:518:LEU:HD13	2.51	0.51
1:A:539:ASP:C	1:A:541:SER:H	2.14	0.51
1:A:67:THR:HB	1:A:488:ARG:HH11	1.75	0.51
1:A:178:ILE:HG12	1:A:250:GLN:HE22	1.75	0.51
1:B:94:ILE:HG23	1:B:95:THR:HG23	1.93	0.51
1:A:653:GLU:OE2	1:A:665:TYR:O	2.28	0.51
1:B:363:ASN:HD22	1:B:409:LEU:CD2	2.23	0.51
1:B:411:GLN:CA	1:B:411:GLN:HE21	2.24	0.51
1:B:523:PHE:HA	5:B:731:HOH:O	2.10	0.51
1:B:60:VAL:O	1:B:61:ILE:HB	2.11	0.51
1:B:662:LYS:HG3	1:B:663:TYR:HD1	1.76	0.51
3:A:684:UDP:O2B	3:A:684:UDP:O5'	2.29	0.50
1:A:154:ILE:CD1	1:A:248:TRP:HZ3	2.24	0.50
1:A:557:ASN:ND2	1:A:557:ASN:H	2.08	0.50
1:B:577:MET:HE3	1:B:579:CYS:O	2.11	0.50
1:B:643:GLN:HG3	1:B:644:LYS:N	2.24	0.50
1:B:559:ILE:CG2	1:B:560:SER:N	2.70	0.50
1:B:107:VAL:HG23	1:B:566:PRO:HG2	1.93	0.50
1:A:250:GLN:HA	1:A:250:GLN:NE2	2.26	0.50
1:A:642:ILE:HG12	5:A:712:HOH:O	2.12	0.50
1:B:334:SER:O	1:B:338:VAL:HG13	2.11	0.50
1:B:367:TYR:O	1:B:370:TYR:HB3	2.12	0.50
1:B:552:ILE:CG2	1:B:553:ASP:N	2.75	0.50
1:A:167:ILE:HD12	1:A:387:GLN:NE2	2.27	0.50
1:A:501:SER:O	1:A:502:ALA:C	2.50	0.50
1:A:435:SER:HB3	1:A:510:CYS:HB3	1.92	0.50
1:A:661:LYS:HD3	5:A:693:HOH:O	2.09	0.50
1:A:190:SER:O	1:B:199:ARG:NH2	2.44	0.50
1:B:327:ASN:HD22	1:B:540:LEU:HB2	1.76	0.50
1:B:438:ILE:N	5:B:709:HOH:O	2.31	0.50
1:B:458:THR:OG1	1:B:527:ASP:HA	2.12	0.50
1:A:544:CYS:HA	1:A:584:MET:O	2.11	0.50
1:B:438:ILE:HG12	1:B:518:LEU:O	2.12	0.50
1:A:214:ASP:OD1	1:A:214:ASP:C	2.50	0.50
1:A:460:THR:HB	5:A:730:HOH:O	2.12	0.50
1:B:167:ILE:CG2	1:B:387:GLN:NE2	2.75	0.50
1:B:80:ASN:O	1:B:82:VAL:N	2.45	0.50
1:A:504:ASN:ND2	1:A:596:PHE:HB2	2.27	0.49
1:B:188:ASP:OD1	1:B:218:GLN:HB2	2.12	0.49
1:B:363:ASN:ND2	1:B:417:TYR:CE2	2.80	0.49
1:B:483:TYR:HB3	1:B:489:VAL:HB	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:212:GLN:HA	5:A:708:HOH:O	2.12	0.49
1:A:490:ARG:HH12	1:A:509:LEU:CD2	2.25	0.49
3:A:684:UDP:O2A	3:A:684:UDP:O1B	2.29	0.49
1:B:420:LYS:HE3	1:B:537:ARG:NH2	2.18	0.49
1:A:564:ASN:O	1:A:566:PRO:HD3	2.13	0.49
3:B:1:UDP:O1B	3:B:1:UDP:O2A	2.30	0.49
1:B:306:GLN:O	1:B:307:ASN:CB	2.60	0.49
1:B:409:LEU:O	1:B:412:LYS:N	2.46	0.49
1:B:536:PHE:HE1	1:B:545:VAL:HG22	1.77	0.49
1:B:565:TRP:CZ2	1:B:572:LYS:HE2	2.48	0.49
1:B:549:ASN:O	1:B:562:GLY:N	2.45	0.49
1:A:197:ILE:O	1:A:200:GLU:HB2	2.11	0.49
1:A:499:ILE:HG13	1:A:604:VAL:HG21	1.94	0.49
1:B:531:LEU:HB3	1:B:621:ILE:HD13	1.95	0.49
1:A:284:GLN:C	1:A:286:SER:H	2.15	0.49
1:A:559:ILE:HD11	1:A:630:LEU:HD23	1.94	0.49
1:A:568:TYR:CE2	1:A:618:PHE:HB2	2.47	0.49
1:B:657:ARG:C	1:B:659:GLY:H	2.16	0.49
1:A:497:LYS:NZ	1:A:501:SER:OG	2.45	0.49
1:B:206:ASN:ND2	5:B:697:HOH:O	2.45	0.49
1:B:360:GLY:O	1:B:364:GLU:N	2.46	0.49
1:A:448:VAL:O	1:A:452:GLU:HG2	2.13	0.49
1:A:88:ILE:O	1:A:91:TYR:HB3	2.13	0.49
1:B:152:LEU:HD12	1:B:249:VAL:HG13	1.94	0.49
1:B:156:ILE:HG23	1:B:238:LEU:O	2.13	0.49
1:B:72:SER:C	1:B:74:ALA:H	2.16	0.49
1:A:344:TRP:CZ3	1:A:347:ARG:HD2	2.47	0.48
1:A:465:CYS:HA	1:A:490:ARG:O	2.13	0.48
1:B:655:LEU:HD22	1:B:658:LEU:HG	1.93	0.48
1:B:668:LEU:O	1:B:668:LEU:CG	2.61	0.48
1:B:490:ARG:HH22	1:B:511:ARG:NH1	2.11	0.48
1:B:65:ALA:O	1:B:66:ALA:C	2.51	0.48
1:B:663:TYR:OH	1:B:681:LYS:HD2	2.13	0.48
1:A:296:THR:HG22	1:A:307:ASN:O	2.14	0.48
1:B:223:ARG:CZ	1:B:335:GLY:HA3	2.44	0.48
1:B:655:LEU:HD23	1:B:657:ARG:HG3	1.95	0.48
1:A:283:SER:OG	1:A:284:GLN:N	2.45	0.48
1:B:352:ASP:OD2	1:B:412:LYS:NZ	2.40	0.48
1:B:91:TYR:CE1	1:B:95:THR:HG21	2.49	0.48
1:A:208:LYS:HE3	1:B:212:GLN:HE21	1.78	0.48
1:A:352:ASP:HB3	1:A:355:PHE:CE2	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:553:ASP:O	1:A:556:GLY:N	2.42	0.48
1:A:251:SER:OG	1:A:381:GLY:HA3	2.14	0.48
1:B:409:LEU:O	1:B:411:GLN:N	2.47	0.48
1:A:669:THR:HG22	1:A:670:ASN:N	2.28	0.48
1:B:477:ARG:HB3	1:B:477:ARG:NH1	2.29	0.48
1:A:273:THR:O	1:A:273:THR:HG23	2.13	0.48
1:A:477:ARG:HD2	1:A:477:ARG:O	2.13	0.48
1:B:360:GLY:HA3	1:B:409:LEU:HD11	1.95	0.48
1:B:490:ARG:HH12	1:B:511:ARG:HH11	1.61	0.48
1:B:553:ASP:O	1:B:554:ARG:C	2.50	0.48
1:A:466:ILE:O	1:A:491:PHE:HA	2.13	0.47
1:B:161:ARG:NE	1:B:392:LYS:HE2	2.28	0.47
1:B:477:ARG:O	1:B:481:GLU:HG2	2.13	0.47
1:A:460:THR:HG21	5:A:714:HOH:O	2.14	0.47
1:B:409:LEU:O	1:B:410:GLN:C	2.53	0.47
1:B:414:PRO:HA	1:B:418:ARG:NH1	2.29	0.47
1:B:499:ILE:CD1	1:B:604:VAL:HG11	2.44	0.47
1:B:91:TYR:HA	1:B:94:ILE:CG2	2.44	0.47
1:A:162:ALA:HB1	1:A:197:ILE:CG1	2.42	0.47
1:A:267:PRO:CG	1:A:383:MET:HE2	2.36	0.47
1:A:642:ILE:CD1	1:A:672:ASN:HD21	2.27	0.47
1:A:110:ILE:O	1:A:111:PRO:C	2.51	0.47
1:B:284:GLN:C	1:B:286:SER:H	2.18	0.47
1:B:474:ASP:O	1:B:477:ARG:N	2.48	0.47
1:B:542:LEU:HD21	1:B:619:LYS:HB2	1.95	0.47
1:A:614:GLU:OE2	1:A:655:LEU:HD21	2.14	0.47
1:A:677:TYR:HE2	1:A:679:TRP:NE1	2.13	0.47
1:B:565:TRP:CE2	1:B:572:LYS:HE2	2.49	0.47
1:B:94:ILE:CG2	1:B:95:THR:HG23	2.45	0.47
1:B:218:GLN:HB3	1:B:221:ALA:CB	2.44	0.47
1:B:79:LEU:HD23	1:B:80:ASN:N	2.29	0.47
1:A:459:ILE:O	1:A:462:LEU:HD22	2.14	0.47
1:A:62:ASP:CG	1:A:63:ILE:H	2.18	0.47
1:B:577:MET:HE2	1:B:583:ARG:NH2	2.30	0.47
1:A:371:ARG:O	1:A:591:ASN:ND2	2.48	0.47
1:A:70:MET:HE3	1:A:488:ARG:HD2	1.97	0.47
1:A:545:VAL:HA	1:A:619:LYS:O	2.14	0.47
1:B:114:TRP:HZ2	1:B:120:LEU:HD13	1.79	0.47
1:B:483:TYR:C	1:B:485:ASN:H	2.18	0.47
1:B:497:LYS:HZ2	1:B:497:LYS:HB2	1.77	0.47
1:B:571:GLU:H	1:B:571:GLU:CD	2.18	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:64:ASP:OD2	1:B:67:THR:HG22	2.15	0.46
1:A:232:TYR:HB3	5:A:709:HOH:O	2.14	0.46
1:A:458:THR:HG1	1:A:530:GLU:CB	2.28	0.46
1:A:460:THR:N	5:A:759:HOH:O	2.47	0.46
1:A:605:ASP:O	1:A:609:TYR:HD2	1.99	0.46
1:B:136:ARG:O	1:B:137:LYS:CB	2.63	0.46
1:A:459:ILE:HD11	1:A:530:GLU:HG3	1.98	0.46
1:A:92:ARG:HG3	1:A:92:ARG:NH1	2.29	0.46
1:B:410:GLN:HE22	1:B:419:LYS:H	1.63	0.46
1:B:449:ARG:HD2	5:B:686:HOH:O	2.15	0.46
1:B:483:TYR:C	1:B:485:ASN:N	2.68	0.46
1:B:564:ASN:HA	1:B:580:HIS:CD2	2.51	0.46
1:B:126:SER:HB2	1:B:327:ASN:OD1	2.15	0.46
1:B:164:ILE:HG21	1:B:241:ASP:CB	2.46	0.46
1:A:285:LYS:HB2	1:A:285:LYS:NZ	2.30	0.46
1:A:299:GLN:NE2	1:A:304:VAL:HG22	2.29	0.46
1:B:306:GLN:O	1:B:307:ASN:HB3	2.16	0.46
1:B:472:THR:OG1	1:B:473:ASP:N	2.48	0.46
1:B:543:ALA:HB2	1:B:616:GLY:HA3	1.97	0.46
1:B:647:HIS:O	1:B:648:PHE:C	2.54	0.46
1:B:649:LYS:H	1:B:649:LYS:CD	2.29	0.46
1:A:125:GLU:OE1	1:A:324:ARG:NH2	2.48	0.46
1:B:295:ILE:HA	1:B:309:SER:OG	2.16	0.46
1:B:433:LEU:O	1:B:433:LEU:HD22	2.16	0.46
1:B:577:MET:SD	1:B:606:TYR:CD1	3.09	0.46
1:B:63:ILE:CG1	1:B:64:ASP:N	2.76	0.46
1:B:72:SER:O	1:B:75:LYS:N	2.49	0.46
1:A:262:VAL:HG13	5:A:691:HOH:O	2.15	0.46
1:B:649:LYS:CG	5:B:706:HOH:O	2.57	0.46
1:A:413:VAL:HG12	5:A:736:HOH:O	2.16	0.46
1:B:420:LYS:NZ	1:B:537:ARG:HH12	2.14	0.46
1:B:552:ILE:HG22	1:B:553:ASP:O	2.15	0.46
1:B:166:ALA:HB1	1:B:278:TYR:CD2	2.51	0.46
1:A:414:PRO:O	1:A:418:ARG:HB3	2.16	0.45
1:A:602:ASN:O	1:A:603:ALA:HB3	2.16	0.45
1:B:130:TYR:CD2	1:B:377:ARG:HD2	2.51	0.45
1:B:483:TYR:O	1:B:485:ASN:N	2.49	0.45
1:B:620:HIS:C	1:B:620:HIS:CD2	2.89	0.45
1:A:443:CYS:O	1:A:447:ILE:HB	2.15	0.45
1:A:657:ARG:C	1:A:659:GLY:H	2.20	0.45
1:B:649:LYS:O	1:B:653:GLU:HG2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:79:LEU:HD23	1:B:80:ASN:O	2.16	0.45
1:A:356:THR:OG1	1:A:358:TRP:HD1	1.99	0.45
1:A:418:ARG:NH2	1:A:431:VAL:O	2.48	0.45
1:A:434:VAL:HB	1:A:462:LEU:CB	2.45	0.45
1:B:67:THR:HG23	1:B:68:LYS:H	1.80	0.45
1:A:219:LEU:O	1:A:222:VAL:HG12	2.17	0.45
1:A:65:ALA:HB1	1:A:87:ILE:HG22	1.99	0.45
1:A:677:TYR:HE2	1:A:679:TRP:HE1	1.65	0.45
1:A:680:GLU:O	1:A:680:GLU:HG3	2.16	0.45
1:B:410:GLN:NE2	1:B:418:ARG:HD3	2.30	0.45
1:B:437:TYR:CZ	1:B:517:GLN:HG3	2.52	0.45
1:B:442:ASN:HD21	1:B:472:THR:HG23	1.81	0.45
1:B:319:ASN:C	1:B:321:ASP:H	2.19	0.45
1:A:108:GLU:HG2	1:A:108:GLU:H	1.40	0.45
1:A:550:ARG:CG	1:A:552:ILE:HD11	2.47	0.45
1:B:136:ARG:O	1:B:137:LYS:CG	2.63	0.45
1:B:572:LYS:HG3	1:B:578:ILE:HG21	1.98	0.45
1:A:511:ARG:N	1:A:511:ARG:HD2	2.31	0.45
1:A:656:SER:O	1:A:659:GLY:N	2.46	0.45
1:B:518:LEU:HG	1:B:524:LEU:HD12	1.99	0.45
1:A:617:PRO:C	1:A:618:PHE:HD1	2.20	0.45
1:A:655:LEU:HD22	1:A:658:LEU:HG	1.98	0.45
1:B:284:GLN:O	1:B:286:SER:N	2.50	0.45
1:B:466:ILE:O	1:B:491:PHE:HA	2.16	0.45
1:A:188:ASP:OD1	1:A:218:GLN:HB2	2.17	0.45
1:A:630:LEU:O	1:A:631:HIS:C	2.54	0.45
1:B:160:ASN:OD1	1:B:192:GLU:HG3	2.17	0.45
1:B:199:ARG:O	1:B:202:GLU:HG3	2.17	0.45
1:B:631:HIS:O	1:B:634:ASN:N	2.49	0.45
1:A:423:ILE:N	1:A:423:ILE:CD1	2.73	0.45
1:A:486:HIS:CE1	1:A:488:ARG:HB2	2.52	0.45
1:B:413:VAL:C	1:B:418:ARG:HH12	2.20	0.45
1:A:114:TRP:HA	1:A:115:PRO:HD3	1.89	0.44
1:A:156:ILE:HA	1:A:238:LEU:O	2.16	0.44
1:A:606:TYR:HE1	5:A:715:HOH:O	1.98	0.44
1:B:217:TYR:CE2	1:B:357:HIS:HA	2.51	0.44
1:B:296:THR:HG22	1:B:297:ASN:N	2.32	0.44
1:B:503:SER:C	1:B:505:THR:N	2.68	0.44
1:A:250:GLN:HE21	1:A:250:GLN:HA	1.83	0.44
1:A:445:LYS:HE2	1:A:446:TYR:OH	2.18	0.44
1:A:451:VAL:HG12	1:A:455:LEU:HD11	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:577:MET:HE3	1:A:579:CYS:O	2.17	0.44
1:B:255:LEU:HD12	1:B:379:VAL:CG2	2.47	0.44
1:B:296:THR:CG2	1:B:297:ASN:N	2.80	0.44
1:B:418:ARG:HB2	1:B:418:ARG:NH1	2.30	0.44
1:B:583:ARG:NH1	1:B:609:TYR:HE2	2.15	0.44
1:A:159:TYR:CE2	1:A:160:ASN:ND2	2.85	0.44
1:B:503:SER:C	1:B:505:THR:H	2.20	0.44
1:B:553:ASP:O	1:B:555:GLU:N	2.50	0.44
1:B:586:THR:CG2	1:B:588:ARG:HB3	2.47	0.44
1:B:522:ASP:OD1	1:B:628:ARG:HA	2.18	0.44
1:B:85:ASN:HA	1:B:88:ILE:HD12	2.00	0.44
1:B:164:ILE:CG2	1:B:241:ASP:HA	2.47	0.44
1:A:150:ASP:N	1:A:150:ASP:OD2	2.47	0.44
1:A:321:ASP:OD1	1:A:324:ARG:NH1	2.50	0.44
1:A:251:SER:HA	1:A:254:GLU:OE2	2.17	0.44
1:A:94:ILE:HG23	1:A:95:THR:HG23	2.00	0.44
1:B:175:GLN:HE22	1:B:248:TRP:H	1.64	0.44
1:B:225:LEU:C	1:B:225:LEU:HD23	2.38	0.44
1:A:210:VAL:CG2	1:A:225:LEU:HD13	2.48	0.44
1:A:409:LEU:HB3	1:A:413:VAL:HB	1.99	0.44
1:A:440:ALA:HB1	1:A:443:CYS:SG	2.58	0.44
1:A:73:ASN:OD1	1:A:424:GLU:O	2.35	0.44
1:B:322:ASN:O	1:B:323:LEU:HB2	2.17	0.44
1:B:433:LEU:HD13	1:B:434:VAL:CG2	2.33	0.44
1:A:242:MET:HG3	1:A:336:GLY:O	2.18	0.44
1:A:451:VAL:HG12	1:A:455:LEU:CD1	2.47	0.44
1:A:614:GLU:CD	1:A:655:LEU:HD21	2.38	0.44
1:B:211:ARG:HG2	1:B:211:ARG:HH11	1.82	0.44
1:B:388:GLU:HA	1:B:389:PRO:HD3	1.76	0.44
1:A:550:ARG:HD2	1:A:552:ILE:HD11	1.99	0.43
1:A:545:VAL:HG12	1:A:619:LYS:HB3	2.00	0.43
1:A:118:LEU:HD21	1:A:660:ILE:HD13	2.00	0.43
1:B:564:ASN:HA	1:B:580:HIS:NE2	2.33	0.43
1:B:645:GLU:O	1:B:649:LYS:HD3	2.18	0.43
1:A:545:VAL:O	1:A:545:VAL:HG23	2.18	0.43
1:B:188:ASP:O	1:B:188:ASP:CG	2.56	0.43
1:B:294:ILE:CD1	1:B:295:ILE:N	2.78	0.43
1:B:565:TRP:CE3	1:B:565:TRP:HA	2.52	0.43
1:B:575:SER:O	1:B:576:ALA:HB2	2.18	0.43
1:A:418:ARG:NH2	1:A:429:LYS:HB3	2.27	0.43
1:A:588:ARG:O	1:A:592:LEU:HG	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:150:ASP:OD2	1:B:150:ASP:N	2.51	0.43
1:A:494:GLN:NE2	1:A:497:LYS:HZ2	2.16	0.43
1:B:450:CYS:O	1:B:451:VAL:C	2.57	0.43
1:B:477:ARG:HA	1:B:480:GLN:OE1	2.18	0.43
1:A:103:GLU:HG3	1:A:103:GLU:H	1.58	0.43
1:A:238:LEU:HD21	1:A:244:PRO:HD3	1.99	0.43
1:A:445:LYS:HE2	1:A:446:TYR:CZ	2.54	0.43
1:A:61:ILE:HD11	5:A:754:HOH:O	2.19	0.43
1:B:552:ILE:HG13	1:B:627:ASN:HB3	2.01	0.43
1:B:610:LEU:HA	1:B:610:LEU:HD12	1.85	0.43
1:B:648:PHE:O	1:B:651:VAL:HB	2.19	0.43
1:A:101:ARG:HG2	1:A:101:ARG:HH11	1.84	0.43
1:A:129:ASP:HA	1:A:324:ARG:HG2	1.99	0.43
1:A:414:PRO:O	1:A:415:TYR:O	2.36	0.43
1:B:220:CYS:O	1:B:221:ALA:C	2.57	0.43
1:B:464:VAL:HG12	1:B:466:ILE:HD11	2.01	0.43
1:A:117:ASP:O	1:A:662:LYS:NZ	2.34	0.43
1:A:287:LEU:O	1:A:291:ILE:HG13	2.19	0.43
1:A:490:ARG:NH1	1:A:509:LEU:HD22	2.30	0.43
1:A:669:THR:HG22	1:A:670:ASN:H	1.84	0.43
1:B:522:ASP:OD1	1:B:628:ARG:HG3	2.19	0.43
1:B:67:THR:HA	1:B:70:MET:HE3	2.00	0.43
1:A:255:LEU:HB2	1:A:264:LEU:HD11	2.00	0.43
1:A:476:LEU:O	1:A:476:LEU:HD12	2.18	0.43
1:A:643:GLN:CG	1:A:644:LYS:N	2.71	0.43
1:B:172:LEU:HA	1:B:175:GLN:HG2	2.01	0.43
1:B:206:ASN:CB	5:B:697:HOH:O	2.66	0.43
1:B:64:ASP:CG	1:B:67:THR:HG22	2.39	0.43
1:A:153:SER:HA	1:A:182:GLU:HG2	2.00	0.43
1:A:284:GLN:O	1:A:286:SER:N	2.50	0.43
1:B:270:TYR:HB3	1:B:296:THR:OG1	2.19	0.43
1:B:572:LYS:HG2	1:B:578:ILE:HD13	2.01	0.43
1:A:270:TYR:O	1:A:293:GLU:HA	2.19	0.42
1:A:265:ILE:HD13	1:A:333:PHE:HA	2.01	0.42
1:A:404:ILE:HD12	1:A:407:GLN:HE21	1.82	0.42
1:A:124:PRO:HB3	1:A:132:TRP:CE3	2.54	0.42
1:A:441:TYR:CE2	1:A:471:SER:HA	2.54	0.42
1:A:490:ARG:HH21	1:A:511:ARG:HD3	1.83	0.42
1:B:84:LYS:O	1:B:87:ILE:HB	2.19	0.42
1:B:68:LYS:HG2	1:B:87:ILE:HD13	2.00	0.42
1:A:503:SER:O	1:A:504:ASN:C	2.58	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:270:TYR:O	1:B:293:GLU:HA	2.20	0.42
1:B:589:ALA:O	1:B:590:TRP:C	2.57	0.42
1:A:167:ILE:HB	1:A:387:GLN:HE22	1.85	0.42
1:A:558:LEU:C	1:A:559:ILE:CG2	2.87	0.42
1:B:291:ILE:HG23	1:B:292:PRO:HD2	2.02	0.42
1:B:449:ARG:HD3	1:B:523:PHE:HB3	2.00	0.42
1:B:653:GLU:O	1:B:656:SER:HB3	2.18	0.42
1:A:605:ASP:CG	1:A:606:TYR:H	2.22	0.42
1:B:125:GLU:OE1	1:B:324:ARG:NH2	2.51	0.42
1:B:549:ASN:CA	1:B:624:ILE:HG23	2.48	0.42
1:A:152:LEU:CD2	1:A:236:ALA:HB2	2.47	0.42
1:A:258:VAL:HG23	1:A:259:ASP:N	2.35	0.42
1:B:155:VAL:O	1:B:157:PRO:HD3	2.20	0.42
1:B:223:ARG:NH2	1:B:335:GLY:HA3	2.34	0.42
1:B:583:ARG:NH1	1:B:609:TYR:CE2	2.88	0.42
1:A:219:LEU:HA	1:A:222:VAL:HG12	2.02	0.42
1:B:312:TRP:CZ2	1:B:313:ARG:HG2	2.54	0.42
1:B:557:ASN:N	1:B:557:ASN:ND2	2.67	0.42
1:B:111:PRO:CG	1:B:572:LYS:HD2	2.45	0.42
1:B:503:SER:HB3	1:B:596:PHE:CE1	2.54	0.42
1:B:630:LEU:HD12	1:B:630:LEU:HA	1.88	0.42
1:A:113:ASP:OD1	1:A:677:TYR:OH	2.27	0.42
1:A:376:PHE:CD2	5:A:748:HOH:O	2.56	0.42
1:A:496:ASN:ND2	1:A:496:ASN:C	2.73	0.42
1:A:533:LEU:O	1:A:537:ARG:HD3	2.20	0.42
1:A:552:ILE:CG2	1:A:553:ASP:N	2.82	0.42
1:B:318:LYS:HB2	1:B:318:LYS:HZ3	1.85	0.42
1:B:414:PRO:CA	1:B:418:ARG:NH1	2.83	0.42
1:B:486:HIS:ND1	1:B:487:PRO:HD2	2.34	0.42
1:B:63:ILE:CG1	1:B:64:ASP:H	2.33	0.42
1:A:460:THR:CB	5:A:730:HOH:O	2.67	0.42
1:A:496:ASN:C	1:A:496:ASN:HD22	2.23	0.42
1:A:620:HIS:CD2	1:A:620:HIS:C	2.92	0.42
1:B:525:GLU:CG	1:B:625:CYS:HA	2.50	0.42
1:B:662:LYS:HG3	1:B:663:TYR:CD1	2.54	0.42
1:B:81:GLU:HG2	1:B:85:ASN:ND2	2.35	0.42
1:A:653:GLU:OE2	1:A:665:TYR:HB3	2.20	0.41
1:B:187:ASP:C	1:B:187:ASP:OD2	2.58	0.41
1:B:329:PRO:HB2	1:B:376:PHE:HB2	2.02	0.41
1:B:552:ILE:CD1	1:B:558:LEU:HA	2.49	0.41
1:B:658:LEU:HD23	1:B:658:LEU:HA	1.73	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:67:THR:HB	1:B:488:ARG:HD3	2.02	0.41
1:A:239:ASP:HB3	1:A:241:ASP:OD1	2.20	0.41
1:A:350:TRP:CD1	1:A:350:TRP:N	2.88	0.41
1:A:418:ARG:HH21	1:A:429:LYS:HG3	1.85	0.41
1:B:158:THR:HG21	1:B:194:ILE:HD12	2.03	0.41
1:B:519:ASP:HB2	1:B:522:ASP:OD2	2.21	0.41
1:A:415:TYR:C	5:A:736:HOH:O	2.58	0.41
1:A:429:LYS:HD3	1:A:429:LYS:HA	1.69	0.41
1:A:550:ARG:HG3	1:A:550:ARG:O	2.19	0.41
1:A:620:HIS:HD2	1:A:621:ILE:O	2.02	0.41
1:B:177:THR:CA	1:B:250:GLN:HE21	2.25	0.41
1:B:272:ASP:OD2	1:B:272:ASP:N	2.48	0.41
1:A:552:ILE:HG22	1:A:553:ASP:N	2.35	0.41
1:A:69:ILE:HD13	1:A:88:ILE:HG12	2.02	0.41
1:B:200:GLU:HB2	5:B:691:HOH:O	2.21	0.41
1:B:323:LEU:O	1:B:325:LEU:N	2.54	0.41
1:B:435:SER:CB	1:B:510:CYS:HB3	2.50	0.41
1:A:215:TYR:CE1	1:A:218:GLN:HG3	2.55	0.41
1:A:234:TYR:N	5:A:709:HOH:O	2.53	0.41
1:B:480:GLN:C	1:B:482:HIS:H	2.24	0.41
1:B:577:MET:HE3	1:B:579:CYS:HB3	2.01	0.41
1:B:596:PHE:CD2	1:B:608:MET:HE3	2.55	0.41
1:B:645:GLU:O	1:B:645:GLU:HG3	2.19	0.41
1:B:91:TYR:CA	1:B:94:ILE:HG22	2.48	0.41
1:A:114:TRP:CZ2	1:A:118:LEU:HD12	2.55	0.41
1:A:156:ILE:HG23	1:A:238:LEU:O	2.20	0.41
1:B:121:PRO:HA	1:B:122:PRO:HD3	1.85	0.41
1:B:363:ASN:ND2	1:B:417:TYR:HE2	2.18	0.41
1:B:523:PHE:CE1	1:B:627:ASN:ND2	2.89	0.41
1:B:601:SER:HB2	1:B:647:HIS:HE1	1.86	0.41
1:A:471:SER:HB3	1:A:473:ASP:OD2	2.21	0.41
1:A:199:ARG:NH2	1:B:211:ARG:HH21	2.18	0.41
1:B:345:LEU:HD23	1:B:345:LEU:HA	1.95	0.41
1:B:649:LYS:N	1:B:649:LYS:CD	2.84	0.41
1:A:560:SER:OG	1:A:561:ASN:N	2.54	0.41
1:B:423:ILE:HD12	1:B:423:ILE:N	2.06	0.41
1:B:81:GLU:HG2	1:B:85:ASN:HD21	1.86	0.41
1:B:126:SER:CA	5:B:737:HOH:O	2.68	0.41
1:B:284:GLN:NE2	1:B:287:LEU:HD22	2.35	0.41
1:B:356:THR:OG1	1:B:357:HIS:N	2.53	0.41
1:B:92:ARG:O	1:B:96:ALA:HB2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:212:GLN:HB2	5:A:708:HOH:O	2.20	0.40
1:A:418:ARG:HB2	1:A:418:ARG:NH1	2.11	0.40
1:A:480:GLN:C	1:A:482:HIS:N	2.74	0.40
1:A:90:LYS:HD2	1:A:90:LYS:HA	1.90	0.40
1:B:227:LEU:HA	1:B:227:LEU:HD23	1.94	0.40
1:A:475:THR:N	5:A:750:HOH:O	2.54	0.40
1:A:213:LYS:CE	1:B:202:GLU:O	2.69	0.40
1:B:283:SER:OG	1:B:284:GLN:N	2.54	0.40
1:B:389:PRO:HA	1:B:390:PRO:HD3	1.83	0.40
1:B:438:ILE:C	5:B:709:HOH:O	2.59	0.40
1:A:422:LYS:HD3	5:A:743:HOH:O	2.20	0.40
1:B:124:PRO:HD3	1:B:132:TRP:CE2	2.57	0.40
1:B:248:TRP:CZ2	1:B:252:TYR:HE2	2.39	0.40
1:B:296:THR:HG22	1:B:297:ASN:O	2.21	0.40
1:B:67:THR:O	1:B:68:LYS:C	2.60	0.40
1:A:61:ILE:CD1	1:A:62:ASP:N	2.82	0.40
1:B:129:ASP:C	1:B:129:ASP:OD1	2.60	0.40
1:B:164:ILE:HG22	1:B:241:ASP:HA	2.03	0.40
1:B:164:ILE:HG21	1:B:241:ASP:HB3	2.03	0.40
1:B:427:THR:CG2	5:B:741:HOH:O	2.69	0.40
1:B:563:TYR:CD1	1:B:564:ASN:N	2.89	0.40
1:A:654:SER:C	1:A:656:SER:N	2.74	0.40
1:A:655:LEU:CD2	1:A:658:LEU:HG	2.52	0.40
1:B:238:LEU:HA	1:B:336:GLY:O	2.21	0.40
1:B:418:ARG:NE	1:B:429:LYS:HG3	2.28	0.40
1:B:511:ARG:CG	1:B:511:ARG:HH11	2.32	0.40
1:B:572:LYS:HB3	1:B:578:ILE:HD13	2.03	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	593/624 (95%)	507 (86%)	63 (11%)	23 (4%)	3	17
1	B	581/624 (93%)	472 (81%)	77 (13%)	32 (6%)	2	10
All	All	1174/1248 (94%)	979 (83%)	140 (12%)	55 (5%)	2	14

All (55) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	60	VAL
1	A	136	ARG
1	A	137	LYS
1	A	337	ASN
1	A	410	GLN
1	A	415	TYR
1	A	444	SER
1	A	638	LYS
1	A	641	ASP
1	B	61	ILE
1	B	63	ILE
1	B	65	ALA
1	B	359	GLY
1	B	420	LYS
1	B	422	LYS
1	B	426	ALA
1	B	527	ASP
1	B	580	HIS
1	A	285	LYS
1	A	423	ILE
1	A	474	ASP
1	A	560	SER
1	A	580	HIS
1	B	66	ALA
1	B	73	ASN
1	B	81	GLU
1	B	285	LYS
1	B	357	HIS
1	B	391	GLY
1	B	410	GLN
1	B	559	ILE
1	B	577	MET
1	B	638	LYS
1	B	648	PHE
1	A	335	GLY

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Mol	Chain	Res	Type
1	A	484	ALA
1	A	640	LEU
1	B	504	ASN
1	B	576	ALA
1	A	111	PRO
1	A	526	PRO
1	A	655	LEU
1	B	85	ASN
1	B	160	ASN
1	B	311	ASP
1	B	320	THR
1	B	554	ARG
1	B	556	GLY
1	A	64	ASP
1	B	481	GLU
1	B	484	ALA
1	A	540	LEU
1	A	559	ILE
1	B	475	THR
1	B	294	ILE

### 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	539/557 (97%)	489 (91%)	50 (9%)	9	33
1	B	530/557 (95%)	493 (93%)	37 (7%)	15	47
All	All	1069/1114 (96%)	982 (92%)	87 (8%)	11	40

All (87) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	60	VAL
1	A	61	ILE
1	A	77	ILE

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Mol	Chain	Res	Type
1	A	101	ARG
1	A	104	LEU
1	A	107	VAL
1	A	111	PRO
1	A	112	LEU
1	A	120	LEU
1	A	152	LEU
1	A	158	THR
1	A	195	GLU
1	A	213	LYS
1	A	219	LEU
1	A	225	LEU
1	A	272	ASP
1	A	273	THR
1	A	298	ASN
1	A	304	VAL
1	A	318	LYS
1	A	325	LEU
1	A	361	GLU
1	A	369	LEU
1	A	371	ARG
1	A	380	GLU
1	A	388	GLU
1	A	409	LEU
1	A	418	ARG
1	A	419	LYS
1	A	423	ILE
1	A	433	LEU
1	A	462	LEU
1	A	496	ASN
1	A	499	ILE
1	A	511	ARG
1	A	518	LEU
1	A	533	LEU
1	A	542	LEU
1	A	554	ARG
1	A	557	ASN
1	A	559	ILE
1	A	579	CYS
1	A	581	HIS
1	A	583	ARG
1	A	612	LEU

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Mol	Chain	Res	Type
1	A	631	HIS
1	A	639	LYS
1	A	654	SER
1	A	655	LEU
1	A	681	LYS
1	B	61	ILE
1	B	71	CYS
1	B	82	VAL
1	B	92	ARG
1	B	93	GLU
1	B	118	LEU
1	B	150	ASP
1	B	195	GLU
1	B	219	LEU
1	B	262	VAL
1	B	318	LYS
1	B	356	THR
1	B	358	TRP
1	B	361	GLU
1	B	369	LEU
1	B	380	GLU
1	B	411	GLN
1	B	418	ARG
1	B	423	ILE
1	B	424	GLU
1	B	449	ARG
1	B	468	ASP
1	B	518	LEU
1	B	537	ARG
1	B	542	LEU
1	B	544	CYS
1	B	574	THR
1	B	575	SER
1	B	581	HIS
1	B	605	ASP
1	B	628	ARG
1	B	631	HIS
1	B	641	ASP
1	B	645	GLU
1	B	654	SER
1	B	655	LEU
1	B	669	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (44) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	146	GLN
1	A	174	ASN
1	A	206	ASN
1	A	212	GLN
1	A	245	ASN
1	A	250	GLN
1	A	289	ASN
1	A	299	GLN
1	A	363	ASN
1	A	387	GLN
1	A	407	GLN
1	A	411	GLN
1	A	494	GLN
1	A	496	ASN
1	A	517	GLN
1	A	549	ASN
1	A	551	ASN
1	A	557	ASN
1	A	620	HIS
1	A	622	ASN
1	A	631	HIS
1	A	643	GLN
1	A	647	HIS
1	B	85	ASN
1	B	174	ASN
1	B	175	GLN
1	B	212	GLN
1	B	245	ASN
1	B	250	GLN
1	B	284	GLN
1	B	289	ASN
1	B	297	ASN
1	B	363	ASN
1	B	387	GLN
1	B	410	GLN
1	B	411	GLN
1	B	494	GLN
1	B	517	GLN
1	B	557	ASN
1	B	620	HIS
1	B	631	HIS

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Mol	Chain	Res	Type
1	B	634	ASN
1	B	643	GLN
1	B	672	ASN

### 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 ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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	$\# Z  > 2$
2	UD2	A	683	4	34,41,41	1.08	3 (8%)	45,62,62	1.49	7 (15%)
3	UDP	A	684	-	20,26,26	1.67	3 (15%)	25,40,40	2.18	7 (28%)
2	UD2	B	683	4	34,41,41	0.86	1 (2%)	45,62,62	1.57	9 (20%)
3	UDP	B	1	4	20,26,26	1.69	4 (20%)	25,40,40	1.97	5 (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
2	UD2	A	683	4	-	8/24/63/63	0/3/3/3
3	UDP	A	684	-	-	4/14/32/32	0/2/2/2
2	UD2	B	683	4	-	11/24/63/63	0/3/3/3
3	UDP	B	1	4	-	5/14/32/32	0/2/2/2

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1	UDP	C6-N1	-4.11	1.30	1.35
3	A	684	UDP	C6-N1	-3.67	1.31	1.35
2	A	683	UD2	C6-N1	3.40	1.40	1.35
3	B	1	UDP	C2-N3	-3.02	1.32	1.38
3	A	684	UDP	C2'-C1'	-2.97	1.49	1.53
2	B	683	UD2	C6-N1	2.87	1.39	1.35
3	A	684	UDP	C2-N3	-2.84	1.32	1.38
3	B	1	UDP	C2'-C1'	-2.60	1.49	1.53
3	B	1	UDP	O4'-C4'	-2.41	1.39	1.45
2	A	683	UD2	C4-N3	2.31	1.37	1.33
2	A	683	UD2	C2B-C1B	-2.00	1.50	1.53

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	684	UDP	PA-O3A-PB	-6.71	109.81	132.83
3	B	1	UDP	PA-O3A-PB	-5.99	112.26	132.83
2	B	683	UD2	C3'-C2'-N2'	-4.19	102.71	110.62
3	A	684	UDP	O3'-C3'-C2'	-3.91	99.17	111.82
2	B	683	UD2	O3A-PB-O1'	-3.66	95.11	102.48
2	B	683	UD2	PB-O3A-PA	-3.60	120.49	132.83
2	A	683	UD2	O4B-C4B-C5B	-3.59	97.57	109.37
3	B	1	UDP	O4'-C1'-C2'	-3.55	101.74	106.93
2	A	683	UD2	PB-O3A-PA	-3.29	121.55	132.83
2	A	683	UD2	O1'-C1'-C2'	3.17	114.14	108.40
3	B	1	UDP	O3B-PB-O3A	-2.95	94.75	104.64
2	A	683	UD2	O5'-C1'-C2'	-2.92	104.87	110.58
3	A	684	UDP	O4'-C1'-C2'	-2.76	102.90	106.93
2	B	683	UD2	O5'-C1'-C2'	-2.65	105.40	110.58
2	B	683	UD2	C6'-C5'-C4'	-2.63	106.85	113.00
3	A	684	UDP	O2'-C2'-C3'	-2.54	103.62	111.82
2	B	683	UD2	O5'-C5'-C6'	2.52	112.70	106.44
3	A	684	UDP	O3'-C3'-C4'	-2.47	103.89	111.05
3	B	1	UDP	O2'-C2'-C3'	-2.46	103.86	111.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	683	UD2	O5'-C5'-C4'	2.36	113.97	109.69
3	A	684	UDP	O3A-PB-O1B	-2.30	98.42	111.19
2	A	683	UD2	O3A-PB-O1'	2.29	107.10	102.48
2	A	683	UD2	C4'-C3'-C2'	-2.28	107.00	110.34
2	B	683	UD2	O3B-C3B-C4B	-2.16	104.79	111.05
2	B	683	UD2	C2B-C3B-C4B	2.15	106.82	102.64
3	A	684	UDP	O2B-PB-O1B	2.13	119.03	110.68
3	B	1	UDP	O3'-C3'-C2'	-2.08	105.09	111.82
2	B	683	UD2	O5'-C5'-C4'	2.01	113.34	109.69

There are no chirality outliers.

All (28) torsion outliers are listed below:

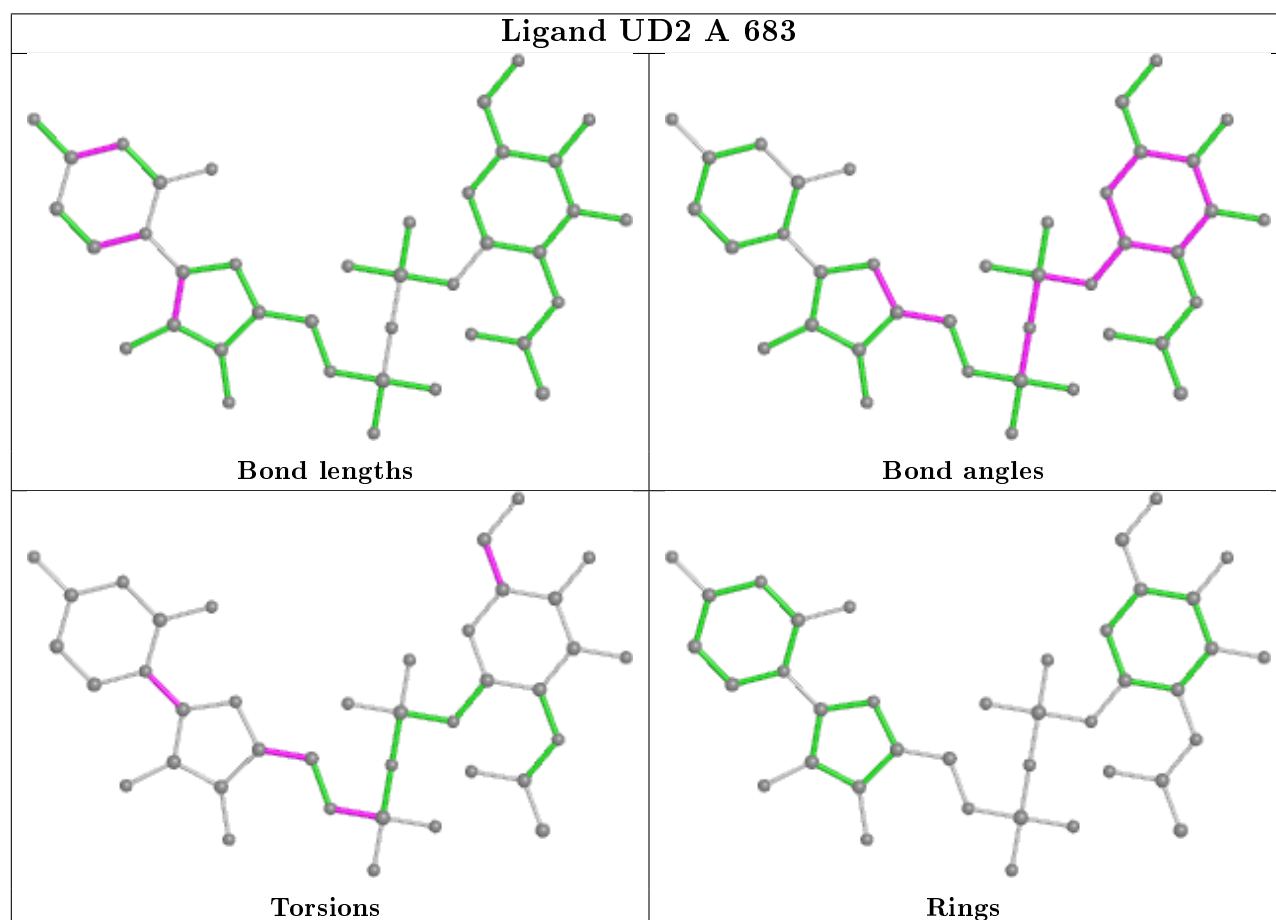
Mol	Chain	Res	Type	Atoms
2	A	683	UD2	C2B-C1B-N1-C6
2	A	683	UD2	O4B-C1B-N1-C6
2	A	683	UD2	C5B-O5B-PA-O1A
2	A	683	UD2	C5B-O5B-PA-O3A
2	B	683	UD2	C1'-C2'-N2'-C7'
2	B	683	UD2	C2B-C1B-N1-C6
2	B	683	UD2	O4B-C1B-N1-C6
3	B	1	UDP	C2'-C1'-N1-C6
3	B	1	UDP	O4'-C1'-N1-C6
3	B	1	UDP	C5'-O5'-PA-O1A
3	B	1	UDP	C5'-O5'-PA-O2A
3	B	1	UDP	C5'-O5'-PA-O3A
3	A	684	UDP	C2'-C1'-N1-C6
3	A	684	UDP	O4'-C1'-N1-C6
2	A	683	UD2	O5'-C5'-C6'-O6'
2	A	683	UD2	C3B-C4B-C5B-O5B
2	A	683	UD2	O4B-C4B-C5B-O5B
2	B	683	UD2	C1'-O1'-PB-O3A
2	B	683	UD2	O5'-C5'-C6'-O6'
3	A	684	UDP	C4'-C5'-O5'-PA
3	A	684	UDP	PB-O3A-PA-O5'
2	A	683	UD2	C4'-C5'-C6'-O6'
2	B	683	UD2	C3'-C2'-N2'-C7'
2	B	683	UD2	PB-O3A-PA-O1A
2	B	683	UD2	PA-O3A-PB-O2B
2	B	683	UD2	PB-O3A-PA-O2A
2	B	683	UD2	PA-O3A-PB-O1B
2	B	683	UD2	C1'-O1'-PB-O1B

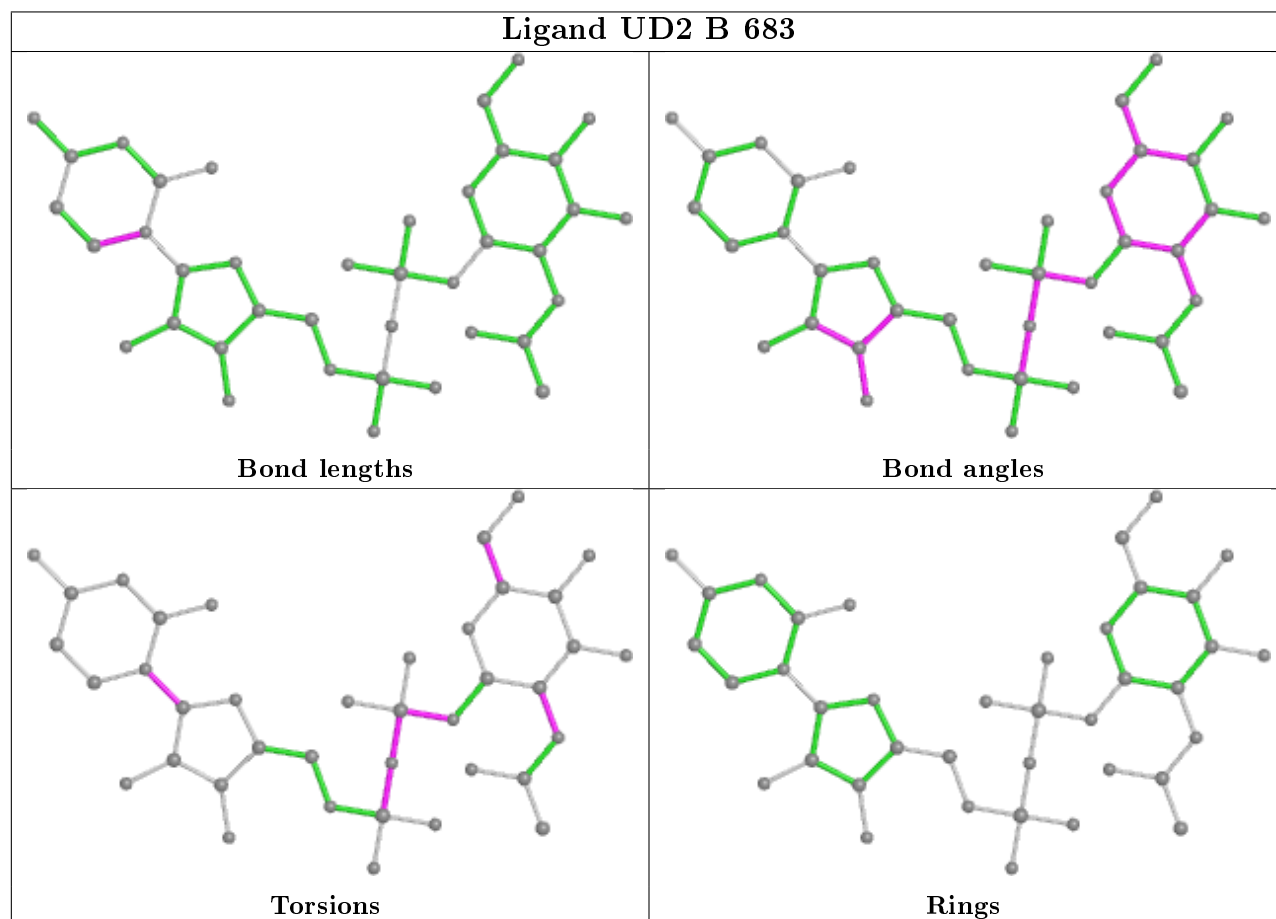
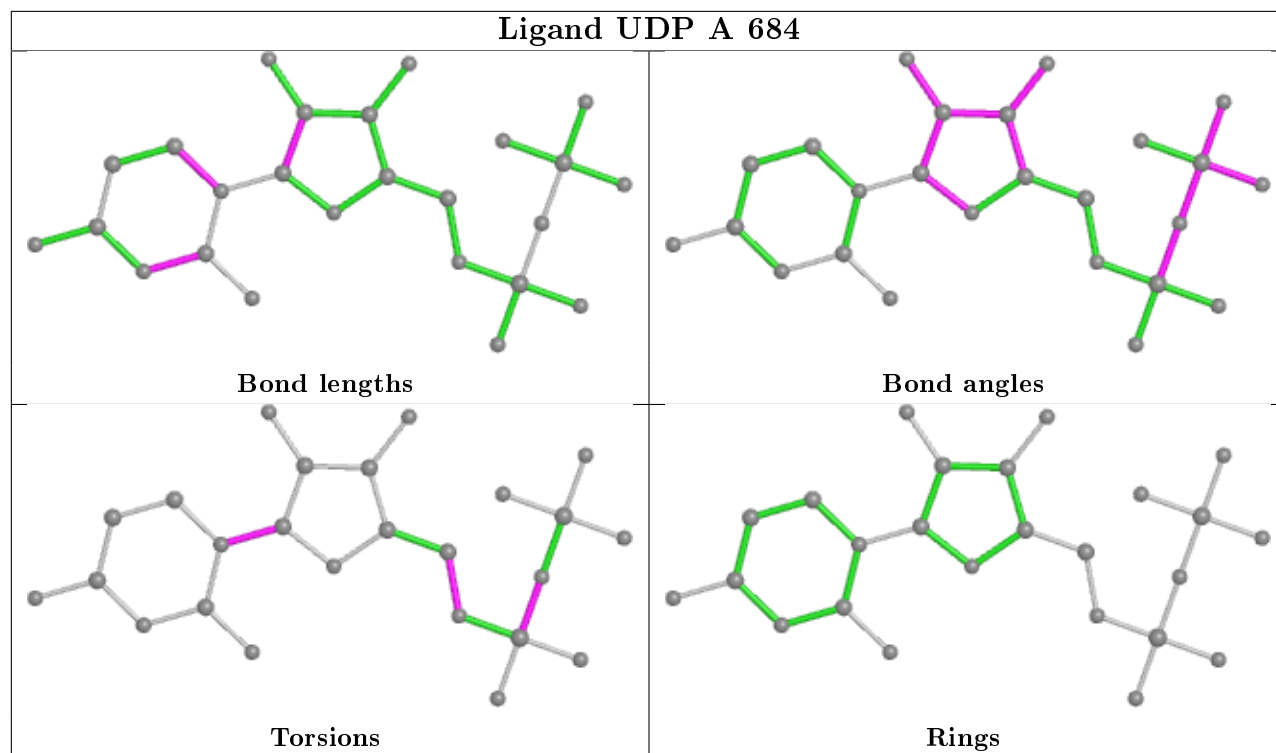
There are no ring outliers.

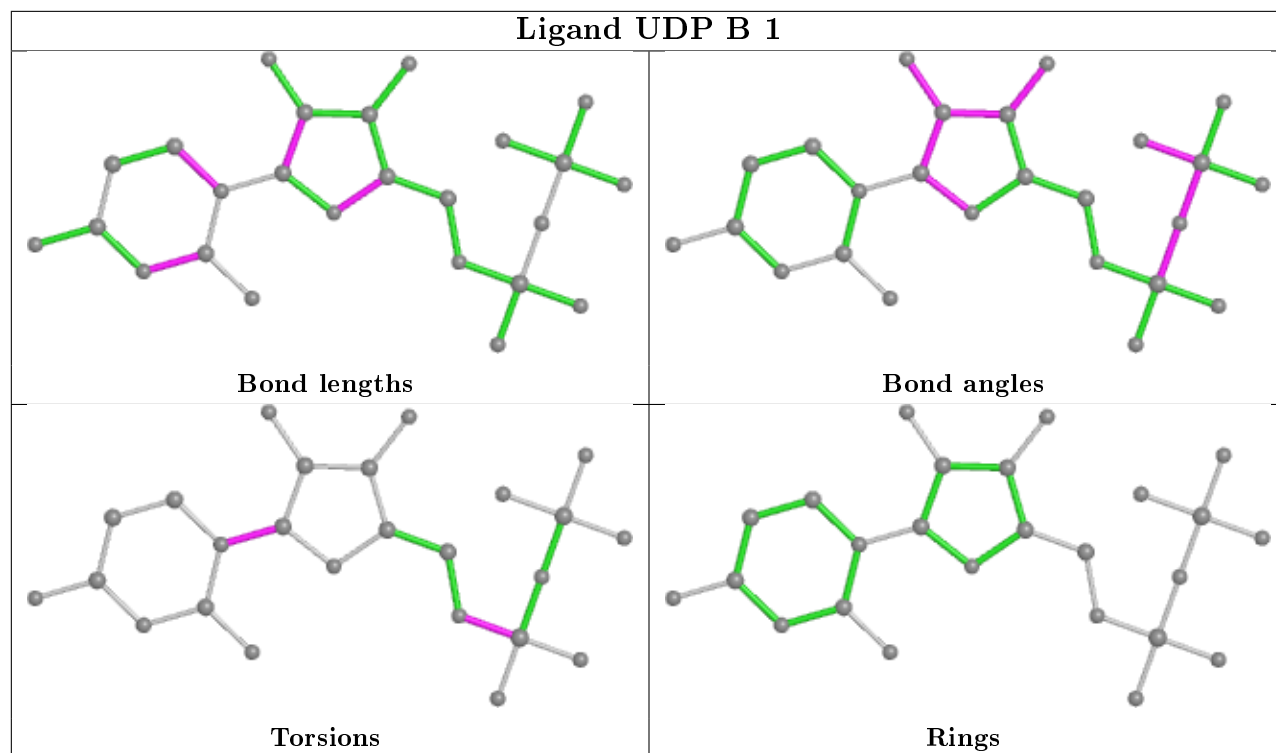
3 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	684	UDP	8	0
2	B	683	UD2	1	0
3	B	1	UDP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

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

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

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	601/624 (96%)	-0.46	6 (0%) 82 59	23, 49, 87, 122	22 (3%)
1	B	591/624 (94%)	-0.39	4 (0%) 87 69	23, 52, 95, 119	21 (3%)
All	All	1192/1248 (95%)	-0.43	10 (0%) 86 65	23, 50, 90, 122	43 (3%)

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	76	ALA	4.6
1	A	77	ILE	3.3
1	A	60	VAL	2.9
1	B	77	ILE	2.8
1	A	61	ILE	2.8
1	A	390	PRO	2.7
1	B	78	SER	2.3
1	A	389	PRO	2.3
1	B	76	ALA	2.2
1	B	446	TYR	2.2

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

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

### 6.3 Carbohydrates [i](#)

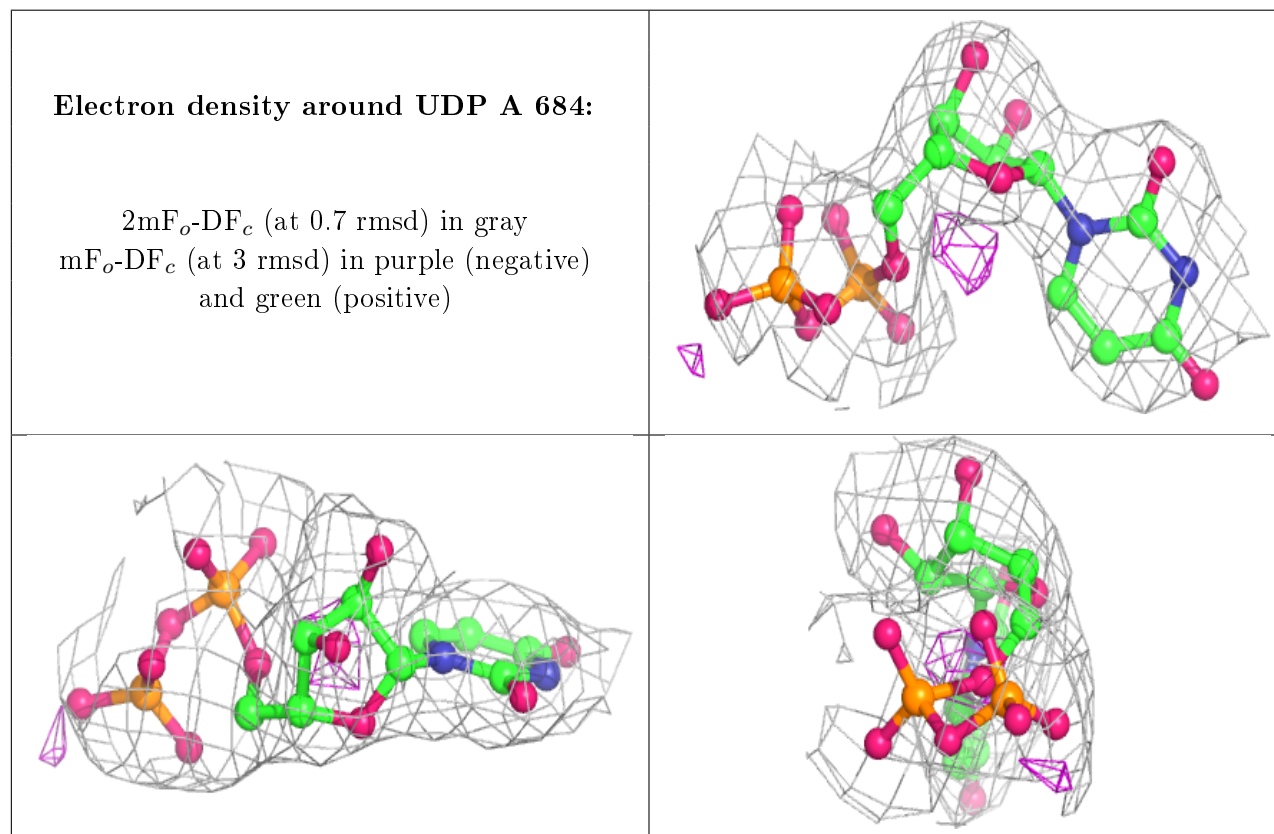
There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

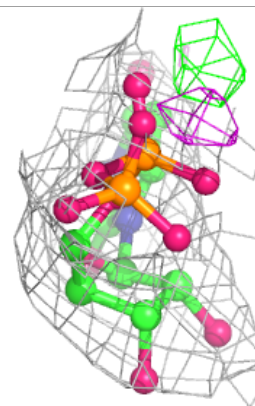
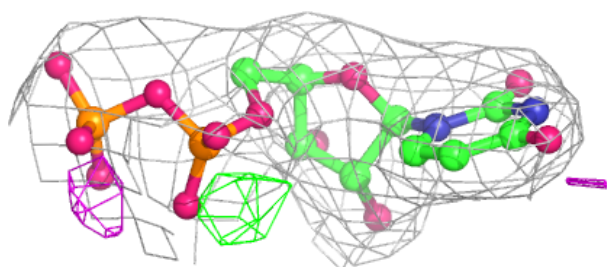
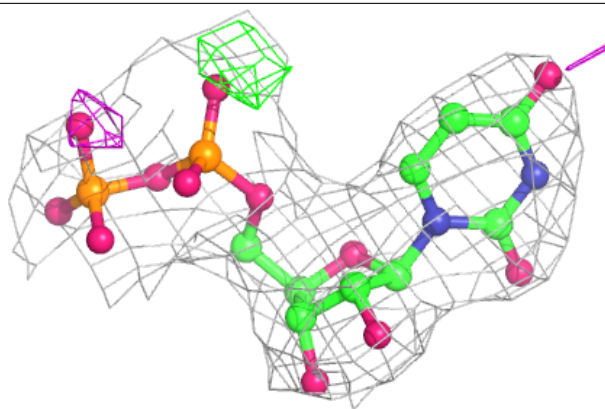
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	MN	B	4	1/1	0.91	0.10	65,65,65,65	0
3	UDP	A	684	25/25	0.91	0.19	52,80,106,110	0
3	UDP	B	1	25/25	0.93	0.18	51,66,124,131	0
4	MN	A	2	1/1	0.96	0.10	62,62,62,62	0
2	UD2	A	683	39/39	0.96	0.18	29,55,99,102	0
2	UD2	B	683	39/39	0.97	0.17	29,55,72,79	0
4	MN	B	3	1/1	0.97	0.13	48,48,48,48	0
4	MN	A	1	1/1	0.99	0.13	47,47,47,47	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

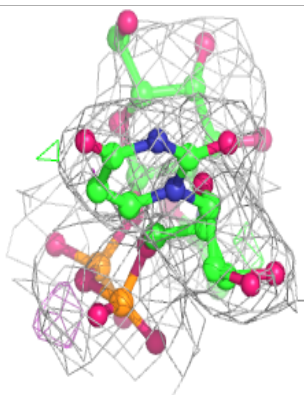
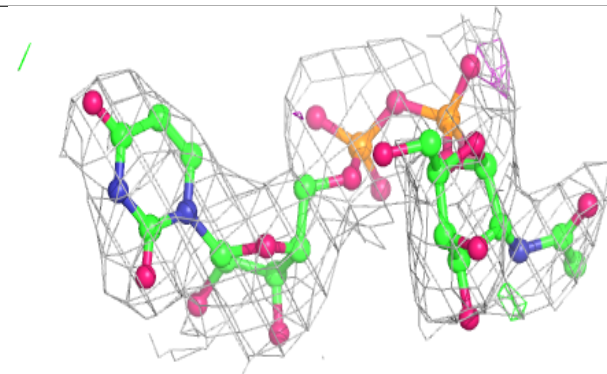
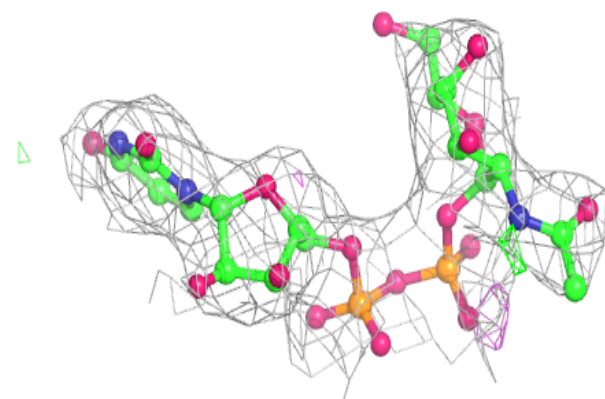


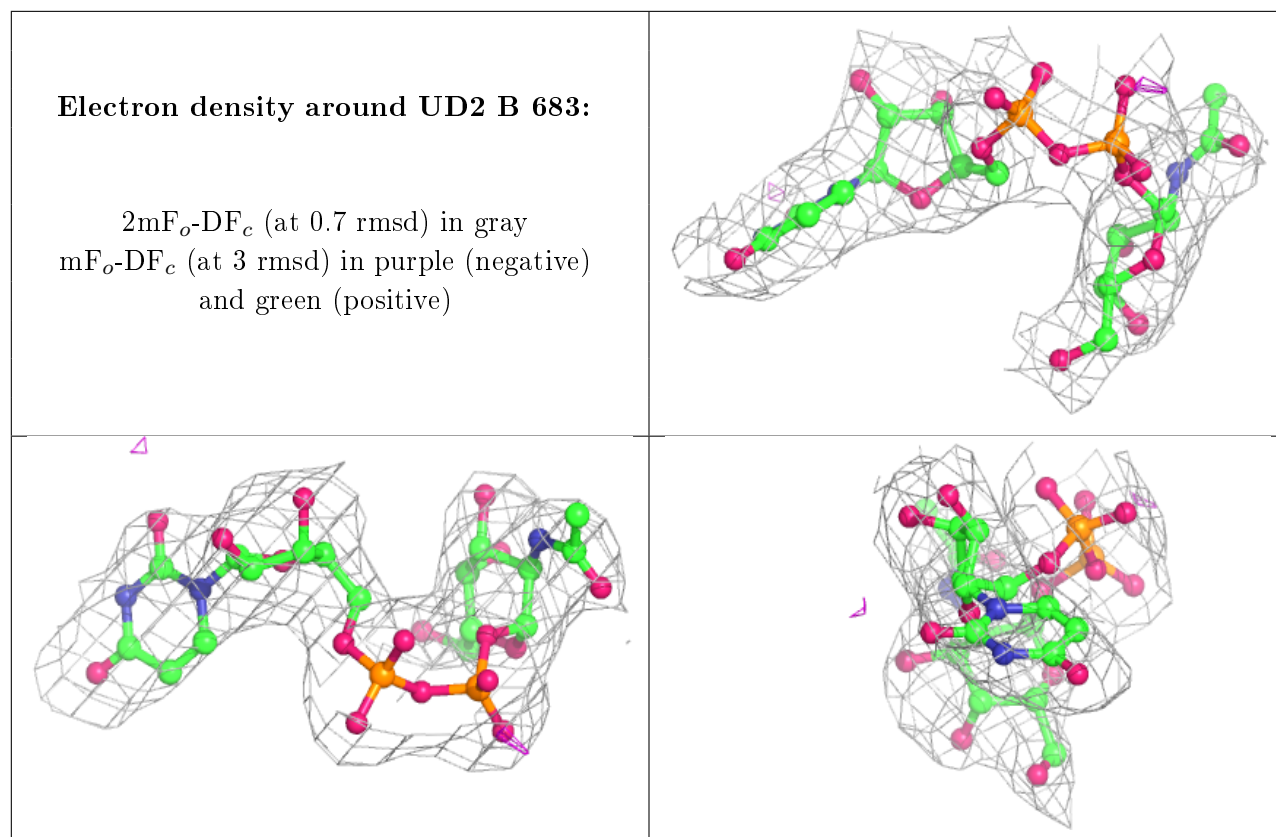
**Electron density around UDP B 1:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around UD2 A 683:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





## 6.5 Other polymers [i](#)

There are no such residues in this entry.