



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 12:41 am GMT

PDB ID : 3OC0
Title : Structure of human DPP-IV with HTS hit (2S,3S,11bS)-3-butyl-9,10-dimethoxy-1,3,4,6,7,11b-hexahydro-2H-pyrido[2,1-a]isoquinolin-2-ylamine
Authors : Hennig, M.; Stihle, M.; Thoma, R.
Deposited on : 2010-08-09
Resolution : 2.70 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

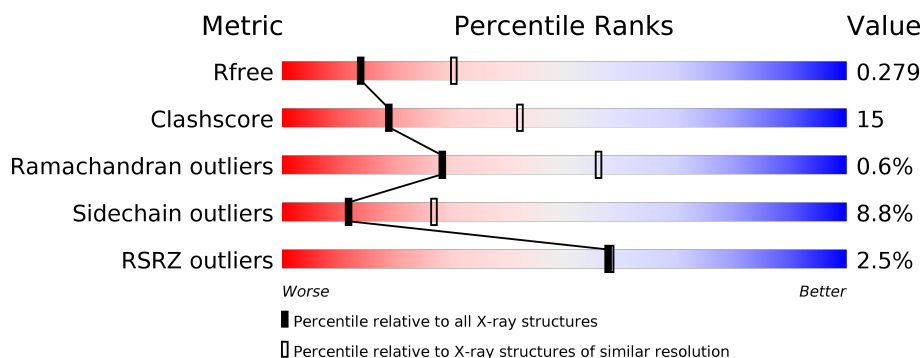
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	100719	2259 (2.70-2.70)
Clashscore	112137	2590 (2.70-2.70)
Ramachandran outliers	110173	2550 (2.70-2.70)
Sidechain outliers	110143	2550 (2.70-2.70)
RSRZ outliers	101464	2275 (2.70-2.70)

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	728	<div> <div>2%</div> <div> <div></div> <div>69%</div> <div>26%</div> <div>.</div> </div> </div>
1	B	728	<div> <div>3%</div> <div> <div></div> <div>67%</div> <div>27%</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
2	NAG	B	793	-	-	-	X
2	NAG	B	796	-	-	-	X
3	B2Q	A	900	X	-	-	-
3	B2Q	B	900	X	-	-	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 12163 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 Dipeptidyl peptidase 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	728	Total	C	N	O	S	0	0	0
			5963	3827	982	1128	26			
1	B	728	Total	C	N	O	S	0	0	0
			5963	3827	982	1128	26			

- Molecule 2 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



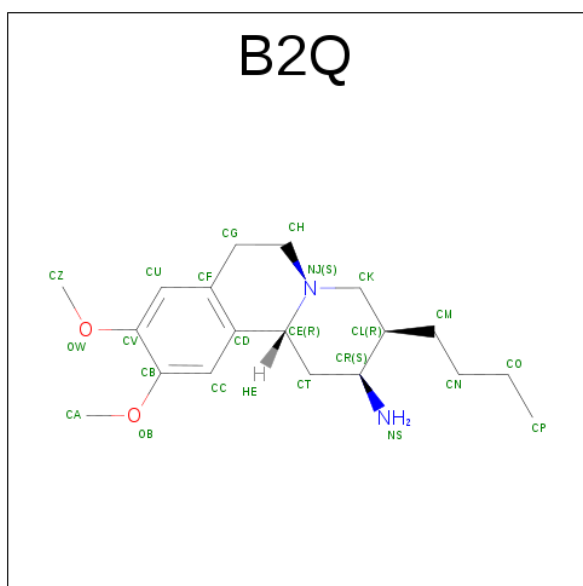
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

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

- Molecule 3 is (2S,3R,11BR)-3-BUTYL-9,10-DIMETHOXY-1,3,4,6,7,11B-HEXAHYDRO-2H-PYRIDO[2,1-A]ISOQUINOLIN-2-AMINE (three-letter code: B2Q) (formula: $C_{19}H_{30}N_2O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			23	19	2	2		
3	B	1	Total	C	N	O	0	0
			23	19	2	2		

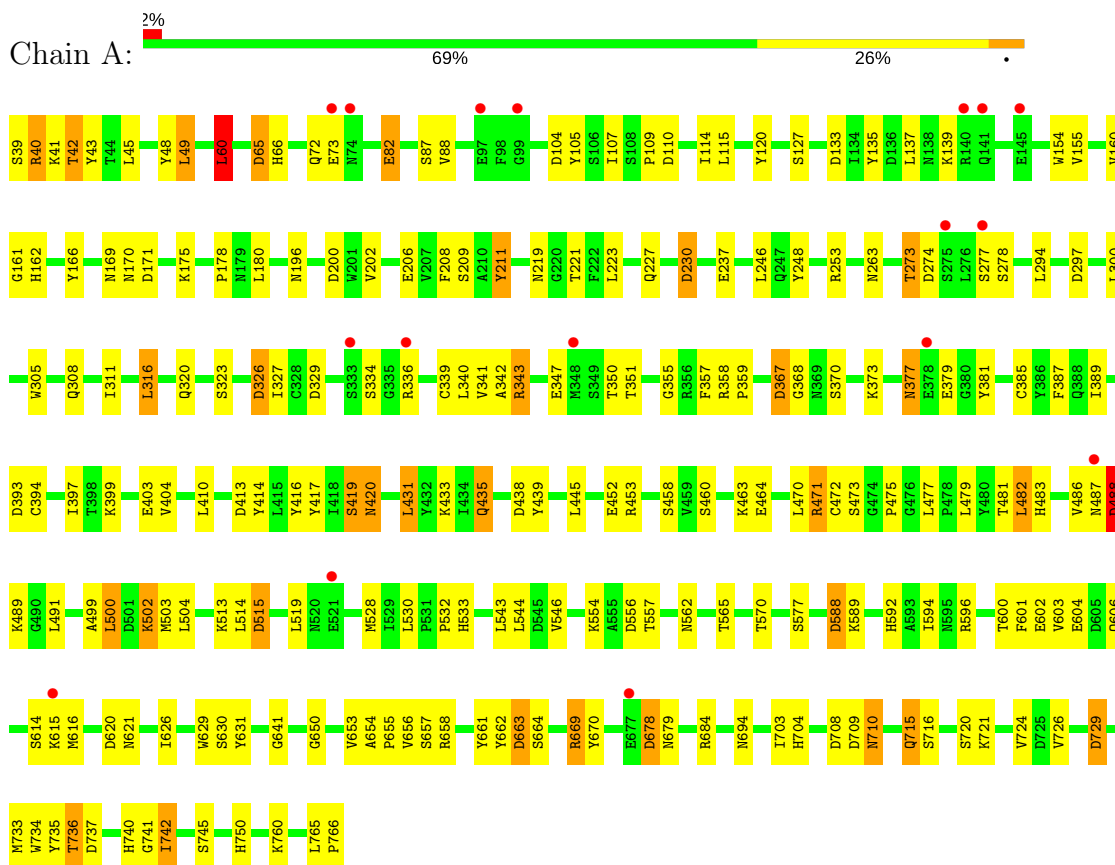
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	41	Total	O	0	0
			41	41		
4	B	38	Total	O	0	0
			38	38		

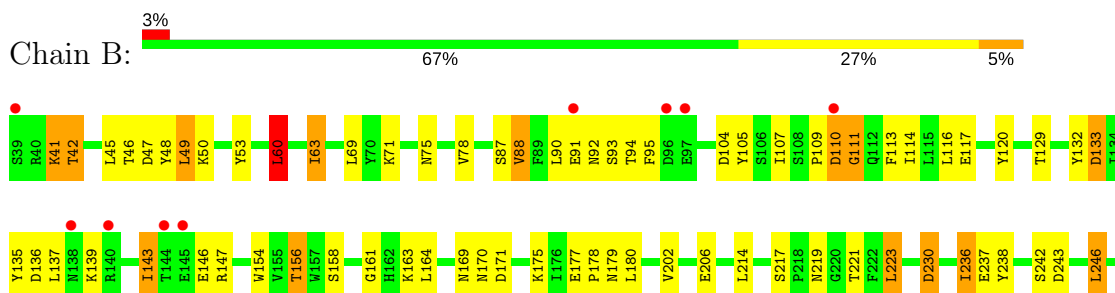
3 Residue-property plots [i](#)

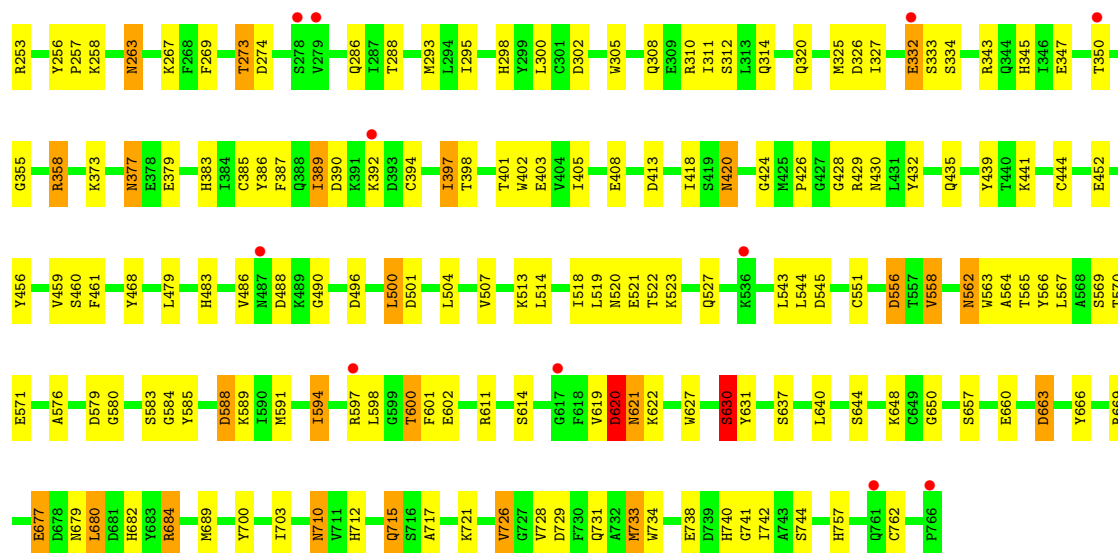
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: Dipeptidyl peptidase 4



• Molecule 1: Dipeptidyl peptidase 4





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	65.56Å 68.49Å 421.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	12.00 – 2.70 10.01 – 2.70	Depositor EDS
% Data completeness (in resolution range)	(Not available) (12.00-2.70) 76.5 (10.01-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.85 (at 2.71Å)	Xtriage
Refinement program	REFMAC 5.0	Depositor
R, R_{free}	0.236 , 0.286 0.221 , 0.279	Depositor DCC
R_{free} test set	2042 reflections (5.37%)	DCC
Wilson B-factor (Å ²)	39.1	Xtriage
Anisotropy	1.105	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 43.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.033 for k,h,-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	12163	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.87% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 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: NAG, B2Q

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	0.76	0/6135	0.94	21/8344 (0.3%)
1	B	0.77	0/6135	0.96	24/8344 (0.3%)
All	All	0.76	0/12270	0.95	45/16688 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	1	0

There are no bond length outliers.

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	358	ARG	NE-CZ-NH2	-7.51	116.55	120.30
1	A	678	ASP	CB-CG-OD2	7.08	124.67	118.30
1	B	110	ASP	CB-CG-OD2	6.92	124.53	118.30
1	B	729	ASP	CB-CG-OD2	6.88	124.49	118.30
1	B	501	ASP	CB-CG-OD2	6.85	124.47	118.30
1	B	133	ASP	CB-CG-OD2	6.85	124.46	118.30
1	B	663	ASP	CB-CG-OD2	6.74	124.37	118.30
1	A	588	ASP	CB-CG-OD2	6.64	124.28	118.30
1	A	230	ASP	CB-CG-OD2	6.62	124.26	118.30
1	A	620	ASP	CB-CG-OD2	6.61	124.25	118.30
1	B	274	ASP	CB-CG-OD2	6.61	124.25	118.30
1	B	579	ASP	CB-CG-OD2	6.46	124.12	118.30
1	A	297	ASP	CB-CG-OD2	6.35	124.02	118.30
1	A	737	ASP	CB-CG-OD2	6.29	123.96	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	367	ASP	CB-CG-OD2	6.28	123.95	118.30
1	B	588	ASP	CB-CG-OD2	6.23	123.90	118.30
1	B	390	ASP	CB-CG-OD2	6.19	123.87	118.30
1	B	111	GLY	N-CA-C	6.13	128.43	113.10
1	A	171	ASP	CB-CG-OD2	6.10	123.79	118.30
1	A	329	ASP	CB-CG-OD2	5.88	123.59	118.30
1	B	620	ASP	CB-CG-OD2	5.86	123.58	118.30
1	A	515	ASP	CB-CG-OD2	5.82	123.54	118.30
1	A	133	ASP	CB-CG-OD2	5.77	123.49	118.30
1	B	243	ASP	CB-CG-OD2	5.65	123.39	118.30
1	B	47	ASP	CB-CG-OD2	5.45	123.20	118.30
1	A	413	ASP	CB-CG-OD2	5.44	123.20	118.30
1	B	230	ASP	CB-CG-OD2	5.42	123.18	118.30
1	B	721	LYS	CD-CE-NZ	5.41	124.13	111.70
1	A	488	ASP	CB-CG-OD2	5.38	123.14	118.30
1	A	200	ASP	CB-CG-OD2	5.35	123.12	118.30
1	A	60	LEU	CA-CB-CG	5.35	127.60	115.30
1	B	60	LEU	CA-CB-CG	5.34	127.58	115.30
1	A	104	ASP	CB-CG-OD2	5.33	123.10	118.30
1	B	171	ASP	CB-CG-OD2	5.33	123.09	118.30
1	B	104	ASP	CB-CG-OD2	5.33	123.09	118.30
1	B	496	ASP	CB-CG-OD2	5.29	123.06	118.30
1	B	488	ASP	CB-CG-OD2	5.28	123.06	118.30
1	B	358	ARG	NE-CZ-NH1	5.27	122.93	120.30
1	A	709	ASP	CB-CG-OD2	5.25	123.02	118.30
1	B	413	ASP	CB-CG-OD2	5.21	122.99	118.30
1	A	65	ASP	CB-CG-OD2	5.16	122.95	118.30
1	B	556	ASP	CB-CG-OD2	5.12	122.91	118.30
1	A	274	ASP	CB-CG-OD2	5.04	122.84	118.30
1	A	729	ASP	CB-CG-OD2	5.03	122.82	118.30
1	A	40	ARG	N-CA-C	5.01	124.52	111.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	40	ARG	CA

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5963	0	5681	146	0
1	B	5963	0	5680	198	0
2	A	56	0	52	2	0
2	B	56	0	52	3	0
3	A	23	0	30	2	0
3	B	23	0	30	4	0
4	A	41	0	0	5	0
4	B	38	0	0	13	0
All	All	12163	0	11525	346	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 15.

All (346) 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:B:600:THR:HG22	1:B:601:PHE:H	1.13	1.12
1:B:267:LYS:HE3	4:B:772:HOH:O	1.56	1.06
1:B:543:LEU:HD21	1:B:627:TRP:HD1	1.22	1.02
1:A:347:GLU:OE2	1:A:373:LYS:NZ	2.01	0.94
1:B:600:THR:HG22	1:B:601:PHE:N	1.83	0.93
1:B:221:THR:O	1:B:273:THR:HB	1.71	0.91
1:A:377:ASN:C	1:A:377:ASN:HD22	1.74	0.90
1:A:160:VAL:HG12	1:A:160:VAL:O	1.68	0.90
1:B:377:ASN:HD22	1:B:377:ASN:C	1.74	0.89
1:B:620:ASP:OD1	1:B:620:ASP:C	2.10	0.88
1:B:267:LYS:CE	4:B:772:HOH:O	2.14	0.87
1:B:680:LEU:HD22	1:B:684:ARG:HD3	1.58	0.86
1:A:704:HIS:HD1	1:A:716:SER:HG	0.87	0.84
1:A:735:TYR:OH	1:A:750:HIS:HD2	1.60	0.84
1:B:253:ARG:HD2	4:B:767:HOH:O	1.77	0.84
1:B:87:SER:OG	2:B:794:NAG:O7	1.97	0.81
1:B:267:LYS:HD2	1:B:286:GLN:NE2	1.95	0.80
1:B:117:GLU:HG3	1:B:132:TYR:CE1	2.17	0.79
1:B:75:ASN:OD1	1:B:92:ASN:HB3	1.81	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:657:SER:H	1:B:715:GLN:NE2	1.81	0.79
1:B:320:GLN:OE1	1:B:669:ARG:HD3	1.83	0.78
1:B:347:GLU:OE2	1:B:373:LYS:NZ	2.14	0.78
3:B:900:B2Q:HH	4:B:11:HOH:O	1.81	0.78
1:A:596:ARG:NH2	1:A:678:ASP:OD1	2.16	0.78
1:B:46:THR:HG22	1:B:50:LYS:HD3	1.66	0.78
1:B:731:GLN:NE2	4:B:779:HOH:O	2.16	0.78
1:B:600:THR:CG2	1:B:601:PHE:H	1.96	0.77
1:B:562:ASN:HD22	1:B:562:ASN:C	1.90	0.75
1:A:487:ASN:O	1:A:489:LYS:N	2.20	0.74
1:A:403:GLU:H	1:A:420:ASN:HD21	1.33	0.74
1:B:175:LYS:NZ	1:B:178:PRO:O	2.21	0.74
1:B:600:THR:CG2	1:B:601:PHE:N	2.49	0.73
1:A:305:TRP:CZ3	1:A:311:ILE:HG12	2.23	0.73
1:B:543:LEU:HD21	1:B:627:TRP:CD1	2.15	0.72
1:A:414:TYR:CE1	1:A:435:GLN:HG3	2.24	0.72
1:B:242:SER:OG	1:B:246:LEU:HD12	1.88	0.72
1:B:621:ASN:HD22	1:B:622:LYS:N	1.88	0.72
1:A:109:PRO:HD2	1:A:161:GLY:O	1.91	0.71
1:B:236:ILE:HD12	1:B:712:HIS:CD2	2.26	0.70
1:B:163:LYS:HZ3	1:B:273:THR:HG22	1.54	0.70
1:B:401:THR:O	1:B:401:THR:HG22	1.90	0.70
1:B:432:TYR:CE2	1:B:444:CYS:HB2	2.27	0.69
2:A:793:NAG:H3	2:A:793:NAG:H83	1.75	0.68
1:A:357:PHE:CE1	3:A:900:B2Q:HGA	2.29	0.68
1:B:377:ASN:C	1:B:377:ASN:ND2	2.47	0.68
1:B:403:GLU:H	1:B:420:ASN:HD21	1.41	0.68
1:B:598:LEU:O	1:B:682:HIS:HE1	1.76	0.68
1:A:514:LEU:HD23	1:A:514:LEU:C	2.15	0.67
1:B:403:GLU:OE1	1:B:585:TYR:HA	1.95	0.67
1:A:160:VAL:CG1	1:A:160:VAL:O	2.40	0.67
1:B:345:HIS:CE1	4:B:28:HOH:O	2.46	0.67
1:A:657:SER:H	1:A:715:GLN:NE2	1.93	0.66
1:B:219:ASN:N	1:B:308:GLN:OE1	2.29	0.66
1:A:221:THR:O	1:A:273:THR:HB	1.95	0.66
1:B:620:ASP:OD1	1:B:622:LYS:N	2.29	0.66
1:A:482:LEU:HD13	1:A:491:LEU:HD12	1.79	0.65
1:B:518:ILE:O	1:B:519:LEU:HD12	1.96	0.65
1:A:397:ILE:HG22	1:A:439:TYR:CE2	2.31	0.65
1:A:735:TYR:OH	1:A:750:HIS:CD2	2.48	0.65
1:A:594:ILE:CD1	1:A:601:PHE:HB2	2.28	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:42:THR:CG2	1:A:570:THR:OG1	2.46	0.64
1:A:377:ASN:ND2	1:A:377:ASN:C	2.44	0.64
1:B:680:LEU:CD2	1:B:684:ARG:HD3	2.26	0.63
1:B:237:GLU:HG2	1:B:253:ARG:HG2	1.81	0.63
1:B:63:ILE:HD13	1:B:69:LEU:HG	1.80	0.63
1:B:163:LYS:NZ	1:B:273:THR:HG22	2.14	0.62
1:B:267:LYS:HD2	1:B:286:GLN:HE22	1.62	0.62
1:B:42:THR:HG23	1:B:570:THR:OG1	2.00	0.62
1:B:621:ASN:C	1:B:621:ASN:HD22	2.02	0.61
1:B:267:LYS:HG3	4:B:772:HOH:O	1.99	0.61
1:B:305:TRP:CZ3	1:B:311:ILE:HG12	2.36	0.61
1:B:660:GLU:OE2	4:B:778:HOH:O	2.16	0.61
1:A:273:THR:O	1:A:273:THR:HG23	2.00	0.60
1:A:351:THR:OG1	1:A:592:HIS:HD2	1.83	0.60
1:A:736:THR:HG21	1:B:717:ALA:O	2.02	0.60
1:B:428:GLY:O	1:B:429:ARG:HG2	2.02	0.60
1:B:75:ASN:OD1	1:B:92:ASN:CB	2.49	0.60
1:B:137:LEU:C	1:B:139:LYS:H	2.04	0.60
1:B:327:ILE:HD13	1:B:389:ILE:HG12	1.84	0.59
1:B:543:LEU:HD23	1:B:544:LEU:N	2.17	0.59
1:A:453:ARG:O	1:A:475:PRO:HD2	2.03	0.59
1:B:594:ILE:HD11	1:B:602:GLU:N	2.17	0.59
1:B:435:GLN:NE2	1:B:441:LYS:HD3	2.18	0.58
1:B:269:PHE:CE1	1:B:286:GLN:HB2	2.38	0.58
1:B:611:ARG:O	1:B:614:SER:HB2	2.02	0.58
1:A:206:GLU:OE2	1:A:663:ASP:OD2	2.19	0.58
1:B:179:ASN:OD1	1:B:180:LEU:HD22	2.02	0.58
1:B:136:ASP:O	1:B:139:LYS:O	2.22	0.58
1:B:42:THR:CG2	1:B:570:THR:OG1	2.51	0.58
1:B:63:ILE:CD1	1:B:69:LEU:CD1	2.81	0.57
1:B:163:LYS:NZ	1:B:273:THR:CG2	2.67	0.57
1:A:305:TRP:CE3	1:A:311:ILE:HG12	2.39	0.57
1:A:340:LEU:O	1:A:342:ALA:N	2.37	0.57
1:B:242:SER:HG	1:B:246:LEU:HD12	1.68	0.57
1:B:257:PRO:CB	1:B:263:ASN:HD22	2.18	0.57
1:B:69:LEU:CD1	1:B:107:ILE:HD12	2.35	0.56
1:A:470:LEU:HD12	1:A:483:HIS:CE1	2.41	0.56
1:A:72:GLN:O	1:A:73:GLU:HB2	2.04	0.56
1:A:115:LEU:HD11	1:A:155:VAL:HG11	1.87	0.56
1:B:657:SER:H	1:B:715:GLN:HE21	1.52	0.56
1:B:598:LEU:O	1:B:682:HIS:CE1	2.58	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:257:PRO:HB2	1:B:263:ASN:ND2	2.21	0.56
1:A:416:TYR:CE2	1:A:433:LYS:HG3	2.41	0.56
1:B:461:PHE:CD1	1:B:468:TYR:HB3	2.41	0.56
1:A:114:ILE:HG23	1:A:135:TYR:HB3	1.87	0.55
1:A:602:GLU:OE2	1:A:631:TYR:OH	2.17	0.55
1:A:614:SER:O	1:A:615:LYS:C	2.44	0.55
1:A:470:LEU:N	1:A:481:THR:O	2.38	0.55
1:A:326:ASP:OD2	1:A:339:CYS:HB3	2.06	0.55
1:A:760:LYS:HE2	4:A:38:HOH:O	2.06	0.55
1:B:710:ASN:C	1:B:710:ASN:HD22	2.09	0.55
1:B:397:ILE:HG13	1:B:439:TYR:CE2	2.42	0.54
3:B:900:B2Q:CH	4:B:11:HOH:O	2.49	0.54
1:A:237:GLU:HG2	1:A:253:ARG:HG2	1.90	0.54
1:B:105:TYR:CD1	1:B:105:TYR:C	2.80	0.54
1:B:703:ILE:HA	1:B:733:MET:O	2.07	0.54
1:B:387:PHE:CE2	1:B:394:CYS:HB3	2.43	0.54
1:B:588:ASP:O	1:B:589:LYS:C	2.44	0.54
1:A:721:LYS:NZ	1:B:242:SER:O	2.39	0.54
1:B:332:GLU:HG2	1:B:333:SER:N	2.23	0.53
1:B:520:ASN:O	1:B:521:GLU:HB2	2.08	0.53
1:B:257:PRO:CB	1:B:263:ASN:ND2	2.72	0.53
1:B:424:GLY:O	1:B:426:PRO:HD3	2.08	0.53
1:B:562:ASN:ND2	1:B:562:ASN:C	2.60	0.53
1:B:69:LEU:HD13	1:B:107:ILE:HD12	1.90	0.53
1:B:680:LEU:O	1:B:680:LEU:HD22	2.09	0.53
1:A:355:GLY:HA3	1:A:358:ARG:O	2.08	0.53
1:A:500:LEU:HA	1:A:503:MET:CE	2.39	0.53
1:B:620:ASP:O	1:B:620:ASP:OD1	2.25	0.53
1:A:641:GLY:O	1:A:694:ASN:ND2	2.36	0.53
1:A:82:GLU:OE1	1:A:82:GLU:HA	2.07	0.53
1:B:387:PHE:CD2	1:B:394:CYS:HB3	2.43	0.53
1:A:334:SER:OG	1:A:336:ARG:HG3	2.09	0.53
1:A:403:GLU:H	1:A:420:ASN:ND2	2.05	0.53
2:A:793:NAG:H3	2:A:793:NAG:C8	2.37	0.53
1:B:594:ILE:HG23	1:B:594:ILE:O	2.08	0.53
1:A:703:ILE:HA	1:A:733:MET:O	2.09	0.53
1:B:405:ILE:HD13	1:B:429:ARG:CD	2.38	0.53
1:A:273:THR:O	1:A:273:THR:CG2	2.57	0.52
1:A:41:LYS:HG2	1:A:42:THR:N	2.24	0.52
1:A:514:LEU:HD23	1:A:515:ASP:N	2.24	0.52
1:A:657:SER:H	1:A:715:GLN:HE21	1.56	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:377:ASN:ND2	1:B:379:GLU:H	2.07	0.52
1:B:386:TYR:HB2	1:B:397:ILE:CD1	2.40	0.52
1:B:267:LYS:NZ	1:B:286:GLN:HE22	2.07	0.52
1:B:594:ILE:HD11	1:B:602:GLU:H	1.73	0.52
1:A:105:TYR:HA	1:A:115:LEU:O	2.10	0.51
1:B:435:GLN:NE2	1:B:441:LYS:CD	2.73	0.51
1:B:377:ASN:ND2	1:B:379:GLU:N	2.57	0.51
1:A:514:LEU:CD2	1:A:514:LEU:C	2.78	0.51
1:A:377:ASN:ND2	1:A:379:GLU:H	2.08	0.51
1:A:463:LYS:O	1:A:464:GLU:HB2	2.09	0.51
1:A:654:ALA:N	1:A:655:PRO:HD3	2.27	0.50
1:A:73:GLU:N	4:A:774:HOH:O	2.39	0.50
1:A:196:ASN:OD1	1:A:227:GLN:HG3	2.10	0.50
1:A:528:MET:CE	1:A:530:LEU:HD21	2.42	0.50
1:A:43:TYR:CD2	1:A:565:THR:HG22	2.46	0.50
1:B:397:ILE:HG13	1:B:439:TYR:CD2	2.47	0.50
1:A:114:ILE:CG2	1:A:135:TYR:HB3	2.41	0.50
1:A:720:SER:O	1:A:724:VAL:HG23	2.11	0.50
1:B:640:LEU:HD11	1:B:650:GLY:HA3	1.93	0.50
1:B:429:ARG:HG3	1:B:456:TYR:CZ	2.47	0.49
1:A:458:SER:OG	1:A:471:ARG:CG	2.60	0.49
1:B:666:TYR:CD2	3:B:900:B2Q:HR	2.47	0.49
1:B:513:LYS:O	1:B:527:GLN:HA	2.12	0.49
1:A:596:ARG:HA	1:A:670:TYR:O	2.13	0.49
1:A:499:ALA:O	1:A:502:LYS:HG3	2.13	0.49
1:B:110:ASP:CG	1:B:161:GLY:H	2.16	0.49
1:B:45:LEU:HG	1:B:49:LEU:HD22	1.95	0.49
1:B:137:LEU:C	1:B:139:LYS:N	2.66	0.49
1:A:594:ILE:HD11	1:A:602:GLU:H	1.78	0.48
1:B:41:LYS:HE3	1:B:53:TYR:OH	2.13	0.48
1:B:420:ASN:C	1:B:420:ASN:HD22	2.16	0.48
1:B:483:HIS:CD2	1:B:490:GLY:HA2	2.48	0.48
1:B:267:LYS:CG	4:B:772:HOH:O	2.59	0.48
1:B:459:VAL:HG22	1:B:460:SER:N	2.29	0.48
1:A:532:PRO:O	1:A:533:HIS:HB2	2.13	0.48
1:A:60:LEU:C	1:A:60:LEU:HD23	2.34	0.48
1:A:66:HIS:ND1	4:A:781:HOH:O	2.35	0.48
1:B:402:TRP:HB2	1:B:420:ASN:ND2	2.28	0.48
1:A:42:THR:HG21	1:A:570:THR:OG1	2.13	0.48
1:A:397:ILE:HG22	1:A:439:TYR:CD2	2.48	0.48
1:A:734:TRP:HE1	1:A:736:THR:HG22	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:500:LEU:HD22	1:B:504:LEU:HG	1.96	0.47
1:B:408:GLU:OE1	4:B:24:HOH:O	2.20	0.47
1:B:163:LYS:HZ3	1:B:273:THR:CG2	2.22	0.47
1:B:46:THR:CG2	1:B:50:LYS:HD3	2.41	0.47
1:B:95:PHE:CZ	1:B:116:LEU:HD11	2.50	0.47
2:B:793:NAG:H3	2:B:793:NAG:C8	2.44	0.47
1:A:741:GLY:O	1:A:742:ILE:C	2.53	0.47
1:B:689:MET:SD	1:B:689:MET:N	2.87	0.47
1:A:458:SER:OG	1:A:471:ARG:HG3	2.15	0.47
1:A:629:TRP:HA	1:A:653:VAL:O	2.15	0.47
1:A:654:ALA:N	1:A:655:PRO:CD	2.77	0.47
1:A:105:TYR:C	1:A:105:TYR:CD1	2.88	0.47
1:A:404:VAL:HG13	1:A:417:TYR:CD2	2.49	0.47
1:A:419:SER:OG	1:A:420:ASN:N	2.45	0.47
1:A:615:LYS:O	1:A:616:MET:C	2.53	0.47
1:B:88:VAL:O	1:B:88:VAL:HG22	2.14	0.47
1:A:656:VAL:HG21	3:A:900:B2Q:HP	1.96	0.47
1:B:562:ASN:ND2	1:B:565:THR:H	2.12	0.47
1:A:137:LEU:O	1:A:139:LYS:O	2.33	0.47
1:B:564:ALA:O	1:B:565:THR:C	2.52	0.47
1:B:92:ASN:OD1	1:B:93:SER:N	2.48	0.47
1:A:323:SER:OG	1:A:347:GLU:HB2	2.14	0.46
1:B:405:ILE:HD13	1:B:429:ARG:NE	2.30	0.46
1:A:340:LEU:HB3	1:A:343:ARG:HD2	1.97	0.46
1:A:596:ARG:N	1:A:670:TYR:O	2.48	0.46
1:B:435:GLN:HE22	1:B:441:LYS:HD3	1.79	0.46
1:B:543:LEU:HD23	1:B:543:LEU:C	2.35	0.46
1:B:677:GLU:H	1:B:677:GLU:HG3	1.45	0.46
1:A:316:LEU:HD22	1:A:320:GLN:HA	1.98	0.46
1:B:164:LEU:HB2	1:B:175:LYS:HB2	1.96	0.46
1:B:343:ARG:O	1:B:343:ARG:HG2	2.16	0.46
1:B:648:LYS:HE3	1:B:762:CYS:O	2.15	0.46
1:B:48:TYR:CD2	1:B:49:LEU:HD13	2.51	0.46
1:A:127:SER:HB3	1:A:211:TYR:CD1	2.51	0.46
1:B:562:ASN:HD21	1:B:564:ALA:HB3	1.80	0.46
1:B:598:LEU:HD22	1:B:631:TYR:OH	2.16	0.46
1:B:741:GLY:O	1:B:742:ILE:C	2.53	0.46
1:B:584:GLY:O	1:B:585:TYR:HB2	2.15	0.46
1:A:300:LEU:HD23	1:A:300:LEU:C	2.36	0.46
1:B:435:GLN:HE21	1:B:441:LYS:HB3	1.81	0.46
1:A:305:TRP:CZ3	1:A:311:ILE:CG1	2.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:546:VAL:HG22	1:A:606:GLN:OE1	2.16	0.46
1:B:405:ILE:HD13	1:B:429:ARG:HD3	1.97	0.46
1:B:42:THR:OG1	1:B:569:SER:O	2.34	0.45
1:A:588:ASP:O	1:A:589:LYS:C	2.53	0.45
1:A:726:VAL:O	1:A:726:VAL:CG1	2.64	0.45
1:B:345:HIS:HE1	4:B:28:HOH:O	1.91	0.45
1:A:154:TRP:O	1:A:166:TYR:HA	2.16	0.45
1:A:219:ASN:N	1:A:308:GLN:OE1	2.49	0.45
1:B:734:TRP:C	1:B:734:TRP:CD1	2.90	0.45
1:A:420:ASN:C	1:A:420:ASN:HD22	2.18	0.44
1:B:206:GLU:O	3:B:900:B2Q:CA	2.65	0.44
1:A:500:LEU:HD11	1:A:504:LEU:HD11	1.99	0.44
1:A:514:LEU:CD1	1:A:557:THR:HG22	2.47	0.44
1:A:710:ASN:C	1:A:710:ASN:HD22	2.21	0.44
1:B:403:GLU:H	1:B:420:ASN:ND2	2.13	0.44
1:A:528:MET:HE2	1:A:530:LEU:HD21	1.99	0.44
1:A:600:THR:O	1:A:603:VAL:N	2.49	0.44
1:B:133:ASP:OD1	1:B:147:ARG:NH1	2.50	0.44
1:B:137:LEU:O	1:B:139:LYS:N	2.50	0.44
1:A:387:PHE:CE2	1:A:394:CYS:HB3	2.52	0.44
1:A:482:LEU:CD1	1:A:491:LEU:HD12	2.46	0.44
1:A:562:ASN:O	1:A:565:THR:HB	2.18	0.44
1:B:117:GLU:HG3	1:B:132:TYR:CZ	2.52	0.44
1:B:293:MET:O	1:B:298:HIS:HD2	2.01	0.44
1:B:556:ASP:OD1	1:B:558:VAL:HG13	2.18	0.44
1:B:63:ILE:CD1	1:B:69:LEU:HG	2.46	0.44
1:A:487:ASN:O	1:A:488:ASP:C	2.55	0.44
1:B:169:ASN:O	1:B:170:ASN:HB2	2.17	0.44
1:A:626:ILE:O	1:A:650:GLY:HA2	2.18	0.44
1:A:669:ARG:HG3	1:A:669:ARG:HH11	1.82	0.44
1:A:760:LYS:CE	4:A:38:HOH:O	2.65	0.44
1:B:383:HIS:HD2	1:B:398:THR:HB	1.83	0.44
1:A:556:ASP:OD1	1:A:556:ASP:C	2.57	0.43
1:A:603:VAL:O	1:A:604:GLU:C	2.56	0.43
1:B:236:ILE:HD12	1:B:712:HIS:NE2	2.33	0.43
1:B:267:LYS:CD	1:B:286:GLN:HE22	2.29	0.43
1:A:658:ARG:HB3	1:A:661:TYR:CD2	2.53	0.43
1:B:177:GLU:HB2	1:B:180:LEU:HD23	2.00	0.43
1:B:355:GLY:HA3	1:B:358:ARG:O	2.18	0.43
1:B:543:LEU:CD2	1:B:543:LEU:C	2.86	0.43
1:B:562:ASN:O	1:B:563:TRP:C	2.55	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:630:SER:OG	1:B:740:HIS:NE2	2.42	0.43
1:B:49:LEU:HA	1:B:49:LEU:HD12	1.74	0.43
1:B:738:GLU:OE2	1:B:744:SER:OG	2.24	0.43
1:A:477:LEU:HD22	1:A:500:LEU:HD12	1.99	0.43
1:B:114:ILE:CG2	1:B:135:TYR:HB3	2.49	0.43
1:B:405:ILE:CD1	1:B:429:ARG:HD3	2.48	0.43
1:A:519:LEU:HA	1:A:519:LEU:HD23	1.64	0.43
1:A:594:ILE:HG23	1:A:594:ILE:O	2.19	0.43
1:B:158:SER:OG	1:B:163:LYS:HB2	2.18	0.43
1:B:253:ARG:CD	4:B:767:HOH:O	2.50	0.43
1:A:370:SER:HB2	1:A:387:PHE:O	2.18	0.43
1:A:729:ASP:OD2	1:B:757:HIS:HD2	2.00	0.43
1:B:551:CYS:HB2	1:B:591:MET:SD	2.59	0.43
1:B:742:ILE:HG22	1:B:742:ILE:O	2.18	0.43
1:B:597:ARG:O	1:B:600:THR:HB	2.19	0.43
1:B:256:TYR:CZ	1:B:663:ASP:HB3	2.54	0.43
1:B:312:SER:OG	1:B:325:MET:HE3	2.19	0.43
1:A:327:ILE:HB	1:A:343:ARG:HG3	2.01	0.42
1:B:63:ILE:HD13	1:B:69:LEU:CG	2.46	0.42
1:B:726:VAL:HG12	1:B:728:VAL:HG23	2.01	0.42
1:A:327:ILE:HD13	1:A:389:ILE:HG12	2.00	0.42
1:A:377:ASN:ND2	1:A:381:TYR:H	2.16	0.42
1:B:428:GLY:C	1:B:429:ARG:HG2	2.39	0.42
1:B:522:THR:HG22	1:B:523:LYS:N	2.33	0.42
1:B:567:LEU:O	1:B:571:GLU:HB2	2.20	0.42
1:B:305:TRP:CE3	1:B:311:ILE:HG12	2.55	0.42
1:A:110:ASP:OD1	1:A:110:ASP:C	2.58	0.42
1:B:320:GLN:OE1	1:B:669:ARG:CD	2.62	0.42
1:A:367:ASP:OD1	1:A:368:GLY:N	2.52	0.42
1:A:765:LEU:HA	1:A:766:PRO:HD3	1.87	0.42
1:B:562:ASN:HD22	1:B:565:THR:H	1.66	0.42
1:B:594:ILE:CD1	1:B:601:PHE:HB2	2.49	0.42
1:B:143:ILE:HG13	1:B:143:ILE:O	2.13	0.41
1:A:45:LEU:HG	1:A:49:LEU:HD22	2.02	0.41
1:A:669:ARG:HG3	1:A:669:ARG:NH1	2.35	0.41
1:A:662:TYR:HE1	1:A:710:ASN:HD22	1.68	0.41
1:B:69:LEU:HD11	1:B:107:ILE:HD12	2.02	0.41
1:B:146:GLU:O	1:B:175:LYS:NZ	2.50	0.41
1:A:358:ARG:HB2	1:A:359:PRO:HD2	2.02	0.41
1:B:594:ILE:HD12	1:B:601:PHE:HB2	2.01	0.41
1:A:340:LEU:C	1:A:342:ALA:N	2.70	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:42:THR:HG23	1:A:43:TYR:N	2.35	0.41
1:A:500:LEU:HD22	1:A:504:LEU:HG	2.02	0.41
1:A:554:LYS:HB3	1:A:577:SER:HB3	2.02	0.41
1:A:65:ASP:N	1:A:65:ASP:OD1	2.52	0.41
1:A:708:ASP:OD2	1:A:740:HIS:HA	2.21	0.41
1:B:310:ARG:NH2	1:B:389:ILE:HD13	2.35	0.41
1:B:543:LEU:CD2	1:B:627:TRP:HD1	2.11	0.41
1:B:69:LEU:HD23	1:B:78:VAL:HG22	2.03	0.41
1:B:154:TRP:NE1	1:B:156:THR:OG1	2.53	0.41
1:B:630:SER:O	1:B:631:TYR:C	2.59	0.41
2:B:793:NAG:H82	2:B:793:NAG:C1	2.51	0.41
1:A:431:LEU:HD13	1:A:445:LEU:HD12	2.01	0.41
1:A:48:TYR:CD2	1:A:49:LEU:HD13	2.55	0.41
1:B:113:PHE:CE1	1:B:178:PRO:HG2	2.56	0.41
1:B:223:LEU:HD23	1:B:223:LEU:HA	1.85	0.41
1:B:236:ILE:HD13	1:B:238:TYR:HD1	1.86	0.41
1:A:248:TYR:CZ	1:B:258:LYS:HD2	2.55	0.41
1:A:340:LEU:C	1:A:342:ALA:H	2.24	0.41
1:B:397:ILE:CG1	1:B:439:TYR:CE2	3.03	0.41
1:B:580:GLY:O	1:B:583:SER:OG	2.26	0.41
1:A:500:LEU:HA	1:A:503:MET:HE2	2.01	0.41
1:A:208:PHE:O	1:A:209:SER:C	2.56	0.41
1:A:662:TYR:HE1	1:A:710:ASN:ND2	2.19	0.41
1:B:120:TYR:CD1	1:B:120:TYR:C	2.94	0.41
1:B:60:LEU:C	1:B:60:LEU:CD2	2.89	0.41
1:A:420:ASN:C	1:A:420:ASN:ND2	2.75	0.41
1:A:263:ASN:HD21	1:A:664:SER:CB	2.34	0.41
1:B:109:PRO:HD2	1:B:161:GLY:O	2.21	0.40
1:B:545:ASP:N	1:B:576:ALA:O	2.54	0.40
1:B:637:SER:HG	1:B:700:TYR:HH	1.69	0.40
1:A:175:LYS:NZ	1:A:178:PRO:O	2.54	0.40
1:B:397:ILE:HG12	1:B:439:TYR:CE1	2.56	0.40
1:A:110:ASP:OD2	1:A:162:HIS:ND1	2.53	0.40
1:B:267:LYS:CE	1:B:286:GLN:HE22	2.34	0.40
1:B:418:ILE:HA	1:B:430:ASN:O	2.20	0.40
1:A:169:ASN:O	1:A:170:ASN:HB2	2.22	0.40
1:A:73:GLU:CA	4:A:774:HOH:O	2.68	0.40
1:A:105:TYR:HB2	1:A:114:ILE:HD11	2.04	0.40
1:B:114:ILE:O	1:B:114:ILE:HG23	2.21	0.40
1:B:500:LEU:HD22	1:B:504:LEU:CD1	2.52	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	726/728 (100%)	676 (93%)	44 (6%)	6 (1%)	22	49
1	B	726/728 (100%)	674 (93%)	50 (7%)	2 (0%)	44	73
All	All	1452/1456 (100%)	1350 (93%)	94 (6%)	8 (1%)	28	56

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	438	ASP
1	A	488	ASP
1	B	111	GLY
1	A	393	ASP
1	B	630	SER
1	A	742	ILE
1	A	341	VAL
1	A	486	VAL

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	653/653 (100%)	599 (92%)	54 (8%)	13	30
1	B	653/653 (100%)	592 (91%)	61 (9%)	10	24
All	All	1306/1306 (100%)	1191 (91%)	115 (9%)	12	27

All (115) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	SER
1	A	40	ARG
1	A	42	THR
1	A	49	LEU
1	A	60	LEU
1	A	82	GLU
1	A	87	SER
1	A	88	VAL
1	A	107	ILE
1	A	120	TYR
1	A	180	LEU
1	A	202	VAL
1	A	211	TYR
1	A	223	LEU
1	A	230	ASP
1	A	246	LEU
1	A	273	THR
1	A	277	SER
1	A	278	SER
1	A	294	LEU
1	A	316	LEU
1	A	326	ASP
1	A	343	ARG
1	A	350	THR
1	A	377	ASN
1	A	385	CYS
1	A	399	LYS
1	A	410	LEU
1	A	419	SER
1	A	420	ASN
1	A	431	LEU
1	A	435	GLN
1	A	452	GLU
1	A	460	SER
1	A	471	ARG
1	A	472	CYS
1	A	473	SER
1	A	479	LEU
1	A	482	LEU
1	A	500	LEU
1	A	502	LYS
1	A	513	LYS
1	A	543	LEU

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Mol	Chain	Res	Type
1	A	544	LEU
1	A	621	ASN
1	A	630	SER
1	A	663	ASP
1	A	669	ARG
1	A	679	ASN
1	A	684	ARG
1	A	710	ASN
1	A	715	GLN
1	A	736	THR
1	A	745	SER
1	B	41	LYS
1	B	42	THR
1	B	49	LEU
1	B	60	LEU
1	B	63	ILE
1	B	71	LYS
1	B	88	VAL
1	B	90	LEU
1	B	91	GLU
1	B	94	THR
1	B	129	THR
1	B	143	ILE
1	B	156	THR
1	B	202	VAL
1	B	214	LEU
1	B	217	SER
1	B	223	LEU
1	B	230	ASP
1	B	236	ILE
1	B	246	LEU
1	B	263	ASN
1	B	273	THR
1	B	288	THR
1	B	295	ILE
1	B	300	LEU
1	B	302	ASP
1	B	314	GLN
1	B	326	ASP
1	B	332	GLU
1	B	334	SER
1	B	350	THR

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Mol	Chain	Res	Type
1	B	377	ASN
1	B	385	CYS
1	B	389	ILE
1	B	392	LYS
1	B	397	ILE
1	B	420	ASN
1	B	452	GLU
1	B	479	LEU
1	B	486	VAL
1	B	500	LEU
1	B	507	VAL
1	B	514	LEU
1	B	558	VAL
1	B	562	ASN
1	B	566	TYR
1	B	594	ILE
1	B	600	THR
1	B	619	VAL
1	B	620	ASP
1	B	621	ASN
1	B	630	SER
1	B	644	SER
1	B	677	GLU
1	B	679	ASN
1	B	680	LEU
1	B	684	ARG
1	B	710	ASN
1	B	715	GLN
1	B	726	VAL
1	B	733	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	123	GLN
1	A	169	ASN
1	A	247	GLN
1	A	263	ASN
1	A	377	ASN
1	A	420	ASN
1	A	483	HIS
1	A	508	GLN

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Mol	Chain	Res	Type
1	A	533	HIS
1	A	592	HIS
1	A	621	ASN
1	A	679	ASN
1	A	710	ASN
1	A	715	GLN
1	A	750	HIS
1	B	126	HIS
1	B	169	ASN
1	B	263	ASN
1	B	286	GLN
1	B	298	HIS
1	B	377	ASN
1	B	383	HIS
1	B	420	ASN
1	B	435	GLN
1	B	483	HIS
1	B	562	ASN
1	B	621	ASN
1	B	679	ASN
1	B	682	HIS
1	B	710	ASN
1	B	715	GLN
1	B	750	HIS
1	B	757	HIS

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

10 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	A	793	1	14,14,15	0.74	1 (7%)	15,19,21	1.68	2 (13%)
2	NAG	A	794	1	14,14,15	0.77	0	15,19,21	1.81	6 (40%)
2	NAG	A	795	1	14,14,15	0.61	0	15,19,21	2.09	3 (20%)
2	NAG	A	796	1	14,14,15	0.86	1 (7%)	15,19,21	1.95	5 (33%)
3	B2Q	A	900	-	25,25,25	0.63	0	33,35,35	2.18	10 (30%)
2	NAG	B	793	1	14,14,15	0.69	0	15,19,21	2.33	6 (40%)
2	NAG	B	794	1	14,14,15	0.73	0	15,19,21	1.23	1 (6%)
2	NAG	B	796	1	14,14,15	0.86	1 (7%)	15,19,21	1.70	1 (6%)
2	NAG	B	797	1	14,14,15	0.45	0	15,19,21	3.02	5 (33%)
3	B2Q	B	900	-	25,25,25	0.93	1 (4%)	33,35,35	2.77	10 (30%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	A	793	1	-	0/6/23/26	0/1/1/1
2	NAG	A	794	1	-	0/6/23/26	0/1/1/1
2	NAG	A	795	1	-	0/6/23/26	0/1/1/1
2	NAG	A	796	1	-	0/6/23/26	0/1/1/1
3	B2Q	A	900	-	2/2/4/4	0/8/33/33	0/3/3/3
2	NAG	B	793	1	-	0/6/23/26	0/1/1/1
2	NAG	B	794	1	-	0/6/23/26	0/1/1/1
2	NAG	B	796	1	-	0/6/23/26	0/1/1/1
2	NAG	B	797	1	-	0/6/23/26	0/1/1/1
3	B2Q	B	900	-	2/2/4/4	0/8/33/33	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	900	B2Q	CL-CR	-3.17	1.47	1.53
2	B	796	NAG	O5-C1	-2.59	1.39	1.43
2	A	796	NAG	O5-C1	-2.44	1.39	1.43
2	A	793	NAG	O5-C1	-2.04	1.40	1.43

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	797	NAG	C1-O5-C5	-7.22	102.22	112.17
3	B	900	B2Q	CL-CK-NJ	-6.77	103.22	112.24
2	B	797	NAG	C1-C2-N2	-5.37	101.31	110.49
2	B	796	NAG	O5-C1-C2	-5.28	104.13	111.47
3	A	900	B2Q	CM-CL-CR	-4.84	107.01	113.11
3	B	900	B2Q	CT-CR-NS	-4.28	95.39	110.94
3	A	900	B2Q	CT-CR-NS	-4.28	95.42	110.94
2	A	795	NAG	C4-C3-C2	-4.19	104.88	111.02
3	A	900	B2Q	CL-CK-NJ	-4.08	106.80	112.24
2	A	796	NAG	C3-C4-C5	-4.03	103.11	110.22
2	A	794	NAG	C4-C3-C2	-3.71	105.58	111.02
3	B	900	B2Q	CF-CD-CE	-3.65	118.01	121.62
3	A	900	B2Q	CF-CD-CE	-3.64	118.01	121.62
2	B	793	NAG	C4-C3-C2	-3.57	105.79	111.02
3	A	900	B2Q	CL-CR-NS	-3.04	100.59	111.41
2	B	797	NAG	C3-C4-C5	-3.02	104.90	110.22
3	B	900	B2Q	CT-CR-CL	-2.97	106.77	111.99
2	A	796	NAG	O3-C3-C2	-2.77	103.46	109.39
3	B	900	B2Q	CL-CR-NS	-2.74	101.65	111.41
2	A	794	NAG	C6-C5-C4	-2.65	106.79	113.00
2	A	794	NAG	C3-C4-C5	-2.57	105.70	110.22
2	A	796	NAG	O5-C1-C2	-2.49	108.01	111.47
2	B	797	NAG	C2-N2-C7	-2.36	119.51	122.94
2	B	793	NAG	C6-C5-C4	-2.20	107.86	113.00
2	A	794	NAG	O7-C7-C8	-2.18	118.08	122.06
2	A	794	NAG	C2-N2-C7	-2.10	119.89	122.94
2	A	794	NAG	O6-C6-C5	-2.04	104.49	111.34
2	B	793	NAG	O3-C3-C2	2.13	113.95	109.39
2	B	793	NAG	C8-C7-N2	2.17	120.03	116.11
2	A	796	NAG	O4-C4-C5	2.35	115.20	109.28
2	B	794	NAG	C1-O5-C5	2.37	115.43	112.17
2	A	793	NAG	C3-C4-C5	2.43	114.50	110.22
2	A	796	NAG	O7-C7-N2	2.44	126.62	121.92
3	A	900	B2Q	CK-CL-CR	2.46	113.09	110.02
3	B	900	B2Q	OW-CV-CB	2.50	118.84	115.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	900	B2Q	OW-CV-CB	2.55	118.91	115.41
3	A	900	B2Q	OB-CB-CV	2.57	118.93	115.41
3	B	900	B2Q	OB-CB-CV	2.59	118.96	115.41
2	B	793	NAG	O5-C1-C2	3.20	115.92	111.47
2	A	793	NAG	C1-O5-C5	3.26	116.66	112.17
3	A	900	B2Q	CN-CM-CL	3.54	128.44	115.29
2	A	795	NAG	C1-C2-N2	3.65	116.72	110.49
3	A	900	B2Q	CH-NJ-CE	3.96	118.54	111.15
3	B	900	B2Q	CH-NJ-CE	3.97	118.55	111.15
2	A	795	NAG	C1-O5-C5	5.13	119.24	112.17
2	B	797	NAG	O5-C1-C2	5.60	119.27	111.47
2	B	793	NAG	C1-O5-C5	6.32	120.88	112.17
3	B	900	B2Q	CN-CM-CL	6.82	140.61	115.29
3	B	900	B2Q	CK-CL-CR	7.23	119.06	110.02

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	B	900	B2Q	CE
3	B	900	B2Q	CL
3	A	900	B2Q	CE
3	A	900	B2Q	CL

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	793	NAG	2	0
3	A	900	B2Q	2	0
2	B	793	NAG	2	0
2	B	794	NAG	1	0
3	B	900	B2Q	4	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	728/728 (100%)	-0.24	17 (2%) 61 61	27, 44, 68, 93	0
1	B	728/728 (100%)	-0.20	20 (2%) 55 55	27, 44, 65, 84	0
All	All	1456/1456 (100%)	-0.22	37 (2%) 58 58	27, 44, 67, 93	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	140	ARG	5.1
1	A	140	ARG	5.1
1	B	97	GLU	4.9
1	B	279	VAL	4.7
1	A	74	ASN	4.4
1	B	278	SER	4.2
1	B	332	GLU	4.0
1	A	141	GLN	3.6
1	A	275	SER	3.3
1	A	99	GLY	3.2
1	B	39	SER	3.1
1	B	138	ASN	3.0
1	B	144	THR	2.9
1	B	487	ASN	2.9
1	A	615	LYS	2.8
1	A	487	ASN	2.8
1	B	145	GLU	2.7
1	B	96	ASP	2.7
1	B	617	GLY	2.6
1	A	378	GLU	2.5
1	B	536	LYS	2.5
1	B	392	LYS	2.5
1	A	677	GLU	2.5
1	A	145	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	97	GLU	2.4
1	A	333	SER	2.4
1	B	110	ASP	2.4
1	A	521	GLU	2.3
1	B	350	THR	2.3
1	A	336	ARG	2.2
1	A	73	GLU	2.2
1	B	91	GLU	2.2
1	A	348	MET	2.2
1	B	597	ARG	2.2
1	A	277	SER	2.1
1	B	766	PRO	2.0
1	B	761	GLN	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](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	NAG	B	793	14/15	0.84	0.35	3.54	72,79,81,82	0
2	NAG	B	796	14/15	0.84	0.26	2.60	57,62,63,65	0
2	NAG	A	796	14/15	0.89	0.20	1.83	49,52,54,56	0
3	B2Q	B	900	23/23	0.93	0.15	1.43	41,48,49,49	0
3	B2Q	A	900	23/23	0.93	0.15	0.46	42,45,46,47	0
2	NAG	A	794	14/15	0.93	0.18	0.45	46,48,53,54	0
2	NAG	B	794	14/15	0.93	0.20	0.31	53,55,56,57	0
2	NAG	A	793	14/15	0.92	0.20	-0.39	71,73,76,76	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	NAG	A	795	14/15	0.67	0.35	-	83,85,87,87	0
2	NAG	B	797	14/15	0.76	0.36	-	81,83,85,85	0

6.5 Other polymers [i](#)

There are no such residues in this entry.