



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:43 AM GMT

PDB ID : 3MX0  
Title : Crystal Structure of EphA2 ectodomain in complex with ephrin-A5  
Authors : Himanen, J.P.; Yermekbayeva, L.; Janes, P.W.; Walker, J.R.; Xu, K.; Atapattu, L.; Rajashankar, K.R.; Mensinga, A.; Lackmann, M.; Nikolov, D.B.; Dhe-Paganon, S.  
Deposited on : 2010-05-06  
Resolution : 3.51 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  
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

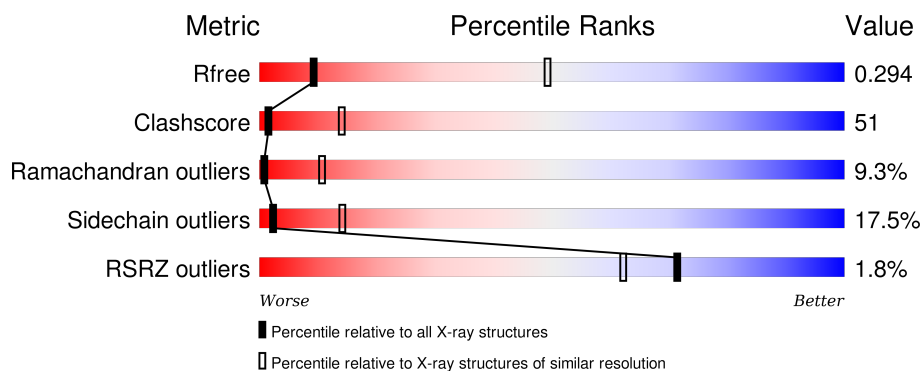
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.51 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	1051 (3.60-3.40)
Clashscore	102246	1157 (3.60-3.40)
Ramachandran outliers	100387	1120 (3.60-3.40)
Sidechain outliers	100360	1121 (3.60-3.40)
RSRZ outliers	91569	1058 (3.60-3.40)

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. 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	409	<div> <div>31%</div> <div>52%</div> <div>15%</div> <div>..</div> </div>
1	C	409	<div> <div>32%</div> <div>52%</div> <div>14%</div> <div>..</div> </div>
2	B	138	<div> <div>2%</div> <div>39%</div> <div>49%</div> <div>10%</div> <div>.</div> </div>
2	D	138	<div> <div>7%</div> <div>29%</div> <div>57%</div> <div>14%</div> <div>.</div> </div>

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 8574 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 Ephrin type-A receptor 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	406	Total	C	N	O	S	0	0	0
			3080	1944	511	597	28			
1	C	406	Total	C	N	O	S	0	0	0
			3080	1944	511	597	28			

- Molecule 2 is a protein called Ephrin-A5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	138	Total	C	N	O	S	0	0	0
			1151	736	198	209	8			
2	D	138	Total	C	N	O	S	0	0	0
			1151	736	198	209	8			

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

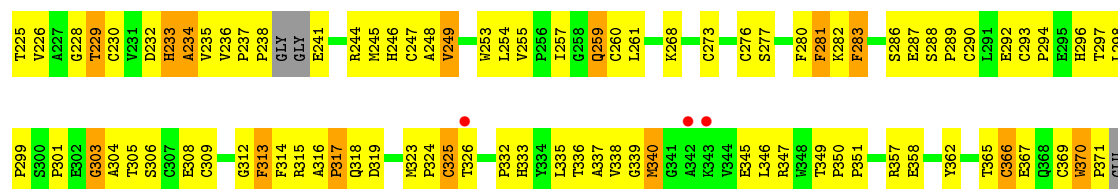


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		

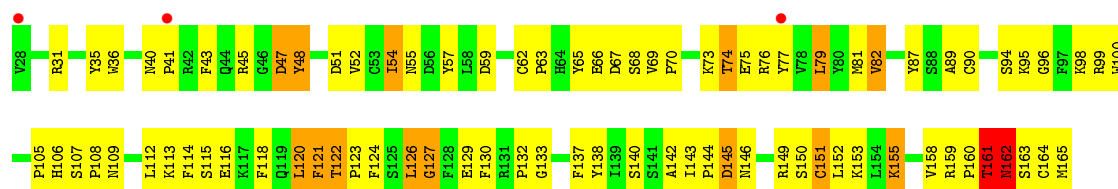
- Molecule 4 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	3	Total	C	N	O	0	0
			42	24	3	15		
4	D	3	Total	C	N	O	0	0
			42	24	3	15		

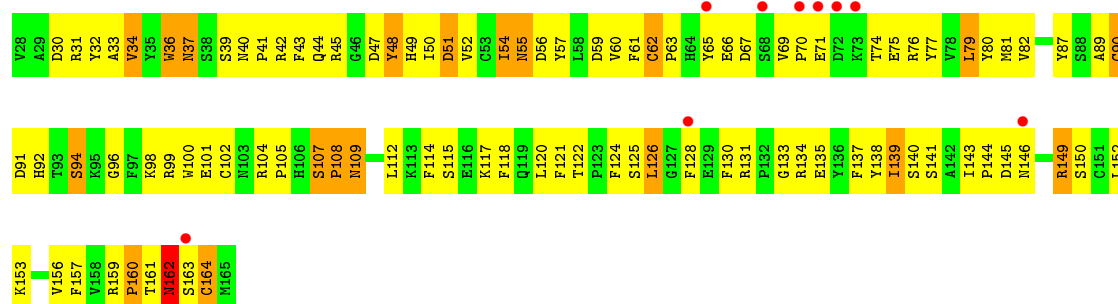




• Molecule 2: Ephrin-A5



• Molecule 2: Ephrin-A5



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	57.86Å 89.05Å 198.15Å 90.00° 96.22° 90.00°	Depositor
Resolution (Å)	45.03 – 3.51 45.03 – 3.51	Depositor EDS
% Data completeness (in resolution range)	88.1 (45.03-3.51) 88.2 (45.03-3.51)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.61 (at 3.48Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.1_357)	Depositor
R, $R_{free}$	0.234 , 0.295 0.223 , 0.294	Depositor DCC
$R_{free}$ test set	1125 reflections (5.02%)	DCC
Wilson B-factor (Å <sup>2</sup> )	78.4	Xtriage
Anisotropy	1.284	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 91.8	EDS
Estimated twinning fraction	0.065 for h,-k,-h-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 23134 reflections	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	8574	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	137.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.32% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG

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	0.54	0/3163	0.73	1/4314 (0.0%)
1	C	0.50	0/3163	0.71	1/4314 (0.0%)
2	B	0.44	0/1190	0.62	0/1610
2	D	0.44	0/1190	0.62	0/1610
All	All	0.50	0/8706	0.69	2/11848 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	54	LEU	CA-CB-CG	5.78	128.60	115.30
1	C	204	LEU	CA-CB-CG	5.60	128.19	115.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3080	0	2863	326	0
1	C	3080	0	2863	307	0
2	B	1151	0	1067	117	0
2	D	1151	0	1067	144	0
3	A	14	0	13	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	14	0	13	1	0
4	B	42	0	37	1	0
4	D	42	0	37	0	0
All	All	8574	0	7960	849	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 51.

All (849) 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:C:103:ARG:HD2	1:C:156:PHE:CZ	1.74	1.21
1:A:190:ALA:HB1	2:B:124:PHE:CZ	1.79	1.18
1:C:71:ASN:HB3	1:C:77:GLN:NE2	1.67	1.09
1:A:200:LYS:HB3	1:A:215:ILE:HD13	1.35	1.05
1:C:139:PHE:HE1	1:C:181:ALA:HB2	1.19	1.04
1:C:103:ARG:HD2	1:C:156:PHE:HZ	0.93	1.04
1:C:224:ALA:HB3	1:C:247:CYS:HB3	1.39	1.04
1:C:370:TRP:HB3	1:C:373:SER:HB3	1.36	1.02
1:A:224:ALA:HB3	1:A:247:CYS:HB3	1.41	1.02
1:C:120:ASN:HB3	1:C:122:TYR:HE1	1.27	0.99
2:B:43:PHE:HB3	2:B:152:LEU:HD21	1.50	0.94
1:C:139:PHE:CE1	1:C:181:ALA:HB2	2.02	0.93
1:C:43:TRP:CD1	1:C:83:THR:HA	2.04	0.93
1:C:100:PHE:CE2	1:C:164:ASN:HB2	2.05	0.92
1:C:67:TYR:CD1	1:C:81:LEU:HD11	2.05	0.92
1:C:59:MET:HB2	1:C:64:ILE:HD13	1.50	0.92
1:C:223:LEU:HD21	1:C:254:LEU:HD12	1.52	0.90
1:A:408:TYR:HB2	1:A:432:VAL:O	1.72	0.90
2:D:81:MET:HG3	2:D:138:TYR:CE2	2.09	0.88
1:C:103:ARG:CD	1:C:156:PHE:HZ	1.84	0.88
1:A:192:LEU:HD21	2:B:124:PHE:HE1	1.38	0.87
1:C:72:VAL:HG21	1:C:108:PHE:CE1	2.09	0.86
1:C:94:ILE:HG12	1:C:173:LEU:HD11	1.58	0.86
1:A:71:ASN:HB3	1:A:77:GLN:HE22	1.39	0.85
1:C:365:THR:OG1	1:C:411:THR:HG23	1.76	0.85
2:D:149:ARG:HG2	2:D:150:SER:N	1.91	0.85
1:A:103:ARG:HD2	1:A:156:PHE:CZ	2.12	0.85
2:D:100:TRP:CD2	2:D:114:PHE:HB3	2.12	0.85
1:C:71:ASN:CB	1:C:77:GLN:NE2	2.41	0.84
1:A:72:VAL:HG11	1:A:108:PHE:CE1	2.13	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:60:VAL:HG11	2:D:79:LEU:HD11	1.59	0.83
2:D:51:ASP:HB3	2:D:159:ARG:HD3	1.62	0.82
2:B:81:MET:HG3	2:B:138:TYR:CE2	2.14	0.82
1:C:87:TYR:HD2	1:C:176:LYS:O	1.64	0.81
2:D:131:ARG:HH11	2:D:134:ARG:NH2	1.77	0.81
1:A:93:ARG:HG2	1:A:95:PHE:HE2	1.45	0.80
1:C:122:TYR:HD2	1:C:139:PHE:O	1.65	0.80
1:C:72:VAL:HG21	1:C:108:PHE:HE1	1.47	0.80
1:C:52:TRP:CD1	1:C:80:TRP:O	2.36	0.78
1:C:91:ALA:HB2	1:C:198:TYR:CG	2.19	0.78
1:A:103:ARG:CZ	2:B:121:PHE:CZ	2.67	0.78
1:C:208:LEU:HD11	1:C:268:LYS:HG3	1.66	0.78
1:C:107:SER:HB3	1:C:153:SER:OG	1.84	0.77
1:C:32:LEU:HD12	1:C:33:ASP:N	1.98	0.77
2:D:34:VAL:HG12	2:D:34:VAL:O	1.83	0.77
1:A:335:LEU:HD12	1:A:336:THR:H	1.47	0.77
1:C:71:ASN:HB3	1:C:77:GLN:HE22	1.50	0.77
2:B:118:PHE:HA	2:B:130:PHE:CD1	2.20	0.77
1:A:212:PRO:HB2	1:A:214:THR:HG23	1.67	0.77
1:A:71:ASN:HB3	1:A:77:GLN:NE2	2.01	0.76
1:A:41:LEU:HD21	1:A:84:ASN:HD22	1.50	0.76
1:A:335:LEU:HD12	1:A:336:THR:N	2.01	0.76
1:C:31:LEU:O	1:C:32:LEU:HB3	1.85	0.76
1:C:82:ARG:HB2	1:C:134:PHE:HE1	1.50	0.76
1:A:188:CYS:SG	2:B:123:PRO:HB3	2.26	0.76
1:C:100:PHE:HE2	1:C:164:ASN:HB2	1.51	0.75
2:D:87:TYR:CD1	2:D:137:PHE:HB3	2.21	0.75
2:D:40:ASN:HB3	2:D:43:PHE:HD2	1.51	0.75
1:A:371:PRO:C	1:A:373:SER:N	2.40	0.74
1:C:93:ARG:HD3	1:C:95:PHE:HE2	1.51	0.74
2:D:122:THR:HG23	2:D:124:PHE:CD1	2.22	0.74
1:A:226:VAL:HG21	1:A:253:TRP:HZ3	1.52	0.74
1:A:43:TRP:CG	1:A:83:THR:HA	2.22	0.74
1:C:134:PHE:HD2	1:C:134:PHE:O	1.70	0.74
1:C:389:PRO:HB2	1:C:390:HIS:CD2	2.23	0.74
2:D:40:ASN:HD22	2:D:43:PHE:HE2	1.35	0.74
1:A:100:PHE:CE1	1:A:119:PHE:HE2	2.05	0.73
1:A:399:VAL:HG12	1:A:402:LEU:HD21	1.69	0.73
1:C:406:MET:HB3	1:C:408:TYR:CD1	2.23	0.73
1:C:95:PHE:HB2	1:C:197:TYR:CE1	2.22	0.73
1:C:276:CYS:HB2	1:C:303:GLY:HA2	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:208:LEU:HD11	1:A:268:LYS:HD2	1.70	0.73
1:C:120:ASN:HB3	1:C:122:TYR:CE1	2.18	0.73
1:C:223:LEU:HD23	1:C:248:ALA:HB2	1.70	0.73
1:C:80:TRP:CE2	1:C:183:GLN:HB2	2.23	0.73
1:C:413:GLU:OE1	1:C:425:ARG:HD2	1.88	0.73
2:B:144:PRO:HB2	2:B:146:ASN:HD21	1.51	0.73
1:C:188:CYS:SG	2:D:121:PHE:CE2	2.82	0.73
1:A:167:GLU:O	1:A:168:ARG:HG2	1.89	0.73
1:C:137:ARG:O	1:C:138:LEU:HD23	1.88	0.73
1:C:244:ARG:HH22	1:C:257:ILE:HG21	1.54	0.72
2:D:51:ASP:OD1	2:D:157:PHE:HB3	1.89	0.72
1:C:108:PHE:CZ	2:D:121:PHE:CE1	2.77	0.72
1:C:134:PHE:CD2	1:C:134:PHE:O	2.43	0.72
2:D:149:ARG:HG2	2:D:150:SER:H	1.51	0.72
1:A:100:PHE:O	1:A:164:ASN:HB2	1.89	0.72
1:C:226:VAL:HG21	1:C:253:TRP:CH2	2.25	0.72
1:A:384:ARG:H	1:A:401:ASP:HB3	1.54	0.72
2:B:87:TYR:HE1	2:B:153:LYS:HB2	1.55	0.72
1:A:41:LEU:HD21	1:A:84:ASN:ND2	2.05	0.71
1:A:411:THR:CB	1:A:429:THR:HG22	2.20	0.71
1:A:54:LEU:HD22	1:A:67:TYR:CE2	2.26	0.71
1:C:357:ARG:O	1:C:358:GLU:HG3	1.90	0.71
1:C:129:ASP:O	1:C:130:TYR:CD2	2.43	0.71
1:A:56:GLN:O	1:A:57:ASN:HB2	1.92	0.70
1:A:314:PHE:CD1	1:A:421:LEU:HD13	2.25	0.70
1:A:246:HIS:HB2	1:A:255:VAL:H	1.57	0.70
1:A:413:GLU:OE1	1:A:425:ARG:HD2	1.92	0.70
1:C:203:GLU:HA	1:C:212:PRO:O	1.91	0.70
1:C:80:TRP:CD2	1:C:183:GLN:HB2	2.27	0.70
2:B:87:TYR:CE1	2:B:153:LYS:HB2	2.25	0.70
2:D:87:TYR:HB2	2:D:137:PHE:HB3	1.73	0.70
1:C:95:PHE:CD2	1:C:169:SER:HB3	2.27	0.70
1:C:99:LYS:HB2	1:C:193:SER:HB3	1.73	0.70
1:A:52:TRP:HA	1:A:69:VAL:HG23	1.74	0.70
1:C:123:TYR:HA	1:C:179:TYR:O	1.90	0.70
2:D:100:TRP:CG	2:D:114:PHE:HB3	2.26	0.69
2:D:121:PHE:CD2	2:D:122:THR:N	2.61	0.69
2:D:59:ASP:HB3	2:D:61:PHE:CE1	2.26	0.69
1:A:32:LEU:HD12	1:A:33:ASP:N	2.07	0.69
1:C:135:GLN:HG3	1:C:137:ARG:HG2	1.74	0.69
1:C:92:GLU:O	1:C:172:PRO:HA	1.91	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:91:ALA:HB2	1:A:198:TYR:CG	2.28	0.69
1:C:200:LYS:HB3	1:C:215:ILE:HG23	1.74	0.69
1:C:411:THR:HB	1:C:429:THR:HG22	1.73	0.69
1:C:366:CYS:HB2	1:C:410:PHE:CE2	2.27	0.69
2:B:31:ARG:HG2	2:B:57:TYR:HB2	1.73	0.69
1:A:66:MET:SD	2:B:124:PHE:CZ	2.86	0.69
2:D:87:TYR:HD1	2:D:137:PHE:HB3	1.57	0.69
1:A:72:VAL:HG11	1:A:108:PHE:HE1	1.53	0.69
1:A:235:VAL:HG13	1:A:236:VAL:N	2.08	0.69
1:A:167:GLU:HG3	1:A:168:ARG:N	2.09	0.68
1:A:411:THR:HB	1:A:429:THR:HG22	1.76	0.68
1:C:103:ARG:NH2	2:D:121:PHE:CE1	2.62	0.68
1:A:88:ARG:HG2	1:A:88:ARG:HH11	1.59	0.68
1:C:406:MET:O	1:C:408:TYR:N	2.27	0.68
1:A:103:ARG:HD2	1:A:156:PHE:HZ	1.59	0.68
1:A:224:ALA:CB	1:A:247:CYS:HB3	2.23	0.68
1:A:234:ALA:HA	1:A:261:LEU:O	1.93	0.68
1:A:120:ASN:HB3	1:A:122:TYR:HE1	1.59	0.68
1:C:415:ARG:NH1	1:C:419:SER:HB3	2.09	0.67
1:A:172:PRO:HB3	1:A:218:SER:CB	2.24	0.67
1:C:244:ARG:NH2	1:C:257:ILE:HG21	2.10	0.67
1:A:192:LEU:HD21	2:B:124:PHE:CE1	2.26	0.67
1:A:102:VAL:HG11	1:A:117:GLU:HB3	1.76	0.67
1:C:282:LYS:HZ3	1:C:286:SER:H	1.40	0.67
1:A:226:VAL:HG21	1:A:253:TRP:CZ3	2.29	0.67
1:A:316:ALA:O	1:A:319:ASP:HB2	1.95	0.67
1:C:326:THR:O	1:C:418:VAL:HG21	1.96	0.66
1:C:47:PRO:HD2	1:C:79:ASN:HA	1.76	0.66
1:A:276:CYS:HB2	1:A:303:GLY:HA2	1.77	0.66
1:C:337:ALA:HB2	1:C:346:LEU:HD23	1.76	0.66
1:A:253:TRP:O	1:A:254:LEU:HD23	1.96	0.66
1:A:84:ASN:O	1:A:179:TYR:CE1	2.48	0.66
2:D:131:ARG:NH1	2:D:134:ARG:NH2	2.44	0.66
1:A:334:TYR:HB2	1:A:349:THR:HB	1.75	0.66
1:C:406:MET:HB3	1:C:408:TYR:CE1	2.30	0.66
1:A:103:ARG:NE	2:B:121:PHE:CZ	2.64	0.66
2:D:48:TYR:HD1	2:D:49:HIS:N	1.93	0.65
1:C:46:HIS:CD2	1:C:46:HIS:C	2.70	0.65
1:A:30:VAL:HG12	1:A:32:LEU:H	1.61	0.65
2:D:82:VAL:HG11	2:D:139:ILE:HD11	1.78	0.65
1:A:242:GLU:O	1:A:258:GLY:HA3	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:139:PHE:CE1	1:C:181:ALA:CB	2.79	0.65
1:C:34:PHE:HB2	1:C:43:TRP:CH2	2.30	0.65
1:C:143:ASP:OD1	1:C:144:THR:N	2.29	0.65
1:A:335:LEU:HD13	1:A:348:TRP:HB3	1.78	0.65
1:A:77:GLN:O	1:A:78:ASP:HB2	1.96	0.65
1:A:167:GLU:C	1:A:168:ARG:HG2	2.16	0.65
1:A:100:PHE:CE1	1:A:119:PHE:CE2	2.85	0.65
1:C:137:ARG:C	1:C:138:LEU:HD23	2.17	0.64
1:C:200:LYS:HA	1:C:215:ILE:HA	1.79	0.64
1:C:234:ALA:HA	1:C:261:LEU:O	1.97	0.64
1:C:103:ARG:CZ	2:D:121:PHE:CE1	2.80	0.64
2:B:150:SER:O	2:B:151:CYS:HB3	1.97	0.64
1:A:182:PHE:CE1	1:A:191:LEU:HD11	2.33	0.64
1:A:296:HIS:HB2	1:A:325:CYS:HB2	1.79	0.64
2:D:76:ARG:HH11	2:D:76:ARG:HG3	1.62	0.64
2:B:62:CYS:HB3	2:B:63:PRO:HD2	1.79	0.64
1:C:74:SER:HB2	1:C:77:GLN:HE22	1.61	0.64
1:A:94:ILE:HG23	1:A:173:LEU:HD12	1.79	0.64
2:B:100:TRP:CH2	2:B:116:GLU:HB2	2.32	0.64
2:D:100:TRP:HB3	2:D:114:PHE:CG	2.32	0.64
1:A:314:PHE:HD1	1:A:421:LEU:HD13	1.61	0.64
2:B:164:CYS:O	2:B:165:MET:HB2	1.98	0.64
1:A:313:PHE:HB3	1:A:325:CYS:HB3	1.79	0.63
1:A:269:VAL:HG12	1:A:270:GLU:HG2	1.80	0.63
1:C:362:TYR:HB2	1:C:392:LEU:HB3	1.79	0.63
1:C:87:TYR:CD2	1:C:176:LYS:O	2.49	0.63
1:A:134:PHE:CD2	1:A:135:GLN:N	2.66	0.63
1:A:348:TRP:O	1:A:395:THR:HB	1.97	0.63
1:C:237:PRO:HB2	1:C:238:PRO:HD3	1.81	0.63
2:B:120:LEU:H	2:B:120:LEU:HD12	1.63	0.63
1:C:82:ARG:HB2	1:C:134:PHE:CE1	2.32	0.63
2:B:82:VAL:HG12	2:B:96:GLY:HA3	1.81	0.63
2:B:105:PRO:HG2	2:B:106:HIS:CD2	2.33	0.63
1:C:127:ASP:OD1	1:C:175:ARG:HB3	1.99	0.63
1:C:137:ARG:HG3	1:C:138:LEU:HD23	1.81	0.63
2:B:43:PHE:HB3	2:B:152:LEU:CD2	2.25	0.63
2:D:40:ASN:OD1	2:D:41:PRO:HD2	1.98	0.63
1:A:235:VAL:HG22	1:A:236:VAL:H	1.62	0.63
1:C:121:LEU:HB2	1:C:145:ILE:HD11	1.80	0.63
1:C:151:THR:HG21	2:D:125:SER:OG	1.99	0.63
1:C:333:HIS:O	1:C:428:ARG:NH1	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:65:TYR:HB3	2:D:69:VAL:HG21	1.79	0.63
1:A:93:ARG:CG	1:A:95:PHE:HE2	2.09	0.62
1:A:367:GLU:HA	1:A:378:PRO:HA	1.80	0.62
1:A:103:ARG:NE	2:B:121:PHE:HZ	1.97	0.62
1:C:369:CYS:HB2	1:C:407:ASN:HB3	1.82	0.62
2:D:33:ALA:O	2:D:34:VAL:HG23	1.98	0.62
2:D:100:TRP:HB3	2:D:114:PHE:CD1	2.34	0.62
2:D:52:VAL:HA	2:D:159:ARG:NH2	2.14	0.62
1:C:246:HIS:ND1	1:C:255:VAL:HG23	2.14	0.62
1:A:277:SER:HB3	1:A:278:PRO:CD	2.30	0.62
2:D:82:VAL:CG1	2:D:139:ILE:HD11	2.30	0.62
1:C:93:ARG:O	1:C:93:ARG:HG3	1.99	0.62
1:A:147:PRO:HB3	1:A:164:ASN:HD21	1.65	0.61
1:C:103:ARG:NE	2:D:121:PHE:CZ	2.69	0.61
1:C:217:GLY:O	1:C:249:VAL:HG13	2.00	0.61
1:C:119:PHE:CE2	1:C:189:VAL:HG11	2.36	0.61
1:C:314:PHE:O	1:C:315:ARG:HG3	2.01	0.61
1:C:221:PRO:HG2	1:C:222:SER:H	1.65	0.61
1:C:103:ARG:CZ	2:D:121:PHE:CZ	2.83	0.61
1:A:71:ASN:CB	1:A:77:GLN:NE2	2.63	0.61
1:C:316:ALA:HB3	1:C:319:ASP:OD1	2.00	0.61
1:A:95:PHE:HB3	1:A:197:TYR:CE2	2.36	0.61
1:C:219:ASP:HB2	1:C:222:SER:HB2	1.81	0.61
1:A:102:VAL:HG21	1:A:147:PRO:HG3	1.82	0.61
2:B:100:TRP:CG	2:B:114:PHE:HB3	2.36	0.61
1:C:198:TYR:CE1	1:C:215:ILE:HG21	2.35	0.61
2:D:77:TYR:O	2:D:143:ILE:HD11	2.01	0.61
1:A:69:VAL:HG21	1:A:79:ASN:HD22	1.65	0.61
2:B:161:THR:O	2:B:162:ASN:HB3	1.99	0.61
2:D:54:ILE:O	2:D:55:ASN:HB2	2.01	0.61
1:A:200:LYS:HB3	1:A:215:ILE:CD1	2.21	0.60
1:A:384:ARG:N	1:A:401:ASP:HB3	2.16	0.60
1:C:411:THR:HB	1:C:429:THR:CG2	2.30	0.60
2:D:89:ALA:O	2:D:90:CYS:C	2.38	0.60
1:C:85:TRP:CZ2	1:C:177:GLY:HA3	2.37	0.60
1:A:29:VAL:HG12	1:A:198:TYR:CE2	2.37	0.60
2:B:100:TRP:CD1	2:B:114:PHE:CD2	2.90	0.60
1:A:224:ALA:HB3	1:A:247:CYS:CB	2.25	0.60
1:A:192:LEU:CD2	2:B:124:PHE:HE1	2.14	0.60
1:A:52:TRP:CG	1:A:81:LEU:HB2	2.37	0.60
1:C:223:LEU:CD2	1:C:254:LEU:HD12	2.29	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:119:PHE:CD2	1:A:189:VAL:HG11	2.37	0.60
1:C:298:LEU:HB2	1:C:308:GLU:O	2.01	0.59
1:C:226:VAL:HG21	1:C:253:TRP:HH2	1.66	0.59
1:C:338:VAL:HG12	1:C:339:GLY:N	2.16	0.59
2:D:79:LEU:HD12	2:D:100:TRP:CE3	2.37	0.59
1:A:52:TRP:CD1	1:A:81:LEU:HB2	2.37	0.59
2:D:79:LEU:HD12	2:D:100:TRP:HE3	1.67	0.59
2:B:98:LYS:O	2:B:98:LYS:HD3	2.02	0.59
1:A:399:VAL:O	1:A:402:LEU:HD11	2.03	0.59
1:A:233:HIS:O	1:A:234:ALA:HB2	2.03	0.59
1:A:246:HIS:ND1	1:A:255:VAL:HG22	2.18	0.59
1:A:77:GLN:O	1:A:78:ASP:CB	2.49	0.59
1:C:107:SER:O	1:C:109:PRO:HD3	2.03	0.59
1:C:233:HIS:O	1:C:273:CYS:SG	2.60	0.59
2:D:91:ASP:OD2	2:D:94:SER:HB2	2.01	0.59
1:A:217:GLY:O	1:A:249:VAL:HG13	2.03	0.59
1:A:282:LYS:HE2	1:A:286:SER:OG	2.02	0.59
1:A:204:LEU:HD22	1:A:205:LEU:N	2.17	0.59
2:B:161:THR:O	2:B:162:ASN:CB	2.51	0.59
2:B:100:TRP:CD1	2:B:114:PHE:HB3	2.38	0.59
1:A:246:HIS:O	1:A:254:LEU:N	2.36	0.59
1:A:406:MET:C	1:A:408:TYR:H	2.05	0.59
1:A:43:TRP:CD1	1:A:83:THR:HA	2.38	0.59
2:D:122:THR:HG22	2:D:124:PHE:H	1.68	0.58
1:A:66:MET:HE2	1:A:192:LEU:HD11	1.84	0.58
2:B:160:PRO:HD2	2:B:163:SER:HB2	1.83	0.58
1:A:71:ASN:CB	1:A:77:GLN:HE22	2.12	0.58
1:C:128:LEU:HD12	1:C:130:TYR:CE2	2.39	0.58
1:A:370:TRP:CD1	1:A:373:SER:HB3	2.39	0.58
2:D:82:VAL:HG12	2:D:96:GLY:HA3	1.83	0.58
1:A:84:ASN:O	1:A:179:TYR:CD1	2.56	0.58
1:A:182:PHE:N	1:A:182:PHE:CD2	2.70	0.58
1:C:93:ARG:CD	1:C:95:PHE:HE2	2.14	0.58
1:A:167:GLU:HG3	1:A:168:ARG:H	1.67	0.58
1:C:223:LEU:CD2	1:C:248:ALA:HB2	2.33	0.58
2:D:52:VAL:HG13	2:D:156:VAL:HG13	1.86	0.58
2:B:43:PHE:CD1	2:B:48:TYR:HD2	2.21	0.58
1:C:91:ALA:HB2	1:C:198:TYR:CD1	2.39	0.58
1:A:95:PHE:CB	1:A:197:TYR:CE2	2.87	0.58
1:C:167:GLU:O	1:C:168:ARG:HD3	2.03	0.58
1:A:313:PHE:C	1:A:314:PHE:CD2	2.77	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:99:ARG:HH11	2:D:99:ARG:HG3	1.69	0.58
1:A:329:PRO:HG2	1:A:414:ALA:O	2.04	0.58
1:C:68:SER:HB3	2:D:124:PHE:HZ	1.67	0.57
2:D:36:TRP:CZ2	2:D:140:SER:HB3	2.39	0.57
1:C:122:TYR:CD2	1:C:139:PHE:O	2.51	0.57
1:A:145:ILE:HD13	1:A:145:ILE:N	2.19	0.57
1:C:152:VAL:O	1:C:155:ASP:HB2	2.03	0.57
2:B:36:TRP:CZ2	2:B:140:SER:HB3	2.39	0.57
1:A:41:LEU:HD22	1:A:43:TRP:CD1	2.39	0.57
1:A:88:ARG:HG2	1:A:88:ARG:NH1	2.18	0.57
1:A:332:PRO:HG2	1:A:412:VAL:HG13	1.86	0.57
2:D:120:LEU:HD23	2:D:130:PHE:O	2.04	0.57
1:A:31:LEU:O	1:A:32:LEU:HB2	2.04	0.57
1:A:175:ARG:HH11	1:A:175:ARG:HG3	1.69	0.57
2:B:132:PRO:HA	2:B:158:VAL:HG11	1.86	0.57
2:D:98:LYS:HD3	2:D:98:LYS:C	2.25	0.57
2:D:34:VAL:CG1	2:D:34:VAL:O	2.53	0.57
1:A:134:PHE:HE2	1:A:136:LYS:HG3	1.68	0.57
1:A:236:VAL:HG22	1:A:236:VAL:O	2.04	0.57
1:C:392:LEU:HD21	1:C:397:VAL:HG11	1.87	0.57
1:C:73:MET:SD	1:C:112:ALA:HB3	2.43	0.57
1:A:57:ASN:HD21	2:B:127:GLY:N	2.03	0.57
2:D:43:PHE:C	2:D:45:ARG:H	2.08	0.57
1:A:114:SER:O	1:A:116:LYS:HE2	2.04	0.57
1:A:108:PHE:CZ	2:B:121:PHE:CZ	2.92	0.57
2:B:133:GLY:H	2:B:158:VAL:HB	1.69	0.57
1:A:108:PHE:CE2	2:B:121:PHE:CZ	2.93	0.57
2:D:48:TYR:HD1	2:D:49:HIS:H	1.52	0.57
1:C:391:GLY:O	1:C:393:THR:HG23	2.04	0.57
1:A:346:LEU:HB3	1:A:348:TRP:HZ3	1.70	0.56
2:B:52:VAL:HG21	2:B:118:PHE:CD2	2.39	0.56
1:A:103:ARG:NH1	1:A:156:PHE:CE2	2.73	0.56
2:D:122:THR:CG2	2:D:124:PHE:H	2.18	0.56
1:C:33:ASP:OD1	1:C:35:ALA:HB3	2.06	0.56
1:C:282:LYS:NZ	1:C:286:SER:H	2.03	0.56
1:A:333:HIS:HB3	1:A:349:THR:CG2	2.35	0.56
2:D:104:ARG:HB2	2:D:112:LEU:HD21	1.87	0.56
1:C:98:LEU:HD11	1:C:121:LEU:CD2	2.36	0.56
2:B:99:ARG:HG3	2:B:99:ARG:HH11	1.71	0.56
2:D:87:TYR:HB2	2:D:137:PHE:CB	2.35	0.56
2:B:74:THR:HG22	2:B:76:ARG:HH11	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:178:PHE:CD1	1:A:178:PHE:C	2.79	0.56
1:A:79:ASN:HB2	1:A:184:ASP:HB3	1.88	0.56
2:B:74:THR:O	2:B:74:THR:HG22	2.05	0.56
1:C:188:CYS:SG	2:D:121:PHE:CD2	2.98	0.56
1:C:169:SER:O	1:C:170:VAL:HB	2.05	0.56
1:A:412:VAL:O	1:A:427:PHE:HB2	2.05	0.56
1:A:103:ARG:NH1	1:A:156:PHE:HE2	2.04	0.56
1:C:43:TRP:HB3	1:C:82:ARG:O	2.05	0.56
2:D:43:PHE:CE1	2:D:48:TYR:HD2	2.23	0.56
1:C:314:PHE:CD1	1:C:421:LEU:HD22	2.41	0.56
1:C:111:GLY:O	1:C:112:ALA:O	2.25	0.55
1:C:198:TYR:HE1	1:C:215:ILE:HG21	1.71	0.55
1:C:370:TRP:HB3	1:C:373:SER:CB	2.23	0.55
2:D:131:ARG:HH11	2:D:134:ARG:HH21	1.52	0.55
1:A:124:ALA:O	1:A:178:PHE:HA	2.06	0.55
1:A:80:TRP:HA	1:A:182:PHE:O	2.06	0.55
1:C:94:ILE:CG1	1:C:173:LEU:HD11	2.33	0.55
2:D:122:THR:O	2:D:122:THR:HG22	2.05	0.55
1:C:32:LEU:C	1:C:32:LEU:HD12	2.27	0.55
2:B:81:MET:HB2	2:B:99:ARG:HG3	1.87	0.55
1:A:348:TRP:CZ3	1:A:396:SER:HA	2.41	0.55
1:C:82:ARG:HG3	1:C:139:PHE:CZ	2.42	0.55
1:A:316:ALA:HB1	1:A:317:PRO:HD2	1.87	0.55
1:C:31:LEU:HD21	1:C:198:TYR:CD2	2.42	0.55
2:D:149:ARG:CG	2:D:150:SER:N	2.64	0.55
1:C:46:HIS:HA	1:C:47:PRO:C	2.27	0.55
1:A:91:ALA:HB2	1:A:198:TYR:CD2	2.41	0.55
1:A:116:LYS:HG2	1:A:186:GLY:O	2.06	0.55
2:B:142:ALA:HB1	2:B:144:PRO:HD2	1.89	0.55
2:D:36:TRP:HZ2	2:D:140:SER:HB3	1.71	0.55
1:C:123:TYR:C	1:C:123:TYR:CD1	2.80	0.55
1:C:224:ALA:CB	1:C:247:CYS:HB3	2.27	0.55
1:C:318:GLN:O	1:C:318:GLN:HG2	2.06	0.55
2:B:121:PHE:HA	2:B:129:GLU:HG2	1.89	0.54
1:C:323:MET:HG3	1:C:324:PRO:HD2	1.89	0.54
2:B:70:PRO:HG2	2:B:73:LYS:HE3	1.89	0.54
1:A:66:MET:SD	2:B:124:PHE:CE2	3.00	0.54
1:C:88:ARG:HD3	1:C:173:LEU:HB2	1.89	0.54
2:D:98:LYS:NZ	2:D:101:GLU:HB2	2.21	0.54
1:A:344:VAL:HG23	1:A:399:VAL:HB	1.88	0.54
1:A:29:VAL:CG1	1:A:198:TYR:CE2	2.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:40:ASN:HB3	2:D:43:PHE:CD2	2.38	0.54
2:B:55:ASN:N	2:B:118:PHE:O	2.36	0.54
2:B:87:TYR:HB2	2:B:137:PHE:HB3	1.89	0.54
1:C:211:PHE:CE1	1:C:228:GLY:HA3	2.42	0.54
1:A:44:LEU:HD23	1:A:44:LEU:C	2.28	0.54
1:C:104:ASP:HB3	1:C:107:SER:OG	2.08	0.54
1:A:120:ASN:HB2	1:A:183:GLN:HB3	1.89	0.54
1:A:246:HIS:ND1	1:A:255:VAL:CG2	2.71	0.54
1:A:277:SER:HB3	1:A:278:PRO:HD2	1.90	0.54
1:A:57:ASN:HD21	2:B:127:GLY:HA2	1.73	0.54
1:A:399:VAL:CG1	1:A:402:LEU:HD21	2.37	0.54
1:C:29:VAL:HB	1:C:198:TYR:CE2	2.43	0.54
1:C:415:ARG:CZ	1:C:419:SER:HB3	2.37	0.54
1:C:84:ASN:O	1:C:85:TRP:C	2.46	0.53
2:D:98:LYS:HZ3	2:D:101:GLU:HB2	1.73	0.53
1:A:104:ASP:HB2	1:A:150:ILE:HG22	1.91	0.53
1:A:172:PRO:HB3	1:A:218:SER:HB2	1.90	0.53
2:B:132:PRO:HA	2:B:158:VAL:CG1	2.38	0.53
1:A:280:PHE:CD1	1:A:280:PHE:N	2.75	0.53
2:D:57:TYR:CE2	2:D:117:LYS:HD2	2.43	0.53
2:D:74:THR:HG21	2:D:105:PRO:HG3	1.89	0.53
2:B:100:TRP:CZ2	2:B:116:GLU:HB2	2.44	0.53
1:C:124:ALA:O	1:C:178:PHE:HA	2.08	0.53
2:B:149:ARG:HG3	2:B:150:SER:H	1.72	0.53
1:A:66:MET:SD	2:B:124:PHE:CE1	3.02	0.53
1:A:203:GLU:HA	1:A:212:PRO:O	2.09	0.53
1:A:92:GLU:O	1:A:172:PRO:HA	2.09	0.53
1:A:280:PHE:N	1:A:280:PHE:HD1	2.07	0.53
1:C:47:PRO:HB2	1:C:50:LYS:CB	2.39	0.53
1:A:411:THR:OG1	1:A:427:PHE:HD1	1.91	0.53
1:A:80:TRP:HH2	1:A:122:TYR:CE2	2.25	0.53
1:C:226:VAL:HG21	1:C:253:TRP:CZ3	2.43	0.52
1:C:211:PHE:CD1	1:C:228:GLY:HA3	2.45	0.52
1:A:103:ARG:HD3	2:B:121:PHE:CE2	2.45	0.52
1:C:43:TRP:CD1	1:C:83:THR:CA	2.87	0.52
2:D:161:THR:O	2:D:162:ASN:HB3	2.08	0.52
1:A:247:CYS:HB2	1:A:253:TRP:CZ3	2.44	0.52
1:C:100:PHE:HA	1:C:190:ALA:O	2.09	0.52
1:C:108:PHE:CZ	2:D:121:PHE:HE1	2.26	0.52
1:A:84:ASN:O	1:A:179:TYR:HE1	1.92	0.52
1:A:411:THR:HG1	1:A:427:PHE:HD1	1.55	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:128:PHE:HD2	2:D:130:PHE:CE2	2.28	0.52
1:A:346:LEU:O	1:A:396:SER:HB2	2.09	0.52
2:D:100:TRP:CD1	2:D:114:PHE:CD2	2.98	0.52
2:D:104:ARG:HB2	2:D:112:LEU:HD11	1.92	0.52
1:A:75:GLY:O	1:A:77:GLN:HG2	2.10	0.52
1:C:52:TRP:HD1	1:C:80:TRP:O	1.87	0.52
1:A:167:GLU:CG	1:A:168:ARG:N	2.73	0.52
1:C:85:TRP:CE2	1:C:177:GLY:HA3	2.45	0.52
1:C:104:ASP:OD2	1:C:152:VAL:HG13	2.09	0.52
1:A:316:ALA:HB1	1:A:318:GLN:HE21	1.73	0.52
1:A:317:PRO:HG2	1:A:318:GLN:HE22	1.75	0.52
2:D:62:CYS:HB3	2:D:63:PRO:HD2	1.92	0.52
1:C:365:THR:HG1	1:C:411:THR:HG23	1.73	0.52
1:C:337:ALA:CB	1:C:346:LEU:HD23	2.38	0.52
2:D:76:ARG:NH1	2:D:76:ARG:HG3	2.25	0.51
1:C:68:SER:CB	2:D:124:PHE:HZ	2.23	0.51
2:B:100:TRP:HB3	2:B:114:PHE:CD1	2.45	0.51
1:A:316:ALA:HB1	1:A:318:GLN:NE2	2.25	0.51
1:C:318:GLN:CD	1:C:318:GLN:H	2.12	0.51
1:C:67:TYR:CD1	1:C:81:LEU:CD1	2.86	0.51
1:A:212:PRO:CB	1:A:214:THR:HG23	2.38	0.51
1:C:413:GLU:HG3	1:C:427:PHE:HB3	1.91	0.51
1:C:357:ARG:NH2	1:C:417:GLY:HA3	2.26	0.51
2:D:76:ARG:HB2	2:D:144:PRO:HD3	1.92	0.51
1:C:281:PHE:HB2	1:C:304:ALA:O	2.11	0.51
1:A:137:ARG:HG3	1:A:138:LEU:HD23	1.93	0.51
1:A:98:LEU:HA	1:A:193:SER:O	2.11	0.51
1:A:101:THR:HG22	1:A:162:LYS:O	2.10	0.51
1:A:103:ARG:HH11	1:A:156:PHE:HE2	1.59	0.51
1:A:95:PHE:HB3	1:A:197:TYR:HE2	1.75	0.51
2:B:160:PRO:HG2	2:B:163:SER:HB2	1.91	0.51
1:A:117:GLU:OE2	1:A:150:ILE:HD12	2.11	0.51
1:A:52:TRP:HD1	1:A:80:TRP:O	1.94	0.51
1:A:94:ILE:HG23	1:A:173:LEU:CD1	2.41	0.51
2:D:133:GLY:HA2	2:D:160:PRO:HD3	1.92	0.51
1:A:276:CYS:O	1:A:277:SER:O	2.29	0.51
2:D:121:PHE:CD2	2:D:121:PHE:C	2.84	0.50
2:D:124:PHE:HB3	2:D:126:LEU:HD12	1.92	0.50
1:A:208:LEU:O	1:A:231:VAL:HG13	2.10	0.50
1:C:98:LEU:HD11	1:C:121:LEU:HD22	1.91	0.50
1:A:220:ALA:HB3	1:A:221:PRO:HD3	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:GLN:NE2	2:B:114:PHE:CD2	2.79	0.50
1:A:57:ASN:HD21	2:B:127:GLY:CA	2.24	0.50
1:A:411:THR:OG1	1:A:429:THR:HG22	2.12	0.50
1:C:335:LEU:HB3	1:C:428:ARG:HG2	1.92	0.50
1:A:124:ALA:HB3	1:A:179:TYR:HB2	1.93	0.50
2:B:77:TYR:O	2:B:143:ILE:HG13	2.11	0.50
2:D:102:CYS:HA	2:D:112:LEU:HD12	1.94	0.50
1:C:184:ASP:CG	1:C:186:GLY:H	2.15	0.50
1:A:418:VAL:HG23	1:A:418:VAL:O	2.12	0.50
1:A:406:MET:C	1:A:408:TYR:N	2.65	0.50
1:A:29:VAL:HG11	1:A:198:TYR:OH	2.12	0.50
2:B:100:TRP:HH2	2:B:116:GLU:HB2	1.74	0.50
2:D:160:PRO:HB2	2:D:163:SER:HB2	1.94	0.50
1:C:135:GLN:CG	1:C:137:ARG:HG2	2.40	0.50
1:A:317:PRO:HG2	1:A:318:GLN:NE2	2.27	0.50
1:C:384:ARG:O	1:C:399:VAL:HA	2.12	0.50
2:B:40:ASN:OD1	2:B:41:PRO:HD2	2.11	0.50
1:A:104:ASP:HB2	1:A:150:ILE:CG2	2.42	0.50
4:B:401:NAG:H61	4:B:402:NAG:C7	2.42	0.50
1:A:134:PHE:CD2	1:A:134:PHE:C	2.85	0.49
1:C:338:VAL:HG12	1:C:339:GLY:H	1.77	0.49
1:A:99:LYS:HA	1:A:164:ASN:O	2.12	0.49
1:A:127:ASP:C	1:A:128:LEU:HD23	2.31	0.49
1:C:82:ARG:NE	1:C:83:THR:O	2.45	0.49
2:D:57:TYR:HE2	2:D:117:LYS:HD2	1.77	0.49
1:C:409:THR:HG23	1:C:431:SER:OG	2.11	0.49
1:A:125:GLU:HB3	1:A:175:ARG:HB2	1.94	0.49
1:C:88:ARG:HD2	1:C:91:ALA:O	2.13	0.49
1:A:167:GLU:O	1:A:168:ARG:NH1	2.39	0.49
1:A:351:PRO:HD3	1:A:362:TYR:OH	2.13	0.49
1:C:129:ASP:O	1:C:130:TYR:HD2	1.91	0.49
1:A:147:PRO:HB3	1:A:164:ASN:ND2	2.27	0.49
1:C:286:SER:OG	1:C:288:SER:HB2	2.13	0.49
1:A:326:THR:OG1	1:A:418:VAL:HG11	2.13	0.49
1:C:72:VAL:HG11	1:C:108:PHE:CE1	2.48	0.49
2:D:118:PHE:HA	2:D:130:PHE:CD1	2.47	0.49
1:C:236:VAL:O	1:C:236:VAL:HG22	2.13	0.49
1:C:323:MET:HG3	1:C:324:PRO:CD	2.43	0.49
2:D:131:ARG:NH1	2:D:134:ARG:HH21	2.09	0.49
1:C:152:VAL:HG12	1:C:153:SER:H	1.78	0.49
1:C:95:PHE:HD2	1:C:169:SER:HB3	1.75	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:59:ASP:OD1	2:D:115:SER:HB2	2.13	0.49
1:A:134:PHE:CE2	1:A:136:LYS:HG3	2.47	0.49
1:A:73:MET:SD	1:A:112:ALA:HB3	2.53	0.49
1:C:74:SER:HB2	1:C:77:GLN:NE2	2.28	0.48
1:A:123:TYR:HA	1:A:179:TYR:O	2.13	0.48
2:D:43:PHE:O	2:D:45:ARG:N	2.44	0.48
1:A:190:ALA:HB1	2:B:124:PHE:HZ	1.64	0.48
1:A:72:VAL:HG21	1:A:108:PHE:CE1	2.48	0.48
1:A:93:ARG:CG	1:A:95:PHE:CE2	2.93	0.48
2:B:65:TYR:HE1	2:B:75:GLU:H	1.60	0.48
1:C:282:LYS:HE2	1:C:288:SER:O	2.13	0.48
1:C:221:PRO:CG	1:C:222:SER:H	2.25	0.48
1:C:82:ARG:HD2	1:C:179:TYR:CD1	2.49	0.48
2:D:43:PHE:CZ	2:D:48:TYR:CD2	3.01	0.48
1:C:145:ILE:HD13	1:C:145:ILE:N	2.28	0.48
1:A:267:GLU:OE1	1:A:290:CYS:HB2	2.13	0.48
1:C:130:TYR:O	1:C:132:THR:N	2.40	0.48
1:C:41:LEU:HD21	1:C:84:ASN:HD21	1.79	0.48
1:C:102:VAL:HG23	1:C:189:VAL:HG13	1.95	0.48
1:A:366:CYS:SG	1:A:410:PHE:HE2	2.36	0.48
1:A:149:GLU:OE1	1:A:162:LYS:HG3	2.13	0.48
1:C:108:PHE:CE1	2:D:121:PHE:CE1	3.01	0.48
1:A:159:ARG:NH2	2:B:126:LEU:O	2.46	0.48
1:C:69:VAL:HG12	1:C:189:VAL:HG23	1.95	0.48
2:D:52:VAL:HG21	2:D:118:PHE:CE2	2.49	0.48
1:A:120:ASN:OD1	1:A:144:THR:HG23	2.13	0.48
1:A:332:PRO:O	1:A:428:ARG:HD2	2.12	0.48
1:A:237:PRO:HB2	1:A:238:PRO:HD3	1.95	0.48
1:A:66:MET:CG	2:B:124:PHE:CZ	2.97	0.48
1:C:244:ARG:HB2	1:C:244:ARG:CZ	2.42	0.48
1:A:366:CYS:SG	1:A:367:GLU:N	2.87	0.48
1:C:338:VAL:HG12	1:C:340:MET:H	1.78	0.48
1:A:387:GLU:HG3	1:A:388:PRO:HD2	1.94	0.48
1:C:380:GLU:O	1:C:383:VAL:HG22	2.13	0.48
1:C:383:VAL:HG12	1:C:402:LEU:HD23	1.94	0.48
1:C:124:ALA:HB2	1:C:139:PHE:CD2	2.48	0.48
2:D:118:PHE:HD1	2:D:130:PHE:CE1	2.32	0.48
1:A:85:TRP:HD1	1:A:179:TYR:CE1	2.32	0.48
1:A:385:TYR:CD2	1:A:399:VAL:HG22	2.49	0.48
1:A:333:HIS:HB3	1:A:349:THR:HG22	1.96	0.48
2:D:54:ILE:HA	2:D:54:ILE:HD12	1.66	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:122:TYR:HB3	1:C:139:PHE:HB3	1.96	0.48
1:A:34:PHE:C	1:A:34:PHE:CD2	2.87	0.48
2:D:43:PHE:CE1	2:D:48:TYR:CD2	3.02	0.48
2:B:54:ILE:O	2:B:55:ASN:HB2	2.13	0.48
1:C:100:PHE:O	1:C:163:LEU:HD12	2.14	0.48
1:A:95:PHE:HB2	1:A:197:TYR:CE2	2.49	0.48
1:C:233:HIS:O	1:C:234:ALA:HB2	2.13	0.48
1:A:279:GLY:C	1:A:280:PHE:HD1	2.17	0.47
2:B:121:PHE:CD2	2:B:121:PHE:C	2.88	0.47
1:C:370:TRP:C	1:C:374:GLY:H	2.18	0.47
1:A:255:VAL:HG23	1:A:255:VAL:O	2.13	0.47
1:A:85:TRP:HD1	1:A:179:TYR:CZ	2.32	0.47
1:A:411:THR:HB	1:A:429:THR:CG2	2.42	0.47
2:B:31:ARG:NH1	2:B:59:ASP:OD2	2.48	0.47
1:A:333:HIS:HB3	1:A:349:THR:HG21	1.96	0.47
2:B:161:THR:O	2:B:162:ASN:OD1	2.32	0.47
2:B:159:ARG:HD2	2:B:163:SER:O	2.15	0.47
1:C:68:SER:HB3	2:D:124:PHE:CZ	2.47	0.47
1:A:235:VAL:HG22	1:A:236:VAL:CG1	2.45	0.47
1:C:335:LEU:HD22	1:C:412:VAL:HG12	1.95	0.47
2:D:32:TYR:N	2:D:57:TYR:O	2.47	0.47
1:A:119:PHE:HD2	1:A:189:VAL:HG11	1.77	0.47
1:C:211:PHE:O	1:C:212:PRO:O	2.31	0.47
2:B:59:ASP:OD1	2:B:113:LYS:HE3	2.15	0.47
1:A:56:GLN:NE2	2:B:114:PHE:HD2	2.13	0.47
2:D:98:LYS:CD	2:D:98:LYS:C	2.83	0.47
1:A:391:GLY:O	1:A:392:LEU:HD12	2.15	0.47
1:C:108:PHE:HB3	1:C:111:GLY:H	1.79	0.47
1:A:115:CYS:O	1:A:116:LYS:NZ	2.41	0.47
1:C:31:LEU:O	1:C:32:LEU:CB	2.59	0.47
1:A:346:LEU:HB3	1:A:348:TRP:CZ3	2.49	0.47
1:A:211:PHE:O	1:A:212:PRO:O	2.32	0.47
1:A:385:TYR:HD2	1:A:399:VAL:HG22	1.80	0.47
1:A:99:LYS:HE3	1:A:165:VAL:CG1	2.45	0.47
1:A:400:SER:O	1:A:401:ASP:HB3	2.15	0.47
1:C:41:LEU:HD21	1:C:84:ASN:ND2	2.30	0.47
2:B:99:ARG:CZ	2:B:99:ARG:HB3	2.43	0.47
1:A:86:VAL:HB	1:A:178:PHE:CE1	2.49	0.47
1:A:102:VAL:HG11	1:A:117:GLU:CB	2.45	0.47
2:B:144:PRO:HB2	2:B:146:ASN:ND2	2.24	0.47
1:C:326:THR:HG21	1:C:357:ARG:CG	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:350:PRO:HA	1:A:362:TYR:OH	2.15	0.47
1:C:229:THR:HG23	1:C:230:CYS:N	2.30	0.47
1:C:345:GLU:HG3	1:C:347:ARG:HG3	1.96	0.47
1:C:366:CYS:HB2	1:C:410:PHE:HE2	1.77	0.47
2:D:62:CYS:HB3	2:D:63:PRO:CD	2.45	0.47
1:A:111:GLY:O	1:A:112:ALA:C	2.52	0.47
1:C:58:ILE:HG22	1:C:58:ILE:O	2.14	0.47
2:B:100:TRP:HD1	2:B:114:PHE:CD2	2.33	0.46
1:C:137:ARG:HG3	1:C:138:LEU:CD2	2.45	0.46
2:D:82:VAL:HG21	2:D:139:ILE:HD11	1.97	0.46
1:A:62:MET:HA	1:A:63:PRO:HD3	1.72	0.46
1:C:296:HIS:O	1:C:325:CYS:SG	2.72	0.46
1:A:370:TRP:HD1	1:A:371:PRO:N	2.13	0.46
2:B:126:LEU:O	2:B:127:GLY:O	2.33	0.46
2:D:56:ASP:O	2:D:118:PHE:HB2	2.16	0.46
1:C:48:TYR:C	1:C:50:LYS:H	2.19	0.46
1:A:355:GLY:O	1:A:357:ARG:HG3	2.15	0.46
1:C:100:PHE:CD2	1:C:100:PHE:N	2.83	0.46
1:A:119:PHE:C	1:A:120:ASN:OD1	2.54	0.46
1:A:135:GLN:HG2	1:A:138:LEU:HD23	1.96	0.46
1:A:235:VAL:O	1:A:237:PRO:HD3	2.15	0.46
1:A:242:GLU:HA	1:A:242:GLU:OE1	2.15	0.46
2:D:82:VAL:CG2	2:D:139:ILE:HD11	2.46	0.46
1:A:215:ILE:O	1:A:216:ALA:O	2.34	0.46
1:C:149:GLU:N	1:C:164:ASN:OD1	2.43	0.46
1:C:197:TYR:CD1	1:C:197:TYR:C	2.89	0.46
1:A:207:GLY:O	1:A:208:LEU:HB2	2.16	0.46
2:B:87:TYR:CE2	2:B:155:LYS:HG3	2.51	0.46
2:B:82:VAL:CG1	2:B:96:GLY:HA3	2.44	0.46
1:C:221:PRO:O	1:C:222:SER:C	2.54	0.46
2:B:160:PRO:CD	2:B:163:SER:HB2	2.45	0.46
1:A:327:ARG:O	1:A:355:GLY:HA3	2.16	0.46
1:C:370:TRP:O	1:C:373:SER:HB3	2.15	0.46
2:B:152:LEU:HA	2:B:152:LEU:HD23	1.49	0.46
2:B:76:ARG:HB2	2:B:144:PRO:HD3	1.97	0.46
2:D:124:PHE:C	2:D:126:LEU:H	2.17	0.46
1:A:72:VAL:HG11	1:A:108:PHE:CZ	2.50	0.46
1:A:86:VAL:CG2	1:A:178:PHE:CE1	2.98	0.46
2:D:122:THR:HG22	2:D:124:PHE:N	2.31	0.46
1:A:32:LEU:C	1:A:32:LEU:HD12	2.36	0.46
2:D:161:THR:O	2:D:162:ASN:CB	2.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:420:GLY:C	1:A:422:VAL:H	2.19	0.46
1:A:400:SER:O	1:A:401:ASP:CB	2.64	0.46
1:A:233:HIS:O	1:A:273:CYS:SG	2.74	0.46
1:C:362:TYR:O	1:C:392:LEU:HB2	2.15	0.46
1:C:392:LEU:HA	1:C:392:LEU:HD12	1.74	0.46
1:C:237:PRO:CB	1:C:238:PRO:HD3	2.44	0.46
2:B:66:GLU:C	2:B:68:SER:H	2.19	0.46
2:B:107:SER:HA	2:B:108:PRO:HD2	1.63	0.46
1:C:103:ARG:NE	2:D:121:PHE:HZ	2.11	0.46
2:B:79:LEU:N	2:B:79:LEU:HD23	2.31	0.46
1:C:33:ASP:O	1:C:34:PHE:C	2.53	0.46
2:B:66:GLU:O	2:B:68:SER:N	2.49	0.46
1:A:107:SER:CB	1:A:153:SER:HB3	2.46	0.46
1:C:70:CYS:O	1:C:70:CYS:SG	2.74	0.46
2:B:35:TYR:N	2:B:35:TYR:CD1	2.84	0.46
1:C:100:PHE:CE1	1:C:119:PHE:CE2	3.04	0.45
1:C:144:THR:C	1:C:145:ILE:HD13	2.36	0.45
1:A:407:ASN:OD1	3:A:501:NAG:O5	2.32	0.45
1:C:103:ARG:NH2	2:D:121:PHE:HE1	2.13	0.45
1:C:68:SER:CB	2:D:124:PHE:CZ	3.00	0.45
1:C:56:GLN:OE1	2:D:114:PHE:HA	2.16	0.45
1:A:80:TRP:NE1	1:A:136:LYS:HG2	2.32	0.45
1:C:367:GLU:OE2	3:C:501:NAG:H82	2.16	0.45
1:A:331:ALA:O	1:A:332:PRO:C	2.55	0.45
1:A:332:PRO:HG2	1:A:412:VAL:CG1	2.46	0.45
1:A:357:ARG:HB3	1:A:359:ASP:OD1	2.17	0.45
1:C:73:MET:O	1:C:75:GLY:N	2.49	0.45
2:B:43:PHE:CD1	2:B:48:TYR:CD2	3.04	0.45
1:C:167:GLU:CG	1:C:168:ARG:N	2.79	0.45
1:A:145:ILE:HD13	1:A:145:ILE:H	1.81	0.45
1:A:149:GLU:CD	1:A:162:LYS:HG3	2.37	0.45
2:B:79:LEU:HB2	2:B:100:TRP:HB2	1.98	0.45
1:A:370:TRP:CD1	1:A:370:TRP:C	2.89	0.45
1:A:120:ASN:HB3	1:A:122:TYR:CE1	2.45	0.45
2:D:61:PHE:CD1	2:D:61:PHE:N	2.84	0.45
1:A:244:ARG:HH12	1:A:257:ILE:HD12	1.82	0.45
1:A:158:ALA:O	1:A:159:ARG:HB2	2.16	0.45
2:B:122:THR:CG2	2:B:124:PHE:H	2.29	0.45
2:B:87:TYR:HB2	2:B:137:PHE:CB	2.46	0.45
1:C:100:PHE:HD2	1:C:100:PHE:H	1.64	0.45
2:D:128:PHE:CD2	2:D:130:PHE:CE2	3.05	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:51:ASP:HB3	2:D:159:ARG:CD	2.40	0.45
1:A:208:LEU:C	1:A:231:VAL:HG13	2.37	0.45
1:C:47:PRO:CD	1:C:79:ASN:HA	2.46	0.45
1:C:236:VAL:HA	1:C:237:PRO:HD3	1.67	0.45
2:B:95:LYS:HG2	2:B:96:GLY:N	2.32	0.45
2:D:118:PHE:HA	2:D:130:PHE:HD1	1.81	0.45
1:C:46:HIS:HD2	1:C:46:HIS:C	2.18	0.45
1:A:350:PRO:HA	1:A:351:PRO:HD3	1.80	0.45
1:A:363:SER:HA	1:A:390:HIS:HA	1.99	0.45
2:D:42:ARG:HH22	2:D:50:ILE:HG22	1.80	0.45
1:A:154:SER:C	1:A:156:PHE:H	2.19	0.45
2:B:100:TRP:CD1	2:B:114:PHE:CG	3.05	0.45
1:A:120:ASN:ND2	1:A:141:LYS:HZ2	2.15	0.45
1:A:411:THR:OG1	1:A:427:PHE:CD1	2.69	0.45
1:A:313:PHE:CB	1:A:325:CYS:HB3	2.44	0.45
2:D:75:GLU:HB3	2:D:77:TYR:CE2	2.52	0.45
2:B:164:CYS:O	2:B:165:MET:CB	2.64	0.45
1:C:335:LEU:HD12	1:C:336:THR:N	2.32	0.45
1:A:139:PHE:N	1:A:139:PHE:CD2	2.85	0.45
2:D:133:GLY:CA	2:D:160:PRO:HD3	2.47	0.44
2:D:66:GLU:O	2:D:69:VAL:HG23	2.17	0.44
2:B:69:VAL:HA	2:B:70:PRO:HD3	1.71	0.44
1:A:180:LEU:O	1:A:181:ALA:HB2	2.17	0.44
1:A:300:SER:HB2	1:A:301:PRO:HD2	1.98	0.44
2:D:159:ARG:HA	2:D:160:PRO:HD2	1.64	0.44
1:A:163:LEU:HG	1:A:164:ASN:N	2.33	0.44
1:A:88:ARG:HD2	1:A:173:LEU:HB3	1.99	0.44
1:A:434:ILE:HG13	1:A:435:ASN:H	1.83	0.44
1:A:406:MET:O	1:A:408:TYR:N	2.36	0.44
1:A:85:TRP:CD1	1:A:179:TYR:CZ	3.06	0.44
1:A:349:THR:HA	1:A:350:PRO:HD3	1.78	0.44
2:D:71:GLU:O	2:D:74:THR:HB	2.17	0.44
1:A:266:TYR:CE1	1:A:275:ALA:HB2	2.52	0.44
2:B:122:THR:HG22	2:B:124:PHE:H	1.82	0.44
1:A:137:ARG:NE	2:D:109:ASN:O	2.50	0.44
1:A:69:VAL:CG2	1:A:79:ASN:HD22	2.28	0.44
2:D:74:THR:HG22	2:D:74:THR:O	2.18	0.44
1:A:310:GLU:OE2	1:A:313:PHE:HE2	2.01	0.44
1:C:55:MET:CE	2:D:117:LYS:HD3	2.47	0.44
1:C:72:VAL:HG11	1:C:108:PHE:CZ	2.52	0.44
1:C:159:ARG:NH2	2:D:126:LEU:O	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:346:LEU:O	1:A:396:SER:CB	2.66	0.44
1:A:69:VAL:HG11	1:A:184:ASP:OD2	2.17	0.44
1:A:344:VAL:HG22	1:A:402:LEU:HD11	1.99	0.44
1:C:326:THR:CB	1:C:357:ARG:HD2	2.48	0.44
2:D:69:VAL:HA	2:D:70:PRO:HD3	1.76	0.44
1:C:54:LEU:HA	1:C:66:MET:O	2.17	0.44
1:A:99:LYS:HG3	1:A:193:SER:HB3	1.99	0.44
1:A:160:HIS:CE1	1:A:162:LYS:HZ2	2.36	0.44
1:C:31:LEU:HD21	1:C:198:TYR:CE2	2.52	0.44
2:B:43:PHE:CE1	2:B:48:TYR:CD2	3.06	0.44
1:C:100:PHE:HD2	1:C:100:PHE:N	2.15	0.44
1:C:232:ASP:O	1:C:273:CYS:HB2	2.18	0.44
1:A:43:TRP:CD1	1:A:84:ASN:N	2.80	0.44
1:A:392:LEU:HA	1:A:392:LEU:HD12	1.80	0.44
1:C:101:THR:H	1:C:190:ALA:HB3	1.83	0.43
2:D:100:TRP:CG	2:D:114:PHE:CG	3.06	0.43
2:D:52:VAL:HG21	2:D:118:PHE:CD2	2.52	0.43
2:B:143:ILE:N	2:B:144:PRO:CD	2.81	0.43
2:D:31:ARG:NH1	2:D:59:ASP:OD2	2.52	0.43
1:A:246:HIS:O	1:A:253:TRP:HA	2.18	0.43
1:C:357:ARG:C	1:C:358:GLU:HG3	2.39	0.43
1:C:238:PRO:HG2	1:C:241:GLU:N	2.32	0.43
1:C:221:PRO:HG2	1:C:222:SER:N	2.32	0.43
1:A:151:THR:HG23	1:A:162:LYS:HB2	2.00	0.43
1:C:280:PHE:CD2	1:C:292:GLU:HA	2.54	0.43
1:C:147:PRO:HB3	1:C:164:ASN:ND2	2.33	0.43
1:A:188:CYS:SG	2:B:121:PHE:CE2	3.12	0.43
2:D:82:VAL:HG21	2:D:139:ILE:CD1	2.47	0.43
2:B:99:ARG:CG	2:B:99:ARG:HH11	2.31	0.43
1:A:31:LEU:HD21	1:A:198:TYR:CE2	2.54	0.43
1:A:241:GLU:HG3	1:A:242:GLU:N	2.33	0.43
1:C:236:VAL:O	1:C:236:VAL:CG2	2.66	0.43
1:A:364:VAL:HG23	1:A:389:PRO:O	2.19	0.43
1:A:223:LEU:HD23	1:A:223:LEU:HA	1.79	0.43
1:C:86:VAL:O	1:C:177:GLY:HA2	2.18	0.43
1:C:102:VAL:HG11	1:C:147:PRO:HG2	2.00	0.43
1:A:43:TRP:CD2	1:A:83:THR:HA	2.53	0.43
1:A:156:PHE:O	1:A:159:ARG:N	2.47	0.43
2:B:126:LEU:H	2:B:126:LEU:HG	1.57	0.43
1:A:47:PRO:O	1:A:48:TYR:C	2.57	0.43
1:A:59:MET:HB3	1:A:59:MET:HE2	1.80	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:72:VAL:HB	1:A:115:CYS:HB2	1.99	0.43
1:C:100:PHE:CD1	1:C:119:PHE:CE2	3.07	0.43
1:C:167:GLU:C	1:C:168:ARG:HG2	2.39	0.43
1:C:281:PHE:HD1	1:C:306:SER:HA	1.84	0.43
1:A:56:GLN:O	1:A:57:ASN:CB	2.64	0.43
1:C:257:ILE:HG22	1:C:257:ILE:O	2.18	0.43
1:C:255:VAL:O	1:C:255:VAL:HG23	2.18	0.43
2:B:77:TYR:CD1	2:B:142:ALA:HA	2.54	0.42
1:C:47:PRO:HG2	1:C:51:GLY:CA	2.49	0.42
2:B:66:GLU:HG3	2:B:66:GLU:H	1.57	0.42
1:C:43:TRP:NE1	1:C:83:THR:HA	2.34	0.42
2:D:52:VAL:HA	2:D:159:ARG:HH21	1.83	0.42
1:A:370:TRP:O	1:A:373:SER:HB3	2.19	0.42
1:A:238:PRO:HG2	1:A:241:GLU:N	2.34	0.42
1:C:48:TYR:C	1:C:50:LYS:N	2.72	0.42
3:A:501:NAG:H3	3:A:501:NAG:O7	2.19	0.42
1:C:116:LYS:HD2	1:C:185:ILE:CG1	2.50	0.42
1:C:259:GLN:HB2	1:C:259:GLN:HE21	1.64	0.42
2:D:122:THR:HG23	2:D:124:PHE:HD1	1.77	0.42
1:A:72:VAL:HB	1:A:115:CYS:CB	2.49	0.42
2:D:47:ASP:O	2:D:48:TYR:C	2.56	0.42
1:C:326:THR:CG2	1:C:357:ARG:HG3	2.49	0.42
1:A:323:MET:O	1:A:324:PRO:O	2.37	0.42
1:C:83:THR:CG2	1:C:180:LEU:HB2	2.49	0.42
2:B:109:ASN:C	1:C:137:ARG:NE	2.73	0.42
1:C:326:THR:HB	1:C:357:ARG:HD2	2.01	0.42
1:C:335:LEU:HD12	1:C:336:THR:H	1.84	0.42
1:C:83:THR:HG21	1:C:180:LEU:HB2	2.02	0.42
1:A:138:LEU:HA	1:A:138:LEU:HD22	1.64	0.42
2:B:65:TYR:CE1	2:B:74:THR:HA	2.54	0.42
1:A:29:VAL:HG11	1:A:198:TYR:CZ	2.55	0.42
1:C:142:ILE:HG22	1:C:143:ASP:N	2.34	0.42
1:A:128:LEU:HD11	1:A:130:TYR:HE2	1.84	0.42
2:B:66:GLU:C	2:B:68:SER:N	2.72	0.42
1:A:72:VAL:CG1	1:A:108:PHE:HE1	2.30	0.42
1:A:190:ALA:HB1	2:B:124:PHE:CE1	2.43	0.42
1:A:235:VAL:HG22	1:A:236:VAL:HG13	2.00	0.42
1:A:422:VAL:HG13	1:A:422:VAL:O	2.18	0.42
2:D:152:LEU:O	2:D:153:LYS:HB3	2.19	0.42
1:C:246:HIS:O	1:C:253:TRP:HA	2.20	0.42
1:C:54:LEU:CD1	1:C:65:TYR:HB3	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:89:ALA:O	2:B:90:CYS:C	2.57	0.42
1:C:211:PHE:HA	1:C:212:PRO:HD3	1.83	0.42
1:C:415:ARG:HH11	1:C:419:SER:HB3	1.81	0.42
1:C:47:PRO:HG2	1:C:51:GLY:N	2.35	0.42
2:D:80:TYR:CE1	2:D:92:HIS:HB2	2.54	0.42
1:C:34:PHE:C	1:C:34:PHE:CD2	2.92	0.42
1:C:87:TYR:CD2	1:C:88:ARG:N	2.88	0.42
1:A:305:THR:HG23	1:A:306:SER:H	1.83	0.42
1:C:129:ASP:OD1	1:C:179:TYR:OH	2.36	0.42
1:C:44:LEU:HD22	1:C:82:ARG:HB3	2.01	0.42
2:D:43:PHE:CD1	2:D:48:TYR:HD2	2.38	0.42
1:A:120:ASN:O	1:A:182:PHE:HA	2.20	0.42
1:C:221:PRO:CG	1:C:222:SER:N	2.83	0.42
1:C:283:PHE:CD1	1:C:283:PHE:O	2.72	0.42
1:C:85:TRP:HE1	1:C:126:SER:HB3	1.86	0.41
2:D:122:THR:C	2:D:124:PHE:H	2.23	0.41
2:B:52:VAL:HG11	2:B:118:PHE:CE2	2.55	0.41
2:D:43:PHE:CZ	2:D:48:TYR:HD2	2.38	0.41
1:A:117:GLU:O	1:A:147:PRO:HD3	2.20	0.41
2:B:122:THR:HG21	2:B:127:GLY:HA3	2.02	0.41
1:C:86:VAL:HG11	1:C:178:PHE:CZ	2.55	0.41
2:B:74:THR:HG23	2:B:105:PRO:HB3	2.01	0.41
1:C:48:TYR:O	1:C:50:LYS:N	2.53	0.41
1:A:121:LEU:HB2	1:A:145:ILE:HD11	2.02	0.41
1:C:225:THR:O	1:C:225:THR:HG22	2.20	0.41
2:D:118:PHE:HD1	2:D:130:PHE:CD1	2.38	0.41
1:C:167:GLU:HG3	1:C:168:ARG:N	2.36	0.41
1:C:199:LYS:O	1:C:216:ALA:N	2.52	0.41
2:B:47:ASP:N	2:B:47:ASP:OD1	2.54	0.41
1:C:95:PHE:CB	1:C:197:TYR:CE1	3.00	0.41
1:A:146:ALA:HA	1:A:147:PRO:HD3	1.83	0.41
1:C:349:THR:HA	1:C:350:PRO:HD3	1.89	0.41
2:D:107:SER:HA	2:D:108:PRO:HD2	1.80	0.41
1:C:146:ALA:HA	1:C:147:PRO:HD3	1.88	0.41
2:D:60:VAL:O	2:D:60:VAL:HG12	2.20	0.41
1:C:128:LEU:CD1	1:C:130:TYR:CE2	3.04	0.41
2:B:54:ILE:HD12	2:B:54:ILE:HA	1.63	0.41
2:B:160:PRO:CG	2:B:163:SER:HB2	2.51	0.41
1:C:53:ASP:HB2	1:C:55:MET:CE	2.50	0.41
1:C:139:PHE:CD1	1:C:181:ALA:CB	3.03	0.41
1:C:94:ILE:HG13	1:C:94:ILE:H	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:128:LEU:CD1	1:C:130:TYR:HE2	2.33	0.41
1:A:226:VAL:CG2	1:A:253:TRP:HZ3	2.27	0.41
1:A:370:TRP:CD1	1:A:371:PRO:N	2.89	0.41
1:C:95:PHE:HB2	1:C:197:TYR:CD1	2.54	0.41
1:A:342:ALA:O	1:A:402:LEU:HD12	2.21	0.41
2:D:143:ILE:HB	2:D:144:PRO:HD3	2.02	0.41
1:A:133:ASN:ND2	1:C:40:GLU:HG3	2.35	0.41
2:D:52:VAL:HG22	2:D:156:VAL:HG12	2.03	0.41
1:A:41:LEU:HD13	1:A:43:TRP:CE2	2.56	0.41
1:A:120:ASN:CB	1:A:122:TYR:HE1	2.29	0.41
2:D:144:PRO:HB2	2:D:146:ASN:HD21	1.86	0.41
2:D:99:ARG:NH1	2:D:99:ARG:HG3	2.34	0.41
1:C:318:GLN:O	1:C:318:GLN:CG	2.69	0.41
1:A:279:GLY:C	1:A:280:PHE:CD1	2.94	0.41
1:C:387:GLU:HG3	1:C:388:PRO:HD2	2.02	0.41
1:C:404:PRO:HB3	1:C:435:ASN:HA	2.02	0.41
1:C:88:ARG:CD	1:C:173:LEU:HB2	2.51	0.40
1:A:34:PHE:CD1	1:A:43:TRP:CH2	3.09	0.40
1:C:238:PRO:HD2	1:C:241:GLU:N	2.36	0.40
1:A:180:LEU:HA	1:A:180:LEU:HD23	1.65	0.40
1:A:190:ALA:CB	2:B:124:PHE:CZ	2.74	0.40
1:C:56:GLN:HG3	1:C:56:GLN:O	2.21	0.40
2:D:159:ARG:O	2:D:164:CYS:SG	2.79	0.40
1:C:93:ARG:CD	1:C:95:PHE:CE2	3.01	0.40
1:A:191:LEU:HA	1:A:191:LEU:HD23	1.85	0.40
2:D:37:ASN:HB2	2:D:75:GLU:OE1	2.21	0.40
1:A:281:PHE:HB2	1:A:304:ALA:O	2.21	0.40
2:B:100:TRP:HZ2	2:B:115:SER:O	2.03	0.40
2:B:121:PHE:CD2	2:B:122:THR:N	2.90	0.40
1:C:369:CYS:C	1:C:371:PRO:HD3	2.41	0.40
1:C:386:SER:HB3	1:C:398:THR:HB	2.03	0.40
1:C:41:LEU:CD2	1:C:84:ASN:ND2	2.85	0.40
1:C:370:TRP:N	1:C:371:PRO:HD3	2.37	0.40
2:D:98:LYS:HE2	2:D:100:TRP:O	2.21	0.40
1:A:339:GLY:HA2	1:A:344:VAL:HG12	2.02	0.40
1:C:316:ALA:O	1:C:317:PRO:C	2.60	0.40
1:A:86:VAL:HB	1:A:178:PHE:CZ	2.56	0.40
1:C:276:CYS:O	1:C:277:SER:C	2.58	0.40
2:D:76:ARG:NH1	2:D:144:PRO:HG3	2.37	0.40
1:C:316:ALA:HB3	1:C:319:ASP:CG	2.42	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	400/409 (98%)	291 (73%)	67 (17%)	42 (10%)	1	8
1	C	400/409 (98%)	309 (77%)	54 (14%)	37 (9%)	1	11
2	B	136/138 (99%)	103 (76%)	24 (18%)	9 (7%)	1	19
2	D	136/138 (99%)	97 (71%)	27 (20%)	12 (9%)	1	12
All	All	1072/1094 (98%)	800 (75%)	172 (16%)	100 (9%)	1	11

All (100) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	78	ASP
1	A	84	ASN
1	A	212	PRO
1	A	216	ALA
1	A	273	CYS
1	A	277	SER
1	A	299	PRO
1	A	324	PRO
1	A	408	TYR
2	B	94	SER
2	B	162	ASN
1	C	112	ALA
1	C	212	PRO
1	C	289	PRO
1	C	407	ASN
2	D	36	TRP
2	D	94	SER
2	D	108	PRO
1	A	42	GLY
1	A	48	TYR
1	A	57	ASN
1	A	74	SER

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Mol	Chain	Res	Type
1	A	128	LEU
1	A	142	ILE
1	A	181	ALA
1	A	190	ALA
1	A	235	VAL
1	A	264	ALA
1	A	294	PRO
1	A	301	PRO
1	A	379	CYS
1	A	407	ASN
2	B	127	GLY
2	B	161	THR
1	C	35	ALA
1	C	70	CYS
1	C	74	SER
1	C	131	GLY
1	C	170	VAL
1	C	219	ASP
1	C	221	PRO
1	C	222	SER
1	C	303	GLY
1	C	313	PHE
2	D	34	VAL
2	D	90	CYS
2	D	109	ASN
2	D	160	PRO
1	A	32	LEU
1	A	112	ALA
1	A	231	VAL
1	A	374	GLY
1	A	391	GLY
2	B	45	ARG
2	B	126	LEU
2	B	151	CYS
1	C	32	LEU
1	C	301	PRO
1	C	312	GLY
1	C	340	MET
1	C	351	PRO
1	C	392	LEU
2	D	44	GLN
2	D	55	ASN

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Mol	Chain	Res	Type
2	D	162	ASN
1	A	70	CYS
1	A	131	GLY
1	A	234	ALA
1	A	289	PRO
1	A	401	ASP
2	B	145	ASP
1	C	49	GLY
1	C	85	TRP
1	C	114	SER
1	C	115	CYS
1	C	132	THR
1	C	154	SER
1	C	234	ALA
1	C	294	PRO
1	C	332	PRO
2	D	39	SER
1	A	109	PRO
1	A	263	GLN
2	B	67	ASP
1	C	60	ASN
1	C	91	ALA
1	C	233	HIS
1	C	424	SER
1	A	233	HIS
1	A	305	THR
1	A	405	HIS
1	C	81	LEU
1	C	142	ILE
1	A	303	GLY
1	A	351	PRO
1	C	317	PRO
1	A	256	PRO
1	C	299	PRO
2	D	62	CYS
1	A	378	PRO

### 5.3.2 Protein sidechains ⓘ

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



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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	330/345 (96%)	262 (79%)	68 (21%)	1	8
1	C	330/345 (96%)	269 (82%)	61 (18%)	2	11
2	B	127/127 (100%)	112 (88%)	15 (12%)	6	31
2	D	127/127 (100%)	111 (87%)	16 (13%)	5	28
All	All	914/944 (97%)	754 (82%)	160 (18%)	2	14

All (160) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	LEU
1	A	41	LEU
1	A	44	LEU
1	A	54	LEU
1	A	66	MET
1	A	67	TYR
1	A	69	VAL
1	A	70	CYS
1	A	72	VAL
1	A	86	VAL
1	A	87	TYR
1	A	93	ARG
1	A	97	GLU
1	A	98	LEU
1	A	100	PHE
1	A	114	SER
1	A	115	CYS
1	A	116	LYS
1	A	118	THR
1	A	123	TYR
1	A	126	SER
1	A	128	LEU
1	A	135	GLN
1	A	138	LEU
1	A	140	THR
1	A	145	ILE
1	A	149	GLU
1	A	151	THR
1	A	161	VAL
1	A	165	VAL

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Mol	Chain	Res	Type
1	A	174	THR
1	A	189	VAL
1	A	197	TYR
1	A	204	LEU
1	A	206	GLN
1	A	219	ASP
1	A	225	THR
1	A	226	VAL
1	A	229	THR
1	A	232	ASP
1	A	235	VAL
1	A	236	VAL
1	A	257	ILE
1	A	261	LEU
1	A	262	CYS
1	A	273	CYS
1	A	280	PHE
1	A	284	GLU
1	A	291	LEU
1	A	297	THR
1	A	298	LEU
1	A	305	THR
1	A	306	SER
1	A	307	CYS
1	A	309	CYS
1	A	319	ASP
1	A	335	LEU
1	A	344	VAL
1	A	349	THR
1	A	364	VAL
1	A	365	THR
1	A	368	GLN
1	A	379	CYS
1	A	392	LEU
1	A	408	TYR
1	A	418	VAL
1	A	426	SER
1	A	432	VAL
2	B	47	ASP
2	B	48	TYR
2	B	51	ASP
2	B	54	ILE

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Mol	Chain	Res	Type
2	B	74	THR
2	B	79	LEU
2	B	82	VAL
2	B	112	LEU
2	B	120	LEU
2	B	121	PHE
2	B	122	THR
2	B	145	ASP
2	B	155	LYS
2	B	161	THR
2	B	162	ASN
1	C	31	LEU
1	C	32	LEU
1	C	41	LEU
1	C	44	LEU
1	C	46	HIS
1	C	48	TYR
1	C	54	LEU
1	C	55	MET
1	C	56	GLN
1	C	72	VAL
1	C	79	ASN
1	C	93	ARG
1	C	94	ILE
1	C	100	PHE
1	C	102	VAL
1	C	107	SER
1	C	114	SER
1	C	118	THR
1	C	123	TYR
1	C	128	LEU
1	C	132	THR
1	C	133	ASN
1	C	145	ILE
1	C	150	ILE
1	C	151	THR
1	C	154	SER
1	C	157	GLU
1	C	169	SER
1	C	170	VAL
1	C	174	THR
1	C	183	GLN

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Mol	Chain	Res	Type
1	C	185	ILE
1	C	188	CYS
1	C	189	VAL
1	C	191	LEU
1	C	214	THR
1	C	215	ILE
1	C	229	THR
1	C	235	VAL
1	C	245	MET
1	C	249	VAL
1	C	259	GLN
1	C	260	CYS
1	C	281	PHE
1	C	283	PHE
1	C	287	GLU
1	C	290	CYS
1	C	293	CYS
1	C	297	THR
1	C	305	THR
1	C	309	CYS
1	C	313	PHE
1	C	325	CYS
1	C	366	CYS
1	C	370	TRP
1	C	379	CYS
1	C	392	LEU
1	C	411	THR
1	C	427	PHE
1	C	429	THR
1	C	432	VAL
2	D	30	ASP
2	D	37	ASN
2	D	48	TYR
2	D	51	ASP
2	D	54	ILE
2	D	67	ASP
2	D	79	LEU
2	D	107	SER
2	D	126	LEU
2	D	135	GLU
2	D	139	ILE
2	D	141	SER

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Mol	Chain	Res	Type
2	D	145	ASP
2	D	149	ARG
2	D	162	ASN
2	D	164	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	ASN
1	A	79	ASN
1	A	259	GLN
1	A	274	GLN
1	A	318	GLN
1	A	368	GLN
2	B	106	HIS
2	B	119	GLN
2	B	146	ASN
2	B	162	ASN
1	C	46	HIS
1	C	60	ASN
1	C	79	ASN
1	C	133	ASN
1	C	259	GLN
1	C	274	GLN
1	C	368	GLN
1	C	390	HIS
2	D	119	GLN
2	D	146	ASN
2	D	162	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

6 carbohydrates are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	NAG	B	401	2,4	14,14,15	0.49	0	15,19,21	1.03	1 (6%)
4	NAG	B	402	4	14,14,15	0.57	0	15,19,21	1.23	3 (20%)
4	NAG	B	403	4	14,14,15	0.69	0	15,19,21	1.59	2 (13%)
4	NAG	D	401	2,4	14,14,15	0.63	0	15,19,21	1.40	2 (13%)
4	NAG	D	402	4	14,14,15	0.65	0	15,19,21	1.37	3 (20%)
4	NAG	D	403	4	14,14,15	0.83	1 (7%)	15,19,21	1.82	2 (13%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	B	401	2,4	-	0/6/23/26	0/1/1/1
4	NAG	B	402	4	-	0/6/23/26	0/1/1/1
4	NAG	B	403	4	-	0/6/23/26	0/1/1/1
4	NAG	D	401	2,4	-	0/6/23/26	0/1/1/1
4	NAG	D	402	4	-	0/6/23/26	0/1/1/1
4	NAG	D	403	4	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	403	NAG	C1-C2	2.47	1.55	1.52

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	401	NAG	C3-C4-C5	-3.62	103.88	110.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	402	NAG	C1-O5-C5	-2.25	109.39	112.25
4	B	402	NAG	O4-C4-C3	-2.21	105.37	110.34
4	B	402	NAG	C3-C4-C5	2.01	113.70	110.20
4	D	402	NAG	O5-C5-C6	2.02	111.71	107.35
4	D	401	NAG	O4-C4-C5	2.20	115.06	109.24
4	D	403	NAG	C3-C2-N2	2.29	116.04	110.56
4	B	402	NAG	C4-C3-C2	2.38	114.92	111.23
4	B	401	NAG	C1-O5-C5	2.55	115.49	112.25
4	D	402	NAG	C4-C3-C2	2.57	115.22	111.23
4	B	403	NAG	C3-C4-C5	2.57	114.68	110.20
4	B	403	NAG	C2-N2-C7	4.28	128.54	123.04
4	D	403	NAG	C2-N2-C7	5.67	130.32	123.04

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	401	NAG	1	0
4	B	402	NAG	1	0

## 5.6 Ligand geometry ⓘ

2 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
3	NAG	A	501	1	14,14,15	0.96	1 (7%)	15,19,21	1.53	3 (20%)
3	NAG	C	501	1	14,14,15	1.12	1 (7%)	15,19,21	1.94	4 (26%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical

component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	A	501	1	-	0/6/23/26	0/1/1/1
3	NAG	C	501	1	-	0/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	501	NAG	C1-C2	2.86	1.56	1.52
3	C	501	NAG	C1-C2	3.66	1.57	1.52

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	501	NAG	O7-C7-C8	-2.44	117.58	122.06
3	C	501	NAG	O7-C7-C8	-2.15	118.11	122.06
3	C	501	NAG	C3-C4-C5	-2.05	106.62	110.20
3	A	501	NAG	O7-C7-N2	2.12	126.19	121.86
3	A	501	NAG	C4-C3-C2	3.09	116.04	111.23
3	C	501	NAG	C2-N2-C7	3.16	127.10	123.04
3	C	501	NAG	C1-O5-C5	4.88	118.45	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	501	NAG	2	0
3	C	501	NAG	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.



## 6 Fit of model and data

### 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, 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	406/409 (99%)	-0.08	3 (0%) 89 82	52, 119, 209, 337	0
1	C	406/409 (99%)	-0.05	5 (1%) 81 72	52, 121, 208, 253	0
2	B	138/138 (100%)	0.26	3 (2%) 65 55	79, 161, 251, 284	0
2	D	138/138 (100%)	0.24	9 (6%) 22 17	78, 161, 255, 350	0
All	All	1088/1094 (99%)	0.02	20 (1%) 71 62	52, 130, 227, 350	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	146	ASN	6.7
2	D	70	PRO	4.8
2	D	73	LYS	3.7
1	A	387	GLU	3.2
2	D	71	GLU	3.2
1	C	343	LYS	2.9
2	B	28	VAL	2.8
1	A	423	THR	2.7
2	D	65	TYR	2.7
1	C	421	LEU	2.6
2	D	72	ASP	2.6
2	B	77	TYR	2.6
1	A	422	VAL	2.6
2	B	41	PRO	2.4
2	D	128	PHE	2.3
2	D	68	SER	2.3
1	C	342	ALA	2.2
2	D	163	SER	2.2
1	C	402	LEU	2.2
1	C	326	THR	2.1

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

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

## 6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	NAG	B	401	14/15	0.91	0.28	0.22	146,146,146,146	0
4	NAG	D	401	14/15	0.93	0.20	-0.89	135,135,135,135	0
4	NAG	B	402	14/15	0.85	0.28	-	146,146,146,146	0
4	NAG	D	402	14/15	0.87	0.22	-	149,149,149,149	0
4	NAG	B	403	14/15	0.63	0.27	-	205,205,205,205	0
4	NAG	D	403	14/15	0.70	0.23	-	184,184,184,184	0

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	NAG	C	501	14/15	0.72	0.20	-0.42	153,153,153,153	0
3	NAG	A	501	14/15	0.85	0.20	-	155,155,155,155	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.