



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:44 AM GMT

PDB ID : 2E4W  
Title : Crystal structure of the extracellular region of the group II metabotropic glutamate receptor complexed with 1S,3S-ACPD  
Authors : Muto, T.; Tsuchiya, D.; Morikawa, K.; Jingami, H.  
Deposited on : 2006-12-17  
Resolution : 2.40 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

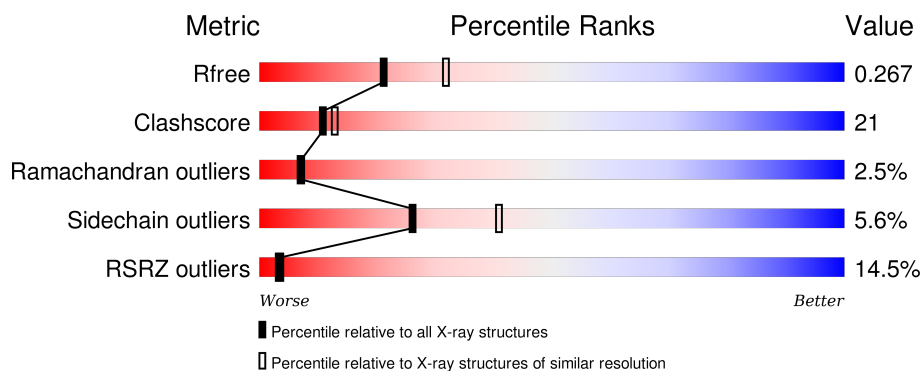
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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	555	 13% 62% 27% • 7%
1	B	555	 14% 60% 29% • 6%

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8602 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.

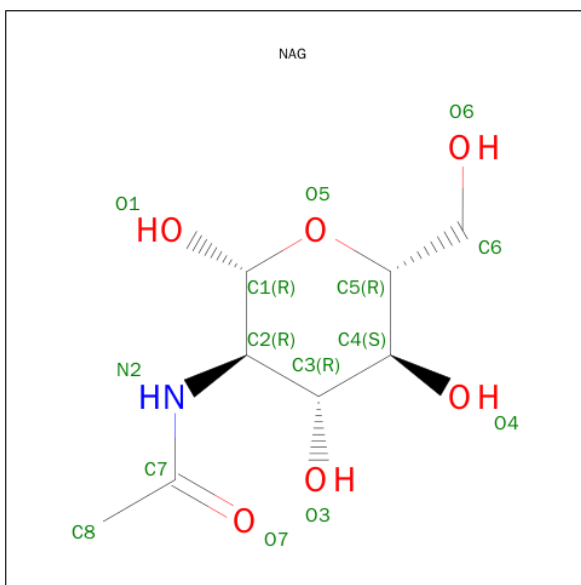
- Molecule 1 is a protein called Metabotropic glutamate receptor 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	518	Total	C	N	O	S	0	0	0
			4118	2606	709	776	27			
1	B	520	Total	C	N	O	S	0	0	0
			4137	2620	711	778	28			

There are 12 discrepancies between the modelled and reference sequences:

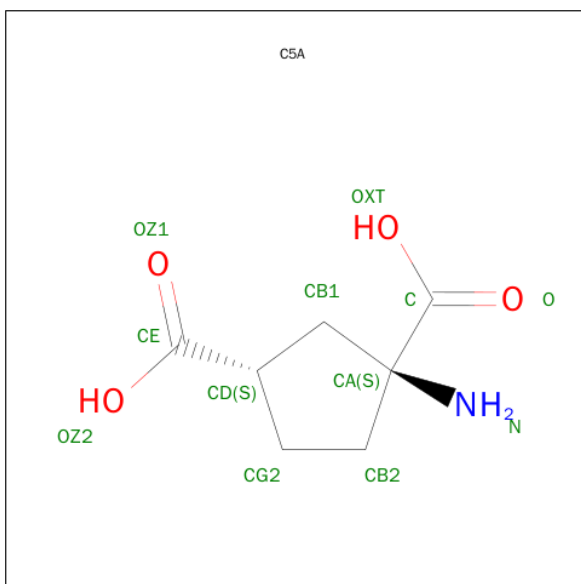
Chain	Residue	Modelled	Actual	Comment	Reference
A	414	GLN	ASN	ENGINEERED	UNP P31422
A	439	GLN	ASN	ENGINEERED	UNP P31422
A	576	LEU	-	CLONING ARTIFACT	UNP P31422
A	577	VAL	-	CLONING ARTIFACT	UNP P31422
A	578	PRO	-	CLONING ARTIFACT	UNP P31422
A	579	ARG	-	CLONING ARTIFACT	UNP P31422
B	414	GLN	ASN	ENGINEERED	UNP P31422
B	439	GLN	ASN	ENGINEERED	UNP P31422
B	576	LEU	-	CLONING ARTIFACT	UNP P31422
B	577	VAL	-	CLONING ARTIFACT	UNP P31422
B	578	PRO	-	CLONING ARTIFACT	UNP P31422
B	579	ARG	-	CLONING ARTIFACT	UNP P31422

- Molecule 2 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	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 (1S,3S)-1-AMINOCYCLOPENTANE-1,3-DICARBOXYLIC ACID (three-letter code: C5A) (formula: C<sub>7</sub>H<sub>11</sub>NO<sub>4</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			12	7	1	4		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			12	7	1	4		

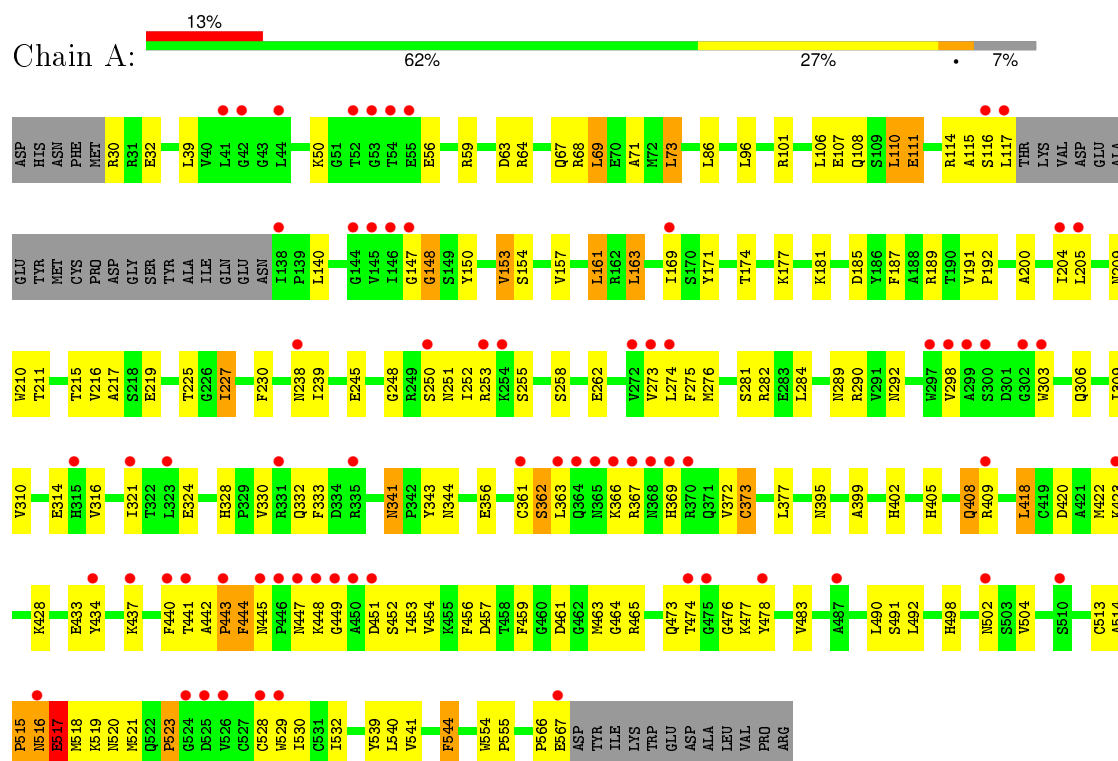
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	166	Total	O	0	0
			166	166		
4	B	129	Total	O	0	0
			129	129		

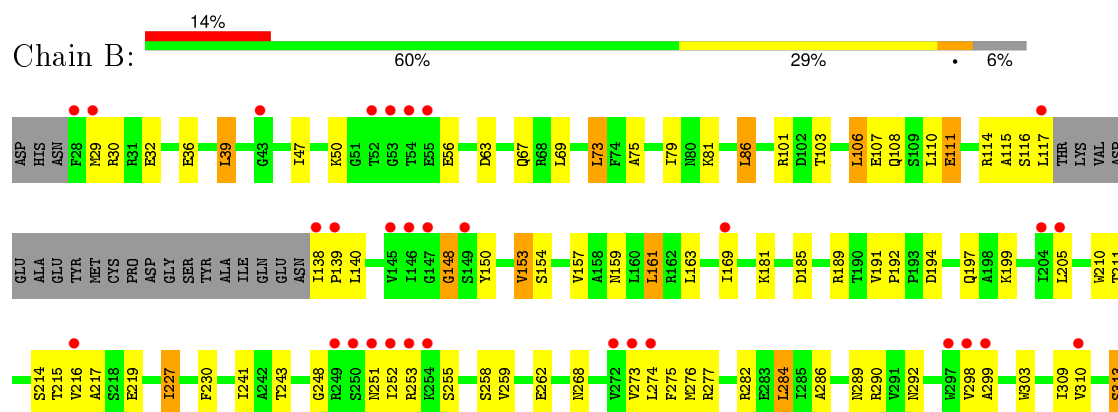
### 3 Residue-property plots

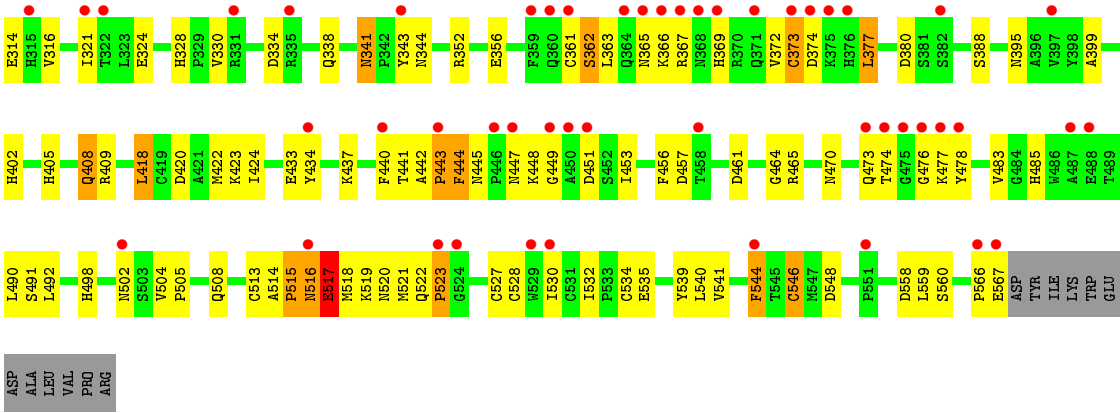
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

#### • Molecule 1: Metabotropic glutamate receptor 3



#### • Molecule 1: Metabotropic glutamate receptor 3





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	83.74Å 97.31Å 107.81Å 90.00° 92.94° 90.00°	Depositor
Resolution (Å)	20.00 – 2.40 29.26 – 2.40	Depositor EDS
% Data completeness (in resolution range)	98.8 (20.00-2.40) 98.8 (29.26-2.40)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.18 (at 2.39Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.236 , 0.267 0.237 , 0.267	Depositor DCC
$R_{free}$ test set	4755 reflections (7.12%)	DCC
Wilson B-factor (Å <sup>2</sup> )	52.2	Xtriage
Anisotropy	0.268	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 58.7	EDS
Estimated twinning fraction	0.024 for h,-k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 66828 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	8602	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.46% 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, C5A

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	0.39	0/4212	0.67	1/5704 (0.0%)
1	B	0.39	0/4232	0.66	2/5730 (0.0%)
All	All	0.39	0/8444	0.66	3/11434 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	148	GLY	N-CA-C	-6.04	97.99	113.10
1	B	148	GLY	N-CA-C	-5.99	98.11	113.10
1	B	546	CYS	CA-CB-SG	-5.37	104.34	114.00

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	4118	0	3993	163	0
1	B	4137	0	4012	186	0
2	A	14	0	13	1	0
2	B	14	0	13	0	0
3	A	12	0	9	0	0
3	B	12	0	9	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	166	0	0	10	0
4	B	129	0	0	13	0
All	All	8602	0	8049	345	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 21.

All (345) 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:402:HIS:HB3	1:B:437:LYS:HE2	1.31	1.11
1:A:514:ALA:H	1:A:518:MET:HE3	1.18	1.06
1:B:30:ARG:HD2	1:B:108:GLN:HE22	1.28	0.98
1:A:356:GLU:HA	1:A:361:CYS:HB2	1.45	0.96
1:A:515:PRO:HG2	1:A:516:ASN:H	1.33	0.94
1:B:514:ALA:H	1:B:518:MET:HE3	1.30	0.94
1:A:420:ASP:HA	1:A:423:LYS:HD3	1.50	0.93
1:B:356:GLU:HA	1:B:361:CYS:HB2	1.49	0.92
1:B:328:HIS:HB2	4:B:2026:HOH:O	1.70	0.91
1:B:216:VAL:HG12	1:B:274:LEU:HD22	1.53	0.90
1:A:276:MET:HE3	1:A:281:SER:HA	1.53	0.89
1:B:216:VAL:CG1	1:B:274:LEU:HD22	2.03	0.89
1:B:274:LEU:HD13	1:B:276:MET:HE2	1.53	0.87
1:A:402:HIS:HB3	1:A:437:LYS:HE2	1.56	0.87
1:B:47:ILE:HD12	1:B:69:LEU:HD12	1.57	0.86
1:A:30:ARG:HA	4:A:1133:HOH:O	1.74	0.86
1:B:341:ASN:HD22	1:B:343:TYR:H	1.18	0.85
1:B:515:PRO:HG2	1:B:516:ASN:H	1.43	0.82
1:A:181:LYS:HE2	1:A:459:PHE:O	1.82	0.80
1:A:289:ASN:HA	1:A:316:VAL:HG21	1.64	0.80
1:B:514:ALA:HB3	1:B:518:MET:HG3	1.61	0.80
1:B:289:ASN:HA	1:B:316:VAL:HG21	1.62	0.79
1:A:216:VAL:CG1	1:A:274:LEU:HD22	2.14	0.78
1:A:514:ALA:HB3	1:A:518:MET:HG3	1.66	0.77
1:A:107:GLU:HB3	4:A:1116:HOH:O	1.82	0.77
1:B:366:LYS:HG2	1:B:367:ARG:H	1.50	0.77
1:B:540:LEU:HD13	1:B:559:LEU:HD23	1.67	0.76
1:B:330:VAL:HG13	1:B:444:PHE:HB3	1.66	0.76
1:A:157:VAL:HG12	1:A:161:LEU:HD22	1.69	0.75
1:B:216:VAL:HG12	1:B:274:LEU:CD2	2.16	0.75
1:B:50:LYS:HG3	1:B:101:ARG:HD3	1.66	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:465:ARG:HH11	1:A:465:ARG:HG3	1.51	0.75
1:B:338:GLN:OE1	1:B:380:ASP:HA	1.88	0.74
1:A:101:ARG:HD3	4:A:1070:HOH:O	1.87	0.74
1:B:440:PHE:CE2	1:B:448:LYS:HB3	2.23	0.74
1:B:103:THR:O	1:B:107:GLU:HG2	1.88	0.73
1:B:514:ALA:H	1:B:518:MET:CE	2.00	0.73
1:A:366:LYS:HG2	1:A:367:ARG:H	1.54	0.72
1:B:362:SER:O	1:B:363:LEU:HD13	1.88	0.72
1:B:409:ARG:HD3	4:B:2033:HOH:O	1.88	0.72
1:A:330:VAL:HG13	1:A:444:PHE:HB3	1.71	0.71
1:A:258:SER:O	1:A:262:GLU:HG3	1.91	0.71
1:A:442:ALA:O	1:A:444:PHE:N	2.24	0.71
1:B:341:ASN:ND2	1:B:344:ASN:H	1.89	0.70
1:A:520:ASN:O	1:A:544:PHE:HB3	1.91	0.70
1:B:442:ALA:O	1:B:444:PHE:N	2.25	0.69
1:B:258:SER:O	1:B:262:GLU:HG3	1.91	0.69
1:B:424:ILE:HG12	4:B:2124:HOH:O	1.91	0.69
1:A:341:ASN:ND2	1:A:344:ASN:H	1.92	0.68
1:A:515:PRO:CG	1:A:516:ASN:H	2.06	0.68
1:A:405:HIS:NE2	1:A:409:ARG:NE	2.42	0.68
1:B:341:ASN:ND2	1:B:343:TYR:H	1.93	0.66
1:B:473:GLN:HE21	1:B:476:GLY:CA	2.09	0.66
1:A:440:PHE:CE2	1:A:448:LYS:HB3	2.31	0.66
1:B:352:ARG:HG3	4:B:2077:HOH:O	1.95	0.66
1:B:521:MET:HB2	1:B:530:ILE:HG13	1.76	0.66
1:B:253:ARG:HG2	1:B:290:ARG:HH22	1.60	0.66
1:B:420:ASP:HA	1:B:423:LYS:HD3	1.77	0.66
1:A:367:ARG:HB2	1:A:369:HIS:CD2	2.31	0.65
1:A:253:ARG:HG2	1:A:290:ARG:HH22	1.59	0.65
1:B:341:ASN:HD22	1:B:343:TYR:N	1.94	0.65
1:B:314:GLU:HG2	1:B:478:TYR:CD2	2.33	0.64
1:B:253:ARG:HG2	1:B:290:ARG:NH2	2.12	0.64
1:B:282:ARG:HG2	1:B:282:ARG:HH11	1.61	0.64
1:A:253:ARG:HG2	1:A:290:ARG:NH2	2.12	0.64
1:A:328:HIS:HB2	4:A:1084:HOH:O	1.98	0.64
1:A:366:LYS:HG2	1:A:367:ARG:N	2.13	0.64
1:B:241:ILE:HG22	4:B:2071:HOH:O	1.97	0.64
1:B:366:LYS:HG2	1:B:367:ARG:N	2.12	0.63
1:A:452:SER:HA	4:A:1147:HOH:O	1.98	0.63
1:B:310:VAL:CG1	1:B:314:GLU:HA	2.28	0.63
1:B:374:ASP:HB3	1:B:377:LEU:HD22	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:515:PRO:O	1:A:517:GLU:N	2.32	0.62
1:B:540:LEU:HD12	1:B:546:CYS:SG	2.38	0.62
1:A:465:ARG:NH1	1:A:465:ARG:HG3	2.15	0.62
1:B:395:ASN:OD1	1:B:441:THR:HG23	2.00	0.61
1:A:110:LEU:O	1:A:114:ARG:HG3	2.00	0.61
1:A:282:ARG:HH11	1:A:282:ARG:HG2	1.65	0.61
1:A:372:VAL:HG22	1:A:373:CYS:N	2.15	0.61
1:A:192:PRO:HG3	1:A:464:GLY:HA2	1.82	0.61
1:A:252:ILE:HG22	1:A:253:ARG:H	1.66	0.61
1:A:402:HIS:CB	1:A:437:LYS:HE2	2.30	0.60
1:B:520:ASN:O	1:B:544:PHE:HB3	2.00	0.60
1:B:215:THR:OG1	1:B:241:ILE:HD11	2.01	0.60
1:B:490:LEU:HD12	1:B:491:SER:H	1.67	0.60
1:B:252:ILE:HG22	1:B:253:ARG:H	1.65	0.59
1:B:483:VAL:O	1:B:492:LEU:HB2	2.02	0.59
1:B:217:ALA:HB2	1:B:227:ILE:HG13	1.84	0.59
1:A:521:MET:HB2	1:A:530:ILE:HG13	1.85	0.59
1:B:367:ARG:HB2	1:B:369:HIS:CD2	2.38	0.59
1:A:216:VAL:HA	1:A:245:GLU:O	2.02	0.58
1:B:47:ILE:CD1	1:B:69:LEU:HD12	2.31	0.58
1:A:169:ILE:HG12	1:A:434:TYR:OH	2.04	0.58
1:A:523:PRO:HD2	1:A:528:CYS:O	2.04	0.58
1:B:310:VAL:HG12	1:B:314:GLU:HA	1.86	0.58
1:A:150:TYR:HB2	1:A:153:VAL:HG13	1.86	0.58
1:B:330:VAL:HG13	1:B:444:PHE:CB	2.35	0.57
1:A:211:THR:HG23	1:A:238:ASN:O	2.04	0.57
1:A:372:VAL:HG22	1:A:373:CYS:H	1.67	0.57
1:B:199:LYS:HD3	4:B:2063:HOH:O	2.04	0.57
1:B:523:PRO:HD2	1:B:528:CYS:O	2.04	0.57
1:A:473:GLN:NE2	1:A:476:GLY:HA2	2.20	0.57
1:B:515:PRO:O	1:B:517:GLU:N	2.38	0.56
1:A:303:TRP:HA	1:A:309:ILE:CD1	2.35	0.56
1:A:282:ARG:HD2	1:A:309:ILE:O	2.05	0.56
1:B:374:ASP:HB3	1:B:377:LEU:CD2	2.34	0.56
1:A:310:VAL:CG1	1:A:314:GLU:HA	2.36	0.56
1:A:189:ARG:HD3	1:A:461:ASP:OD1	2.06	0.56
1:A:330:VAL:HG13	1:A:444:PHE:CB	2.36	0.56
1:B:86:LEU:H	1:B:405:HIS:HD1	1.53	0.55
1:B:473:GLN:HE21	1:B:476:GLY:HA2	1.70	0.55
1:A:314:GLU:HG2	1:A:478:TYR:CD2	2.41	0.55
1:B:303:TRP:HA	1:B:309:ILE:CD1	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:362:SER:C	1:A:363:LEU:HD22	2.27	0.55
1:B:441:THR:O	1:B:442:ALA:C	2.43	0.55
1:B:251:ASN:HD22	1:B:255:SER:HB3	1.72	0.55
1:B:81:LYS:HG3	4:B:2098:HOH:O	2.06	0.55
1:A:56:GLU:HG2	1:A:101:ARG:HH22	1.72	0.54
1:B:473:GLN:NE2	1:B:476:GLY:HA2	2.21	0.54
1:A:169:ILE:CD1	1:A:434:TYR:OH	2.55	0.54
1:A:216:VAL:HG13	1:A:274:LEU:HD22	1.89	0.54
1:B:219:GLU:OE2	1:B:248:GLY:HA3	2.08	0.54
1:A:483:VAL:O	1:A:492:LEU:HB2	2.08	0.54
1:A:367:ARG:HB2	1:A:369:HIS:NE2	2.22	0.54
1:A:399:ALA:HB1	1:A:434:TYR:HE1	1.73	0.54
1:B:181:LYS:HE2	1:B:181:LYS:HA	1.90	0.54
1:B:465:ARG:HH11	1:B:465:ARG:HG3	1.73	0.54
1:A:363:LEU:HD22	1:A:363:LEU:N	2.23	0.54
1:A:115:ALA:HB1	1:A:140:LEU:O	2.08	0.53
1:B:86:LEU:HD13	1:B:405:HIS:HB2	1.89	0.53
1:A:209:ASN:ND2	2:A:801:NAG:H82	2.23	0.53
1:B:157:VAL:HG12	1:B:161:LEU:HD22	1.90	0.53
1:A:405:HIS:NE2	1:A:409:ARG:CZ	2.72	0.53
1:B:169:ILE:HG12	1:B:434:TYR:OH	2.09	0.53
1:B:189:ARG:HG3	1:B:191:VAL:O	2.09	0.53
1:B:150:TYR:HB2	1:B:153:VAL:HG13	1.89	0.53
1:B:252:ILE:HG22	1:B:253:ARG:N	2.23	0.53
1:A:473:GLN:HE21	1:A:476:GLY:CA	2.22	0.53
1:B:108:GLN:O	1:B:111:GLU:HB2	2.09	0.53
1:B:214:SER:OG	1:B:243:THR:HG22	2.08	0.53
1:B:63:ASP:O	1:B:67:GLN:HB2	2.09	0.53
1:B:418:LEU:HD22	1:B:422:MET:HE3	1.90	0.53
1:A:408:GLN:HB2	1:A:422:MET:HE1	1.90	0.53
1:A:441:THR:O	1:A:442:ALA:C	2.46	0.52
1:B:56:GLU:HG2	1:B:101:ARG:NH2	2.24	0.52
1:A:252:ILE:HG22	1:A:253:ARG:N	2.24	0.52
1:A:554:TRP:CG	1:A:555:PRO:HD2	2.44	0.52
1:B:30:ARG:HD2	1:B:108:GLN:NE2	2.11	0.52
1:B:341:ASN:HD22	1:B:341:ASN:C	2.13	0.52
1:A:418:LEU:HD22	1:A:422:MET:HE3	1.91	0.52
1:B:324:GLU:HG2	1:B:388:SER:OG	2.10	0.52
1:A:341:ASN:HD22	1:A:343:TYR:H	1.56	0.52
1:A:515:PRO:HG2	1:A:516:ASN:N	2.14	0.52
1:B:211:THR:O	1:B:211:THR:HG22	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:451:ASP:OD1	1:A:453:ILE:HG12	2.10	0.52
1:A:189:ARG:HG3	1:A:191:VAL:O	2.10	0.52
1:B:169:ILE:CD1	1:B:434:TYR:OH	2.58	0.51
1:B:282:ARG:HD2	1:B:309:ILE:O	2.09	0.51
1:B:539:TYR:CZ	1:B:541:VAL:HG22	2.46	0.51
1:A:457:ASP:HB2	1:A:461:ASP:H	1.75	0.51
1:A:504:VAL:HG13	1:A:504:VAL:O	2.10	0.51
1:A:362:SER:O	1:A:363:LEU:HD13	2.11	0.51
1:B:334:ASP:O	1:B:338:GLN:HG3	2.10	0.51
1:A:216:VAL:CG1	1:A:274:LEU:CD2	2.88	0.51
1:A:298:VAL:HA	1:A:321:ILE:O	2.11	0.51
1:B:169:ILE:CD1	1:B:434:TYR:CZ	2.94	0.51
1:A:64:ARG:O	1:A:68:ARG:HD2	2.10	0.51
1:A:169:ILE:HD13	1:A:434:TYR:OH	2.10	0.50
1:A:332:GLN:HB2	4:A:1125:HOH:O	2.11	0.50
1:B:115:ALA:HB1	1:B:140:LEU:O	2.11	0.50
1:A:215:THR:HG22	1:A:273:VAL:HB	1.93	0.50
1:A:303:TRP:HA	1:A:309:ILE:HD13	1.93	0.50
1:A:310:VAL:HG12	1:A:314:GLU:HA	1.92	0.50
1:B:116:SER:O	1:B:117:LEU:HD12	2.10	0.50
1:B:362:SER:OG	1:B:366:LYS:HD3	2.11	0.50
1:A:362:SER:OG	1:A:366:LYS:HD3	2.12	0.50
1:A:50:LYS:NZ	1:A:250:SER:H	2.10	0.50
1:A:306:GLN:NE2	1:A:309:ILE:HD11	2.27	0.50
1:B:402:HIS:CB	1:B:437:LYS:HE2	2.23	0.50
1:A:513:CYS:HB3	1:A:518:MET:HB2	1.94	0.50
1:A:428:LYS:NZ	4:A:1018:HOH:O	2.40	0.50
1:B:362:SER:C	1:B:363:LEU:HD22	2.32	0.49
1:B:255:SER:O	1:B:259:VAL:HG23	2.12	0.49
1:B:408:GLN:HB2	1:B:422:MET:CE	2.42	0.49
1:A:114:ARG:HG2	1:B:114:ARG:HH21	1.76	0.49
1:B:372:VAL:HG22	1:B:373:CYS:H	1.76	0.49
1:A:289:ASN:CA	1:A:316:VAL:HG21	2.40	0.49
1:A:108:GLN:O	1:A:111:GLU:HB2	2.12	0.49
1:B:485:HIS:HB2	4:B:2054:HOH:O	2.11	0.49
1:B:366:LYS:HE2	1:B:369:HIS:CD2	2.48	0.49
1:B:216:VAL:HG13	1:B:276:MET:SD	2.53	0.49
1:B:268:ASN:HB3	1:B:508:GLN:O	2.13	0.49
1:B:514:ALA:N	1:B:518:MET:HE3	2.13	0.49
1:A:56:GLU:HG2	1:A:101:ARG:NH2	2.28	0.48
1:A:169:ILE:CG1	1:A:434:TYR:OH	2.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:219:GLU:HB2	1:A:248:GLY:HA2	1.94	0.48
1:B:75:ALA:O	1:B:79:ILE:HG13	2.13	0.48
1:A:163:LEU:HD11	1:B:159:ASN:HB3	1.95	0.48
1:B:328:HIS:CD2	4:B:2128:HOH:O	2.66	0.48
1:A:492:LEU:N	1:A:492:LEU:HD23	2.28	0.48
1:B:519:LYS:HG2	1:B:532:ILE:HB	1.95	0.48
1:B:189:ARG:HD3	1:B:461:ASP:OD1	2.14	0.48
1:B:408:GLN:HB2	1:B:422:MET:HE1	1.95	0.48
1:A:274:LEU:HD13	1:A:276:MET:CE	2.44	0.47
1:A:252:ILE:N	1:A:252:ILE:HD12	2.29	0.47
1:B:515:PRO:CG	1:B:516:ASN:H	2.16	0.47
1:B:516:ASN:HB2	1:B:517:GLU:OE2	2.14	0.47
1:B:539:TYR:OH	1:B:541:VAL:HG22	2.14	0.47
1:A:515:PRO:CG	1:A:516:ASN:N	2.73	0.47
1:A:395:ASN:OD1	1:A:441:THR:HG23	2.14	0.47
1:A:341:ASN:C	1:A:341:ASN:HD22	2.18	0.47
1:B:217:ALA:HB2	1:B:227:ILE:CG1	2.44	0.47
1:B:282:ARG:NH1	1:B:282:ARG:HG2	2.29	0.47
1:A:211:THR:HG23	1:A:239:ILE:HA	1.97	0.47
1:A:177:LYS:HE3	1:A:225:THR:HG21	1.97	0.47
1:B:434:TYR:OH	1:B:456:PHE:CZ	2.67	0.47
1:B:138:ILE:N	1:B:139:PRO:HD2	2.30	0.47
1:A:443:PRO:C	1:A:445:ASN:H	2.18	0.47
1:A:181:LYS:HE3	1:A:187:PHE:O	2.15	0.47
1:B:558:ASP:O	1:B:559:LEU:HB2	2.15	0.47
1:B:169:ILE:HD13	1:B:434:TYR:OH	2.14	0.46
1:A:449:GLY:C	1:A:451:ASP:H	2.18	0.46
1:B:30:ARG:NH2	1:B:32:GLU:OE1	2.48	0.46
1:A:418:LEU:HD22	1:A:422:MET:CE	2.45	0.46
1:A:116:SER:O	1:A:117:LEU:HD12	2.14	0.46
1:B:341:ASN:HD21	1:B:343:TYR:HB2	1.81	0.46
1:A:169:ILE:CD1	1:A:434:TYR:CZ	2.98	0.46
1:A:473:GLN:HE21	1:A:476:GLY:HA2	1.78	0.46
1:A:441:THR:HG22	4:A:1045:HOH:O	2.15	0.46
1:B:39:LEU:HA	1:B:39:LEU:HD12	1.82	0.46
1:B:341:ASN:HD21	1:B:344:ASN:H	1.61	0.46
1:A:211:THR:HG22	1:A:211:THR:O	2.16	0.46
1:B:504:VAL:HG13	1:B:504:VAL:O	2.16	0.46
1:A:147:GLY:HA2	1:A:171:TYR:CE2	2.51	0.46
1:A:473:GLN:NE2	1:A:476:GLY:CA	2.79	0.45
1:A:516:ASN:C	1:A:517:GLU:HG3	2.36	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:274:LEU:HD13	1:B:276:MET:CE	2.37	0.45
1:B:363:LEU:HD22	1:B:363:LEU:N	2.32	0.45
1:A:282:ARG:HG2	1:A:282:ARG:NH1	2.31	0.45
1:B:286:ALA:O	1:B:290:ARG:HG3	2.16	0.45
1:A:523:PRO:HD3	1:A:529:TRP:HA	1.98	0.45
1:A:310:VAL:HG12	1:A:310:VAL:O	2.16	0.45
1:B:205:LEU:CD2	1:B:210:TRP:HE3	2.29	0.45
1:A:230:PHE:CZ	1:A:273:VAL:HG21	2.52	0.45
1:A:217:ALA:HB2	1:A:227:ILE:HG13	1.98	0.45
1:A:341:ASN:HD22	1:A:343:TYR:N	2.15	0.45
1:B:69:LEU:CD2	1:B:73:LEU:HD22	2.46	0.45
1:A:174:THR:C	1:A:189:ARG:NH2	2.71	0.45
1:B:399:ALA:HB1	1:B:434:TYR:HE1	1.81	0.44
1:B:558:ASP:OD2	1:B:560:SER:HB3	2.17	0.44
1:A:444:PHE:CD2	1:A:444:PHE:N	2.84	0.44
1:B:473:GLN:HA	1:B:477:LYS:O	2.17	0.44
1:A:539:TYR:CZ	1:A:541:VAL:HG22	2.53	0.44
1:A:96:LEU:HD13	1:A:108:GLN:HB3	1.98	0.44
1:B:276:MET:CE	1:B:284:LEU:HD12	2.48	0.44
1:A:519:LYS:HG2	1:A:532:ILE:HB	1.99	0.44
1:A:463:MET:HG2	4:A:1079:HOH:O	2.17	0.44
1:B:192:PRO:HG3	1:B:464:GLY:HA2	2.00	0.44
1:B:148:GLY:HA3	1:B:154:SER:OG	2.18	0.44
1:B:492:LEU:N	1:B:492:LEU:HD23	2.32	0.44
1:B:465:ARG:NH1	1:B:465:ARG:HG3	2.30	0.44
1:A:408:GLN:HB2	1:A:422:MET:CE	2.48	0.44
1:B:241:ILE:O	1:B:241:ILE:HG23	2.18	0.44
1:A:490:LEU:HD12	1:A:491:SER:H	1.82	0.44
1:B:451:ASP:OD1	1:B:453:ILE:HG12	2.17	0.44
1:B:513:CYS:HB3	1:B:518:MET:HB2	2.00	0.43
1:A:63:ASP:O	1:A:67:GLN:HB2	2.18	0.43
1:B:548:ASP:HB2	4:B:2083:HOH:O	2.18	0.43
1:A:366:LYS:CG	1:A:367:ARG:H	2.26	0.43
1:A:434:TYR:CZ	1:A:456:PHE:CZ	3.07	0.43
1:B:289:ASN:CA	1:B:316:VAL:HG21	2.41	0.43
1:A:251:ASN:HD22	1:A:255:SER:HB3	1.84	0.43
1:B:405:HIS:NE2	1:B:409:ARG:NE	2.67	0.43
1:B:377:LEU:HA	1:B:377:LEU:HD13	1.79	0.43
1:A:434:TYR:OH	1:A:456:PHE:CZ	2.70	0.43
1:A:473:GLN:HA	1:A:477:LYS:O	2.18	0.43
1:B:443:PRO:C	1:B:445:ASN:H	2.21	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:437:LYS:HA	1:B:437:LYS:HD2	1.75	0.43
1:A:185:ASP:OD2	1:A:185:ASP:N	2.42	0.43
1:B:344:ASN:C	4:B:2119:HOH:O	2.56	0.43
1:B:169:ILE:HD11	1:B:434:TYR:CZ	2.54	0.43
1:A:116:SER:C	1:A:117:LEU:HD12	2.39	0.43
1:A:71:ALA:HA	1:A:333:PHE:CE1	2.54	0.43
1:A:30:ARG:O	1:A:30:ARG:HG3	2.18	0.43
1:B:230:PHE:CZ	1:B:273:VAL:HG21	2.54	0.43
1:B:453:ILE:HG13	1:B:453:ILE:O	2.18	0.43
1:A:148:GLY:HA3	1:A:154:SER:OG	2.18	0.43
1:B:366:LYS:CG	1:B:367:ARG:H	2.26	0.42
1:A:114:ARG:NH2	1:B:114:ARG:HG2	2.34	0.42
1:B:522:GLN:NE2	1:B:522:GLN:HA	2.35	0.42
1:B:366:LYS:HE2	1:B:369:HIS:HD2	1.84	0.42
1:A:408:GLN:HE21	1:A:409:ARG:HA	1.84	0.42
1:A:252:ILE:HD12	1:A:252:ILE:H	1.83	0.42
1:B:219:GLU:HB2	1:B:248:GLY:HA2	2.01	0.42
1:A:402:HIS:HB3	1:A:437:LYS:CE	2.37	0.42
1:A:324:GLU:HG3	4:A:1146:HOH:O	2.20	0.42
1:B:227:ILE:HD13	1:B:227:ILE:HA	1.85	0.42
1:B:185:ASP:N	1:B:185:ASP:OD2	2.53	0.42
1:A:420:ASP:O	1:A:423:LYS:HB2	2.20	0.42
1:B:169:ILE:HG12	1:B:434:TYR:CZ	2.55	0.42
1:A:205:LEU:HD22	1:A:210:TRP:HE3	1.84	0.42
1:B:440:PHE:HE2	1:B:448:LYS:HB3	1.77	0.42
1:B:372:VAL:HG22	1:B:373:CYS:N	2.35	0.42
1:B:205:LEU:HD22	1:B:210:TRP:HE3	1.85	0.42
1:B:367:ARG:HB2	1:B:369:HIS:NE2	2.34	0.42
1:B:215:THR:HG22	1:B:273:VAL:HB	2.00	0.42
1:B:150:TYR:HE2	1:B:277:ARG:HB3	1.85	0.42
1:A:163:LEU:HB3	1:B:106:LEU:HD11	2.01	0.42
1:B:517:GLU:O	1:B:534:CYS:N	2.48	0.41
1:B:56:GLU:HG2	1:B:101:ARG:HH22	1.85	0.41
1:B:449:GLY:C	1:B:451:ASP:H	2.24	0.41
1:B:73:LEU:HD12	1:B:73:LEU:HA	1.94	0.41
1:A:59:ARG:HB2	1:A:59:ARG:HH11	1.85	0.41
1:A:30:ARG:NH2	1:A:32:GLU:OE1	2.53	0.41
1:B:341:ASN:C	1:B:341:ASN:ND2	2.74	0.41
1:A:440:PHE:HE2	1:A:448:LYS:HB3	1.82	0.41
1:A:443:PRO:O	1:A:445:ASN:N	2.54	0.41
1:A:205:LEU:CD2	1:A:210:TRP:HE3	2.33	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:200:ALA:O	1:A:204:ILE:HG13	2.20	0.41
1:B:356:GLU:OE1	1:B:366:LYS:HB2	2.21	0.41
1:A:366:LYS:CG	1:A:367:ARG:N	2.81	0.41
1:B:405:HIS:NE2	1:B:409:ARG:CZ	2.83	0.41
1:B:169:ILE:CG1	1:B:434:TYR:OH	2.67	0.41
1:B:36:GLU:HB3	4:B:2037:HOH:O	2.20	0.41
1:A:69:LEU:HD22	1:A:73:LEU:HD22	2.02	0.41
1:A:361:CYS:HB3	1:A:362:SER:H	1.31	0.41
1:A:274:LEU:HD13	1:A:276:MET:HE2	2.03	0.41
1:B:540:LEU:CD1	1:B:546:CYS:SG	3.08	0.41
1:B:211:THR:HG22	1:B:527:CYS:SG	2.61	0.41
1:A:437:LYS:HA	1:A:437:LYS:HD2	1.88	0.41
1:B:69:LEU:HD23	1:B:69:LEU:C	2.41	0.41
1:B:418:LEU:HD22	1:B:422:MET:CE	2.51	0.41
1:B:298:VAL:HA	1:B:321:ILE:O	2.21	0.41
1:B:515:PRO:CG	1:B:516:ASN:N	2.82	0.40
1:B:442:ALA:C	1:B:444:PHE:H	2.24	0.40
1:A:372:VAL:CG2	1:A:373:CYS:N	2.83	0.40
1:B:535:GLU:HA	1:B:535:GLU:OE2	2.21	0.40
1:A:442:ALA:C	1:A:444:PHE:N	2.74	0.40
1:B:313:SER:N	1:B:314:GLU:OE1	2.54	0.40
1:B:365:ASN:OD1	1:B:365:ASN:O	2.38	0.40
1:B:409:ARG:NH1	4:B:2115:HOH:O	2.53	0.40
1:B:299:ALA:HB2	1:B:303:TRP:CE3	2.56	0.40
1:A:169:ILE:HG12	1:A:434:TYR:CZ	2.56	0.40
1:B:194:ASP:OD1	1:B:197:GLN:NE2	2.53	0.40
1:B:181:LYS:CA	1:B:181:LYS:HE2	2.51	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	514/555 (93%)	456 (89%)	46 (9%)	12 (2%)	8	8
1	B	516/555 (93%)	453 (88%)	49 (10%)	14 (3%)	6	6
All	All	1030/1110 (93%)	909 (88%)	95 (9%)	26 (2%)	7	7

All (26) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	443	PRO
1	A	474	THR
1	A	502	ASN
1	A	516	ASN
1	A	523	PRO
1	B	443	PRO
1	B	502	ASN
1	B	516	ASN
1	A	362	SER
1	A	444	PHE
1	A	517	GLU
1	B	362	SER
1	B	474	THR
1	B	523	PRO
1	A	515	PRO
1	B	444	PHE
1	B	447	ASN
1	B	505	PRO
1	B	515	PRO
1	B	517	GLU
1	A	433	GLU
1	A	447	ASN
1	B	313	SER
1	B	433	GLU
1	B	566	PRO
1	A	566	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	447/481 (93%)	422 (94%)	25 (6%)	26	41
1	B	449/481 (93%)	424 (94%)	25 (6%)	26	41
All	All	896/962 (93%)	846 (94%)	50 (6%)	26	41

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	LEU
1	A	69	LEU
1	A	73	LEU
1	A	86	LEU
1	A	106	LEU
1	A	110	LEU
1	A	111	GLU
1	A	153	VAL
1	A	161	LEU
1	A	163	LEU
1	A	227	ILE
1	A	275	PHE
1	A	284	LEU
1	A	292	ASN
1	A	341	ASN
1	A	373	CYS
1	A	377	LEU
1	A	408	GLN
1	A	418	LEU
1	A	454	VAL
1	A	498	HIS
1	A	517	GLU
1	A	540	LEU
1	A	544	PHE
1	A	567	GLU
1	B	29	MET
1	B	39	LEU
1	B	73	LEU
1	B	86	LEU
1	B	106	LEU
1	B	110	LEU
1	B	111	GLU
1	B	153	VAL
1	B	161	LEU
1	B	163	LEU

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Mol	Chain	Res	Type
1	B	227	ILE
1	B	275	PHE
1	B	284	LEU
1	B	292	ASN
1	B	341	ASN
1	B	373	CYS
1	B	377	LEU
1	B	408	GLN
1	B	418	LEU
1	B	457	ASP
1	B	470	ASN
1	B	498	HIS
1	B	517	GLU
1	B	544	PHE
1	B	567	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	251	ASN
1	A	292	ASN
1	A	306	GLN
1	A	341	ASN
1	A	365	ASN
1	A	408	GLN
1	A	473	GLN
1	A	522	GLN
1	B	108	GLN
1	B	251	ASN
1	B	292	ASN
1	B	306	GLN
1	B	341	ASN
1	B	365	ASN
1	B	369	HIS
1	B	408	GLN
1	B	473	GLN
1	B	522	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

4 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	C5A	A	1001	-	5,12,12	1.03	0	7,18,18	1.75	2 (28%)
2	NAG	A	801	1	14,14,15	0.60	0	15,19,21	0.74	1 (6%)
3	C5A	B	2001	-	5,12,12	1.00	0	7,18,18	1.79	1 (14%)
2	NAG	B	802	1	14,14,15	0.54	0	15,19,21	0.64	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	C5A	A	1001	-	-	0/0/21/21	0/1/1/1
2	NAG	A	801	1	-	0/6/23/26	0/1/1/1
3	C5A	B	2001	-	-	0/0/21/21	0/1/1/1
2	NAG	B	802	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1001	C5A	CA-CB1-CD	-2.23	101.73	104.73

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Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
2	A	801	NAG	C2-N2-C7	-2.09	120.35	123.04
3	A	1001	C5A	CB2-CA-CB1	2.64	107.15	102.72
3	B	2001	C5A	CB2-CA-CB1	2.78	107.38	102.72

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	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	518/555 (93%)	0.87	71 (13%) 4 4	28, 58, 98, 133	0
1	B	520/555 (93%)	0.82	80 (15%) 3 3	27, 59, 100, 133	0
All	All	1038/1110 (93%)	0.85	151 (14%) 3 3	27, 58, 99, 133	0

All (151) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	516	ASN	14.6
1	A	516	ASN	11.7
1	A	368	ASN	10.5
1	B	368	ASN	10.3
1	A	449	GLY	10.2
1	A	250	SER	9.8
1	A	365	ASN	9.2
1	B	369	HIS	8.8
1	B	250	SER	8.6
1	B	28	PHE	8.4
1	A	367	ARG	8.2
1	B	367	ARG	7.9
1	B	474	THR	7.8
1	A	450	ALA	7.4
1	B	567	GLU	7.1
1	B	366	LYS	7.1
1	A	443	PRO	7.1
1	B	29	MET	7.1
1	A	370	ARG	6.9
1	A	446	PRO	6.8
1	A	369	HIS	6.5
1	B	365	ASN	6.1
1	B	566	PRO	6.0
1	A	524	GLY	5.8

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Mol	Chain	Res	Type	RSRZ
1	B	449	GLY	5.6
1	B	450	ALA	5.5
1	A	478	TYR	5.5
1	B	343	TYR	5.5
1	B	54	THR	5.4
1	A	116	SER	5.3
1	A	366	LYS	5.3
1	B	443	PRO	5.3
1	A	54	THR	5.3
1	A	474	THR	5.0
1	A	272	VAL	4.9
1	A	254	LYS	4.6
1	A	55	GLU	4.5
1	A	451	ASP	4.4
1	B	273	VAL	4.4
1	B	475	GLY	4.4
1	A	447	ASN	4.4
1	B	298	VAL	4.3
1	B	364	GLN	4.3
1	A	299	ALA	4.3
1	A	274	LEU	4.2
1	B	299	ALA	4.2
1	B	440	PHE	4.2
1	A	448	LYS	4.2
1	A	361	CYS	4.1
1	B	478	TYR	4.1
1	B	52	THR	4.1
1	B	272	VAL	4.0
1	B	315	HIS	4.0
1	A	273	VAL	3.9
1	A	147	GLY	3.8
1	B	252	ILE	3.8
1	A	146	ILE	3.8
1	B	373	CYS	3.8
1	B	249	ARG	3.7
1	A	297	TRP	3.7
1	B	473	GLN	3.7
1	A	364	GLN	3.6
1	A	298	VAL	3.6
1	B	376	HIS	3.6
1	B	53	GLY	3.6
1	A	434	TYR	3.5

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Mol	Chain	Res	Type	RSRZ
1	B	446	PRO	3.5
1	A	502	ASN	3.4
1	B	146	ILE	3.4
1	A	205	LEU	3.3
1	A	529	TRP	3.3
1	B	274	LEU	3.3
1	B	335	ARG	3.3
1	B	254	LYS	3.3
1	B	331	ARG	3.2
1	B	359	PHE	3.2
1	B	374	ASP	3.2
1	B	502	ASN	3.2
1	A	253	ARG	3.1
1	B	251	ASN	3.1
1	A	138	ILE	3.1
1	B	361	CYS	3.1
1	B	551	PRO	3.1
1	A	145	VAL	3.1
1	A	528	CYS	3.0
1	A	204	ILE	3.0
1	B	297	TRP	2.9
1	A	321	ILE	2.9
1	B	477	LYS	2.9
1	A	53	GLY	2.9
1	A	315	HIS	2.9
1	A	487	ALA	2.9
1	A	526	VAL	2.9
1	B	523	PRO	2.9
1	B	139	PRO	2.9
1	B	447	ASN	2.9
1	B	117	LEU	2.8
1	A	440	PHE	2.8
1	B	434	TYR	2.7
1	B	253	ARG	2.7
1	B	451	ASP	2.7
1	A	117	LEU	2.7
1	B	310	VAL	2.7
1	B	147	GLY	2.7
1	B	145	VAL	2.7
1	A	423	LYS	2.7
1	A	300	SER	2.6
1	B	371	GLN	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	530	ILE	2.5
1	A	441	THR	2.5
1	B	487	ALA	2.5
1	B	322	THR	2.5
1	A	409	ARG	2.5
1	B	476	GLY	2.4
1	B	55	GLU	2.4
1	B	529	TRP	2.4
1	A	475	GLY	2.4
1	A	525	ASP	2.4
1	A	331	ARG	2.4
1	B	360	GLN	2.4
1	A	41	LEU	2.3
1	A	144	GLY	2.3
1	A	363	LEU	2.3
1	A	437	LYS	2.3
1	A	44	LEU	2.3
1	A	323	LEU	2.3
1	B	397	VAL	2.3
1	A	445	ASN	2.3
1	B	382	SER	2.3
1	B	138	ILE	2.3
1	B	321	ILE	2.3
1	B	524	GLY	2.2
1	A	335	ARG	2.2
1	B	458	THR	2.2
1	A	567	GLU	2.2
1	A	302	GLY	2.2
1	B	43	GLY	2.2
1	B	149	SER	2.1
1	A	510	SER	2.1
1	B	488	GLU	2.1
1	A	238	ASN	2.1
1	B	205	LEU	2.1
1	B	216	VAL	2.1
1	A	42	GLY	2.1
1	B	544	PHE	2.1
1	A	52	THR	2.1
1	A	303	TRP	2.1
1	A	169	ILE	2.0
1	B	375	LYS	2.0
1	B	169	ILE	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	204	ILE	2.0

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

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

## 6.3 Carbohydrates [i](#)

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, 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	C5A	B	2001	12/12	0.96	0.23	0.66	36,39,40,41	0
3	C5A	A	1001	12/12	0.99	0.24	0.56	35,37,38,42	0
2	NAG	B	802	14/15	0.84	0.23	-	86,90,92,93	0
2	NAG	A	801	14/15	0.85	0.21	-	87,89,93,94	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.