



# Full wwPDB X-ray Structure Validation Report ⓘ

May 17, 2020 – 11:59 pm BST

PDB ID : 1XDK  
Title : Crystal Structure of the RARbeta/RXRalpha Ligand Binding Domain Heterodimer in Complex with 9-cis Retinoic Acid and a Fragment of the TRAP220 Coactivator  
Authors : Pogenberg, V.; Guichou, J.F.; Vivat-Hannah, V.; Kammerer, S.; Perez, E.; Germain, P.; De Lera, A.R.; Gronemeyer, H.; Royer, C.A.; Bourguet, W.  
Deposited on : 2004-09-07  
Resolution : 2.90 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

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

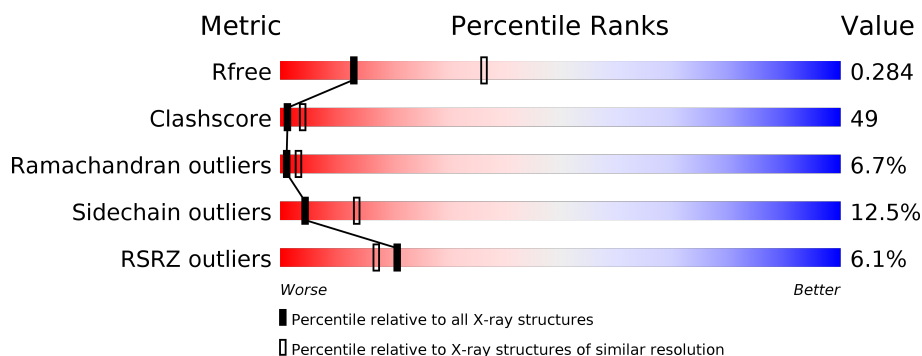
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	238	<div> <div>3%</div> <div> <div>33%</div> <div>46%</div> <div>12%</div> <div>9%</div> </div> </div>
1	E	238	<div> <div>5%</div> <div> <div>32%</div> <div>46%</div> <div>13%</div> <div>9%</div> </div> </div>
2	B	303	<div> <div>5%</div> <div> <div>33%</div> <div>39%</div> <div>9%</div> <div>19%</div> </div> </div>
2	F	303	<div> <div>6%</div> <div> <div>32%</div> <div>40%</div> <div>8%</div> <div>19%</div> </div> </div>
3	C	14	<div> <div>14%</div> <div> <div>7%</div> <div>36%</div> <div>29%</div> <div>7%</div> <div>21%</div> </div> </div>
3	D	14	<div> <div>50%</div> <div>21%</div> <div>29%</div> </div>

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Mol	Chain	Length	Quality of chain
3	G	14	
3	H	14	

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7682 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 Retinoic acid receptor RXR-alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	217	Total	C	N	O	S	0	0	0
			1700	1091	290	309	10			
1	E	217	Total	C	N	O	S	0	0	0
			1700	1091	290	309	10			

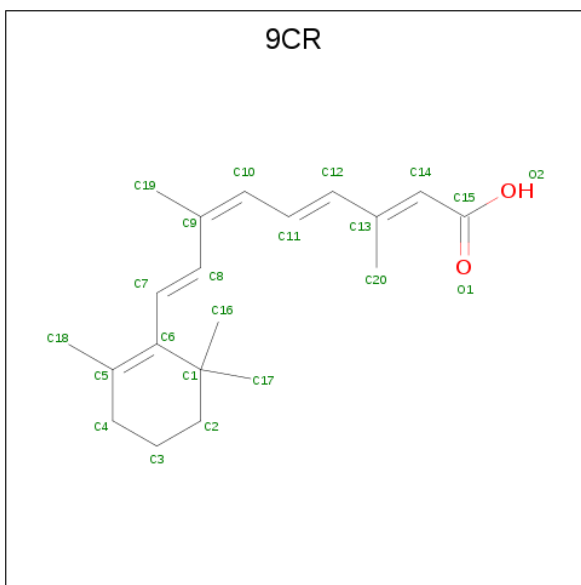
- Molecule 2 is a protein called Retinoic acid receptor, beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	245	Total	C	N	O	S	0	0	0
			1919	1220	325	360	14			
2	F	245	Total	C	N	O	S	0	0	0
			1919	1220	325	360	14			

- Molecule 3 is a protein called Thyroid Receptor Associated Protein 220.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	11	Total	C	N	O	S	0	0	0
			90	57	16	15	2			
3	D	10	Total	C	N	O	S	0	0	0
			82	53	14	13	2			
3	G	11	Total	C	N	O	S	0	0	0
			90	57	16	15	2			
3	H	10	Total	C	N	O	S	0	0	0
			82	53	14	13	2			

- Molecule 4 is (9cis)-retinoic acid (three-letter code: 9CR) (formula: C<sub>20</sub>H<sub>28</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			22	20	2		
4	B	1	Total	C	O	0	0
			22	20	2		
4	E	1	Total	C	O	0	0
			22	20	2		
4	F	1	Total	C	O	0	0
			22	20	2		

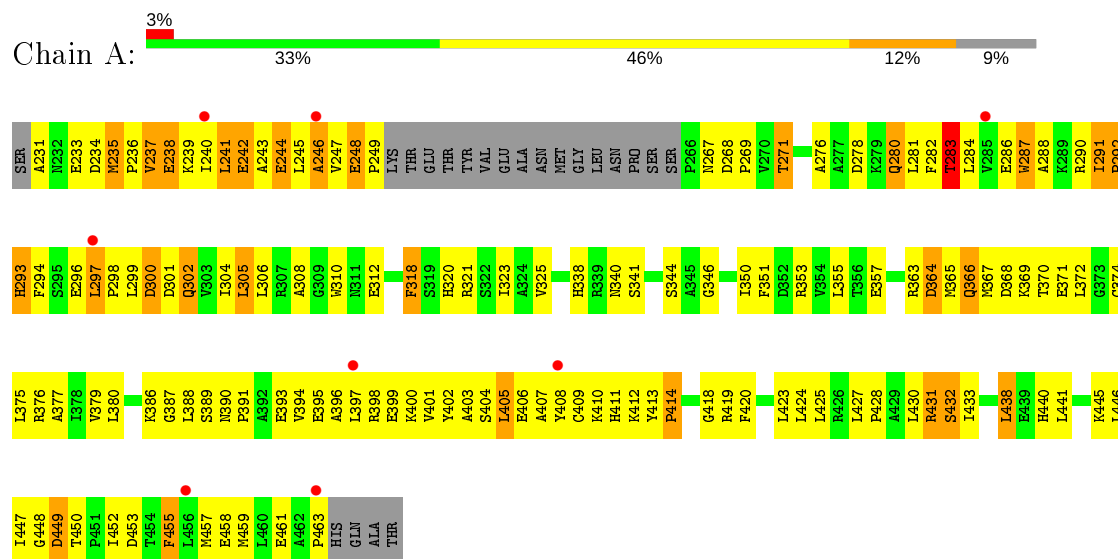
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	4	Total	O	0	0
			4	4		
5	B	2	Total	O	0	0
			2	2		
5	E	4	Total	O	0	0
			4	4		
5	F	2	Total	O	0	0
			2	2		

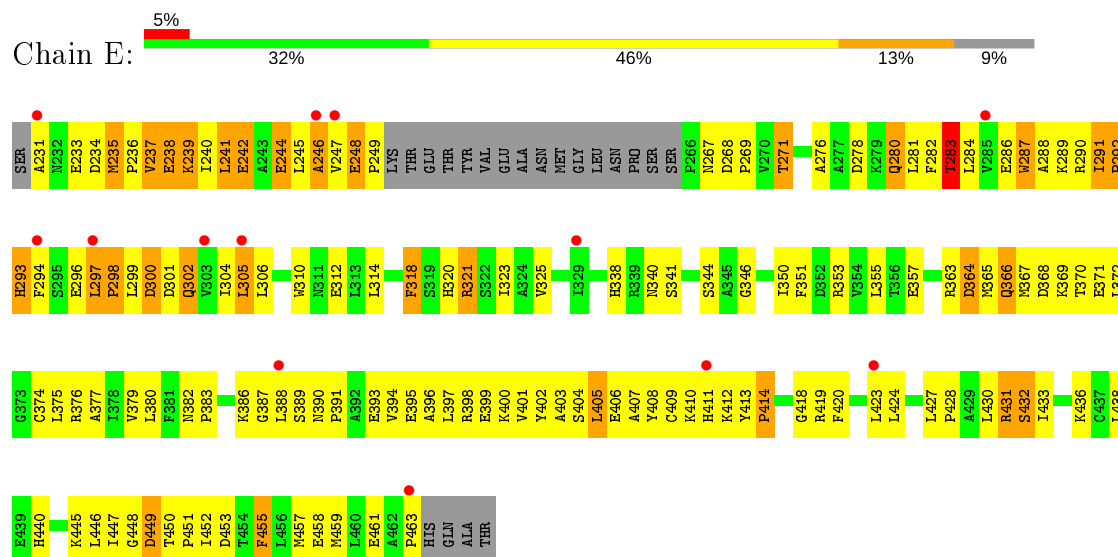
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $\text{RSRZ} > 2$ ). 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.

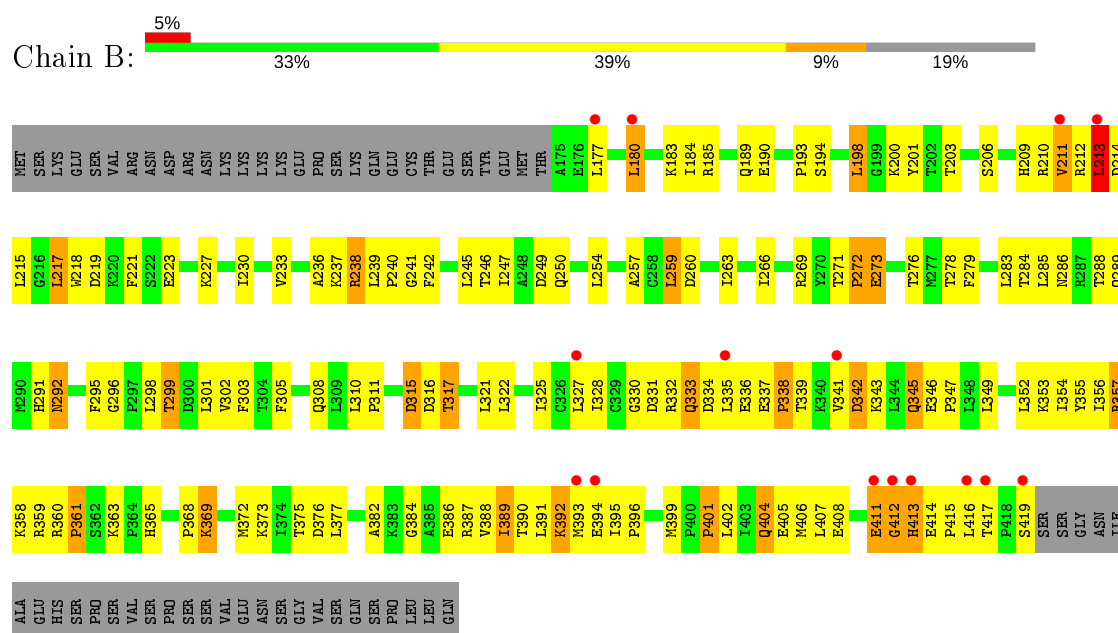
- Molecule 1: Retinoic acid receptor RXR-alpha



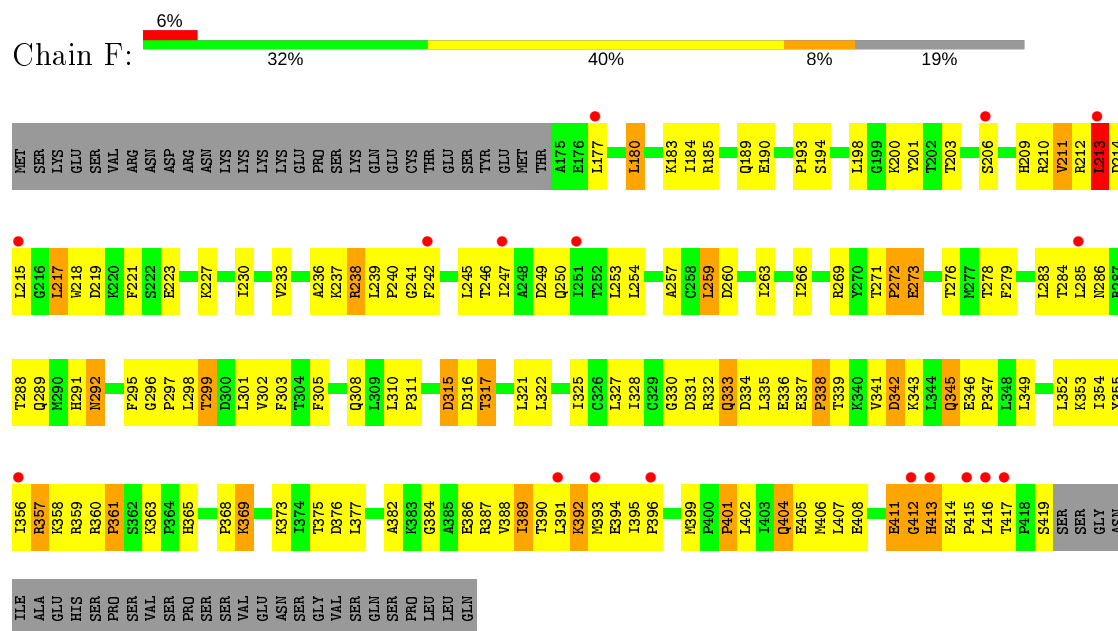
- Molecule 1: Retinoic acid receptor RXR-alpha



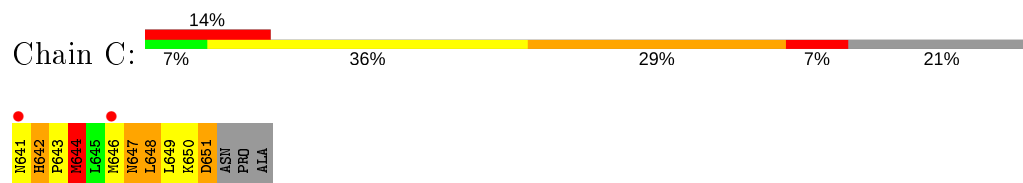
- Molecule 2: Retinoic acid receptor, beta



- Molecule 2: Retinoic acid receptor, beta

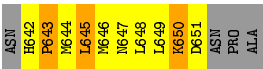


- Molecule 3: Thyroid Receptor Associated Protein 220

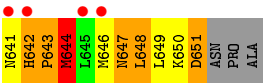


- Molecule 3: Thyroid Receptor Associated Protein 220

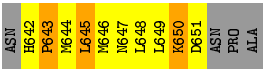
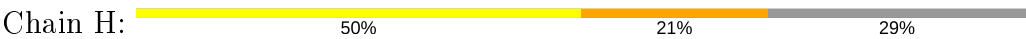




● Molecule 3: Thyroid Receptor Associated Protein 220



● Molecule 3: Thyroid Receptor Associated Protein 220





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	115.70Å 115.70Å 247.20Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 2.90 37.43 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.6 (30.00-2.90) 99.5 (37.43-2.90)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.30 (at 2.90Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.253 , 0.296 0.247 , 0.284	Depositor DCC
$R_{free}$ test set	1372 reflections (3.19%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	74.0	Xtriage
Anisotropy	0.605	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 60.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.480 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	7682	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.34% of the height of the origin peak. No significant pseudotranslation is detected.*

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

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

## 5 Model quality [i](#)

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

Bond lengths and bond angles in the following residue types are not validated in this section: 9CR

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.74	0/1734	0.92	0/2345
1	E	0.73	0/1734	0.92	0/2345
2	B	0.64	0/1952	0.84	1/2638 (0.0%)
2	F	0.64	0/1952	0.84	1/2638 (0.0%)
3	C	0.58	0/91	1.06	0/121
3	D	0.57	0/83	0.70	0/110
3	G	0.59	0/91	1.06	0/121
3	H	0.59	0/83	0.69	0/110
All	All	0.68	0/7720	0.88	2/10428 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	213	LEU	CA-CB-CG	5.64	128.27	115.30
2	F	213	LEU	CA-CB-CG	5.59	128.16	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	1700	0	1728	189	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	1700	0	1728	191	0
2	B	1919	0	1979	191	0
2	F	1919	0	1979	190	0
3	C	90	0	93	17	0
3	D	82	0	87	12	0
3	G	90	0	93	19	0
3	H	82	0	87	12	0
4	A	22	0	27	3	0
4	B	22	0	27	3	0
4	E	22	0	27	2	0
4	F	22	0	27	3	0
5	A	4	0	0	0	0
5	B	2	0	0	0	0
5	E	4	0	0	1	0
5	F	2	0	0	0	0
All	All	7682	0	7882	768	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 49.

All (768) 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)
2:B:343:LYS:HA	2:B:346:GLU:HG3	1.26	1.16
2:F:343:LYS:HA	2:F:346:GLU:HG3	1.26	1.14
2:F:315:ASP:HB3	2:F:359:ARG:HH12	1.09	1.13
2:F:357:ARG:HH11	2:F:357:ARG:HG3	1.13	1.09
1:A:237:VAL:HG23	1:A:238:GLU:H	1.14	1.07
2:B:357:ARG:HH11	2:B:357:ARG:HG3	1.13	1.06
2:B:315:ASP:HB3	2:B:359:ARG:HH12	1.11	1.06
1:E:237:VAL:HG23	1:E:238:GLU:H	1.14	1.04
2:B:401:PRO:HB2	3:D:644:MET:HE1	1.43	1.01
1:E:299:LEU:HA	1:E:302:GLN:HE21	1.26	1.01
1:A:299:LEU:HA	1:A:302:GLN:HE21	1.26	1.01
2:F:315:ASP:HB3	2:F:359:ARG:NH1	1.74	1.01
2:B:315:ASP:HB3	2:B:359:ARG:NH1	1.76	1.00
2:F:386:GLU:O	2:F:390:THR:HG23	1.65	0.95
1:A:299:LEU:HA	1:A:302:GLN:NE2	1.82	0.95
2:B:386:GLU:O	2:B:390:THR:HG23	1.64	0.95
2:F:246:THR:HB	2:F:249:ASP:HB2	1.49	0.94
1:E:299:LEU:HA	1:E:302:GLN:NE2	1.82	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:401:PRO:HB2	3:H:644:MET:HE1	1.48	0.93
1:A:305:LEU:HD22	1:A:380:LEU:O	1.69	0.92
2:B:246:THR:HB	2:B:249:ASP:HB2	1.50	0.92
1:E:305:LEU:HD22	1:E:380:LEU:O	1.71	0.90
1:E:413:TYR:N	1:E:414:PRO:HD3	1.87	0.90
1:A:237:VAL:HG23	1:A:238:GLU:N	1.87	0.89
1:A:413:TYR:N	1:A:414:PRO:HD3	1.86	0.89
2:F:237:LYS:HD3	3:H:649:LEU:HA	1.55	0.87
1:E:237:VAL:HG23	1:E:238:GLU:N	1.87	0.87
2:F:190:GLU:OE2	2:F:238:ARG:NH2	2.10	0.85
1:E:297:LEU:HD21	1:E:397:LEU:CD1	2.07	0.85
2:B:190:GLU:OE2	2:B:238:ARG:NH2	2.09	0.84
2:B:237:LYS:HD3	3:D:649:LEU:HA	1.57	0.84
1:A:366:GLN:HE21	1:A:366:GLN:N	1.76	0.83
1:A:297:LEU:HD21	1:A:397:LEU:CD1	2.08	0.82
1:E:366:GLN:N	1:E:366:GLN:HE21	1.77	0.82
2:B:401:PRO:HB2	3:D:644:MET:CE	2.08	0.82
2:F:401:PRO:HB2	3:H:644:MET:CE	2.08	0.82
1:A:286:GLU:HG3	1:A:290:ARG:HD2	1.62	0.81
2:F:254:LEU:HD23	2:F:327:LEU:HD11	1.60	0.81
2:B:254:LEU:HD23	2:B:327:LEU:HD11	1.62	0.81
2:F:392:LYS:HB3	2:F:399:MET:HE3	1.63	0.80
2:B:210:ARG:HD3	2:B:291:HIS:CD2	2.17	0.80
2:F:210:ARG:HD3	2:F:291:HIS:CD2	2.17	0.79
1:E:286:GLU:HG3	1:E:290:ARG:HD2	1.63	0.79
1:E:299:LEU:O	1:E:302:GLN:HG2	1.84	0.79
1:A:299:LEU:O	1:A:302:GLN:HG2	1.84	0.78
2:F:259:LEU:O	2:F:263:ILE:HG13	1.84	0.77
1:A:237:VAL:CG2	1:A:238:GLU:H	1.95	0.77
2:B:259:LEU:O	2:B:263:ILE:HG13	1.83	0.77
2:B:414:GLU:HB3	2:B:415:PRO:HA	1.66	0.77
1:E:240:ILE:HG23	1:E:291:ILE:HD11	1.65	0.77
1:E:388:LEU:HD21	1:E:394:VAL:HG21	1.67	0.77
2:F:227:LYS:NZ	2:F:227:LYS:HB3	2.00	0.77
2:B:227:LYS:NZ	2:B:227:LYS:HB3	1.99	0.77
2:B:315:ASP:CB	2:B:359:ARG:HH12	1.97	0.76
2:F:414:GLU:HB3	2:F:415:PRO:HA	1.66	0.76
1:A:413:TYR:N	1:A:414:PRO:CD	2.46	0.76
1:E:237:VAL:CG2	1:E:238:GLU:H	1.95	0.76
1:A:240:ILE:HG23	1:A:291:ILE:HD11	1.67	0.76
1:A:388:LEU:HD21	1:A:394:VAL:HG21	1.67	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:391:LEU:C	2:F:393:MET:H	1.89	0.76
1:E:413:TYR:N	1:E:414:PRO:CD	2.47	0.76
2:B:391:LEU:C	2:B:393:MET:H	1.90	0.75
2:F:315:ASP:CB	2:F:359:ARG:HH12	1.95	0.75
1:A:431:ARG:HH11	1:A:431:ARG:HG2	1.52	0.75
1:E:406:GLU:HG2	1:E:410:LYS:HE2	1.67	0.75
1:A:235:MET:HB3	1:A:404:SER:OG	1.87	0.74
3:G:642:HIS:O	3:G:646:MET:HB2	1.87	0.74
1:A:407:ALA:O	1:A:410:LYS:HB2	1.88	0.74
1:E:431:ARG:HG2	1:E:431:ARG:HH11	1.52	0.74
2:F:279:PHE:HE1	2:F:285:LEU:HD12	1.52	0.74
1:E:236:PRO:HB2	1:E:239:LYS:HB2	1.70	0.74
2:B:401:PRO:CB	3:D:644:MET:HE1	2.18	0.73
3:C:642:HIS:O	3:C:646:MET:HB2	1.87	0.73
1:E:374:CYS:CB	1:E:405:LEU:HD22	2.19	0.73
2:B:210:ARG:HG2	2:B:291:HIS:ND1	2.03	0.73
1:A:374:CYS:CB	1:A:405:LEU:HD22	2.19	0.73
2:F:211:VAL:HG23	2:F:213:LEU:H	1.54	0.73
2:F:279:PHE:CE1	2:F:285:LEU:HD12	2.24	0.73
1:A:374:CYS:O	1:A:377:ALA:HB3	1.88	0.72
1:E:374:CYS:O	1:E:377:ALA:HB3	1.89	0.72
1:E:407:ALA:O	1:E:410:LYS:HB2	1.88	0.72
2:F:210:ARG:HG2	2:F:291:HIS:ND1	2.04	0.72
1:A:236:PRO:HB2	1:A:239:LYS:HB2	1.72	0.72
1:E:235:MET:HB3	1:E:404:SER:OG	1.89	0.72
2:F:357:ARG:NH1	2:F:357:ARG:HG3	1.92	0.72
1:A:463:PRO:HB3	3:C:642:HIS:NE2	2.05	0.72
1:A:406:GLU:HG2	1:A:410:LYS:HE2	1.70	0.72
2:B:211:VAL:HG23	2:B:213:LEU:H	1.55	0.72
1:E:463:PRO:HB3	3:G:642:HIS:NE2	2.04	0.72
2:B:279:PHE:HE1	2:B:285:LEU:HD12	1.53	0.71
2:B:357:ARG:NH1	2:B:357:ARG:HG3	1.93	0.71
2:B:278:THR:HG23	2:B:284:THR:OG1	1.90	0.71
2:B:279:PHE:CE1	2:B:285:LEU:HD12	2.26	0.71
2:F:257:ALA:O	2:F:260:ASP:HB2	1.90	0.70
2:F:363:LYS:HB3	2:F:365:HIS:HE1	1.56	0.70
2:B:330:GLY:HA3	2:B:342:ASP:OD1	1.91	0.70
2:B:363:LYS:HB3	2:B:365:HIS:HE1	1.56	0.70
2:F:330:GLY:HA3	2:F:342:ASP:OD1	1.91	0.70
2:B:286:ASN:OD1	2:B:289:GLN:HG3	1.91	0.70
1:A:410:LYS:O	1:A:414:PRO:HG3	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:297:LEU:HD21	1:E:397:LEU:HD11	1.73	0.70
2:B:212:ARG:O	2:B:213:LEU:HB2	1.92	0.70
2:F:305:PHE:CZ	2:F:377:LEU:HD13	2.27	0.70
2:B:389:ILE:HA	2:B:392:LYS:HG2	1.73	0.69
2:F:389:ILE:HA	2:F:392:LYS:HG2	1.74	0.69
1:E:406:GLU:O	1:E:410:LYS:HG3	1.91	0.69
2:F:278:THR:HG23	2:F:284:THR:OG1	1.91	0.69
2:F:328:ILE:O	2:F:345:GLN:NE2	2.24	0.69
2:B:257:ALA:O	2:B:260:ASP:HB2	1.92	0.69
1:E:410:LYS:O	1:E:414:PRO:HG3	1.92	0.69
1:A:399:GLU:HA	1:A:402:TYR:HD2	1.57	0.69
2:F:212:ARG:O	2:F:213:LEU:HB2	1.92	0.69
1:A:400:LYS:O	1:A:403:ALA:HB3	1.93	0.69
2:B:328:ILE:O	2:B:345:GLN:NE2	2.25	0.69
1:A:297:LEU:HD21	1:A:397:LEU:HD11	1.74	0.69
2:F:387:ARG:NH2	2:F:391:LEU:HD23	2.07	0.69
1:A:365:MET:C	1:A:366:GLN:HE21	1.96	0.69
1:E:323:ILE:HG23	1:E:363:ARG:HB2	1.74	0.69
1:A:323:ILE:HG23	1:A:363:ARG:HB2	1.75	0.69
1:A:353:ARG:HH11	1:A:353:ARG:HG2	1.58	0.69
1:E:400:LYS:O	1:E:403:ALA:HB3	1.93	0.69
2:F:286:ASN:OD1	2:F:289:GLN:HG3	1.92	0.69
2:B:387:ARG:NH2	2:B:391:LEU:HD23	2.09	0.68
1:A:406:GLU:O	1:A:410:LYS:HG3	1.91	0.68
1:E:399:GLU:HA	1:E:402:TYR:HD2	1.57	0.68
2:F:315:ASP:CB	2:F:359:ARG:NH1	2.56	0.68
2:F:401:PRO:CB	3:H:644:MET:HE1	2.22	0.68
1:E:375:LEU:O	1:E:379:VAL:HG23	1.94	0.68
1:E:398:ARG:HD3	1:E:402:TYR:OH	1.93	0.68
2:B:394:GLU:HA	2:F:413:HIS:H	1.59	0.68
2:B:285:LEU:HD22	2:B:289:GLN:HB3	1.75	0.68
1:E:365:MET:C	1:E:366:GLN:HE21	1.97	0.68
2:B:305:PHE:CZ	2:B:377:LEU:HD13	2.29	0.68
1:A:458:GLU:OE2	3:C:644:MET:HG2	1.94	0.67
2:B:413:HIS:H	2:F:394:GLU:HA	1.59	0.67
2:B:210:ARG:HG2	2:B:291:HIS:CE1	2.29	0.67
1:E:374:CYS:HB2	1:E:405:LEU:HD22	1.76	0.67
2:F:357:ARG:HH11	2:F:357:ARG:CG	1.98	0.67
1:A:320:HIS:O	1:A:323:ILE:HG12	1.94	0.67
1:A:323:ILE:CG2	1:A:363:ARG:HB2	2.24	0.67
2:B:419:SER:HB3	2:F:215:LEU:HB3	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:401:PRO:HB2	3:D:644:MET:SD	2.34	0.67
1:A:447:ILE:O	1:A:447:ILE:HG22	1.94	0.67
2:B:357:ARG:HH11	2:B:357:ARG:CG	1.98	0.67
1:A:374:CYS:HB2	1:A:405:LEU:HD22	1.77	0.67
2:F:388:VAL:HG21	2:F:407:LEU:HB3	1.77	0.67
1:A:375:LEU:O	1:A:379:VAL:HG23	1.95	0.67
1:E:447:ILE:O	1:E:447:ILE:HG22	1.94	0.67
2:B:276:THR:HG22	2:B:286:ASN:HA	1.76	0.67
2:B:388:VAL:HG21	2:B:407:LEU:HB3	1.77	0.67
1:E:320:HIS:O	1:E:323:ILE:HG12	1.95	0.67
2:F:401:PRO:HB2	3:H:644:MET:SD	2.35	0.67
1:E:323:ILE:CG2	1:E:363:ARG:HB2	2.24	0.67
1:A:398:ARG:HD3	1:A:402:TYR:OH	1.95	0.66
2:B:213:LEU:HD21	2:B:218:TRP:HB2	1.76	0.66
2:F:210:ARG:HG2	2:F:291:HIS:CE1	2.31	0.66
2:F:276:THR:HG22	2:F:286:ASN:HA	1.76	0.66
2:B:365:HIS:O	2:B:369:LYS:HB2	1.95	0.66
1:A:395:GLU:O	1:A:399:GLU:HG2	1.95	0.66
1:A:408:TYR:CE2	1:A:412:LYS:HD3	2.29	0.66
2:F:285:LEU:HD22	2:F:289:GLN:HB3	1.77	0.66
1:E:408:TYR:CE2	1:E:412:LYS:HD3	2.30	0.66
1:E:458:GLU:OE2	3:G:644:MET:HG2	1.95	0.66
3:G:641:ASN:HD22	3:G:642:HIS:H	1.43	0.66
3:C:641:ASN:HD22	3:C:642:HIS:H	1.42	0.65
2:F:213:LEU:HD21	2:F:218:TRP:HB2	1.78	0.65
1:E:412:LYS:C	1:E:414:PRO:HD3	2.16	0.65
2:B:352:LEU:HD11	2:B:356:ILE:HD11	1.79	0.65
1:E:395:GLU:O	1:E:399:GLU:HG2	1.95	0.65
1:A:412:LYS:C	1:A:414:PRO:HD3	2.16	0.65
2:B:215:LEU:HB3	2:F:419:SER:HB3	1.79	0.65
2:B:413:HIS:CE1	2:F:393:MET:HG3	2.32	0.64
2:B:298:LEU:O	2:B:302:VAL:HG13	1.98	0.64
1:E:353:ARG:HH11	1:E:353:ARG:HG2	1.61	0.64
1:A:395:GLU:O	1:A:399:GLU:CG	2.45	0.64
2:F:365:HIS:O	2:F:369:LYS:HB2	1.97	0.64
2:F:269:ARG:HH11	2:F:269:ARG:HG3	1.62	0.64
2:F:298:LEU:O	2:F:302:VAL:HG13	1.97	0.64
2:B:393:MET:HG3	2:F:413:HIS:CE1	2.33	0.64
2:F:352:LEU:HD11	2:F:356:ILE:HD11	1.80	0.64
2:B:254:LEU:HD23	2:B:327:LEU:CD1	2.28	0.64
3:H:642:HIS:O	3:H:646:MET:HB2	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:647:ASN:O	3:G:649:LEU:N	2.31	0.64
2:B:288:THR:HG22	2:B:292:ASN:ND2	2.13	0.63
3:D:642:HIS:O	3:D:646:MET:HB2	1.97	0.63
2:B:315:ASP:CB	2:B:359:ARG:NH1	2.57	0.63
2:B:269:ARG:HH11	2:B:269:ARG:HG3	1.63	0.63
2:B:299:THR:O	2:B:302:VAL:HG22	1.98	0.63
2:B:206:SER:OG	2:B:214:ASP:HB2	1.99	0.63
1:E:237:VAL:O	1:E:239:LYS:N	2.32	0.63
1:E:395:GLU:O	1:E:399:GLU:CG	2.46	0.63
1:E:405:LEU:O	1:E:405:LEU:HD12	1.99	0.63
2:F:185:ARG:HG3	2:F:317:THR:HG22	1.81	0.63
2:B:180:LEU:HD12	2:B:240:PRO:HG2	1.81	0.63
2:F:288:THR:HG22	2:F:292:ASN:ND2	2.14	0.63
1:A:237:VAL:HG21	1:A:408:TYR:CD1	2.34	0.62
2:B:185:ARG:HG3	2:B:317:THR:HG22	1.82	0.62
1:E:353:ARG:NH1	1:E:357:GLU:OE1	2.33	0.62
2:F:299:THR:O	2:F:302:VAL:HG22	1.99	0.62
1:A:237:VAL:HG21	1:A:408:TYR:HD1	1.64	0.62
2:B:392:LYS:HB3	2:B:399:MET:CE	2.30	0.62
1:E:299:LEU:O	1:E:301:ASP:N	2.33	0.62
1:A:405:LEU:O	1:A:405:LEU:HD12	2.00	0.62
2:F:399:MET:HB3	2:F:404:GLN:NE2	2.15	0.62
2:B:399:MET:HB3	2:B:404:GLN:NE2	2.15	0.62
3:C:647:ASN:O	3:C:649:LEU:N	2.33	0.62
1:E:281:LEU:HB3	1:E:455:PHE:CE1	2.34	0.62
2:F:180:LEU:HD12	2:F:240:PRO:HG2	1.81	0.62
1:A:237:VAL:O	1:A:239:LYS:N	2.32	0.62
1:E:237:VAL:HG21	1:E:408:TYR:CD1	2.35	0.62
1:A:237:VAL:HG11	1:A:408:TYR:HD1	1.65	0.61
1:A:353:ARG:NH1	1:A:357:GLU:OE1	2.33	0.61
1:E:338:HIS:CD2	1:E:340:ASN:H	2.17	0.61
1:A:338:HIS:CD2	1:A:340:ASN:H	2.18	0.61
1:A:291:ILE:HG22	1:A:294:PHE:HB2	1.82	0.61
2:B:411:GLU:O	2:B:412:GLY:O	2.18	0.61
2:F:206:SER:OG	2:F:214:ASP:HB2	1.99	0.61
2:F:254:LEU:HD23	2:F:327:LEU:CD1	2.28	0.61
1:E:291:ILE:HG22	1:E:294:PHE:HB2	1.82	0.61
1:E:338:HIS:HD2	1:E:340:ASN:HB2	1.65	0.61
2:F:392:LYS:HB3	2:F:399:MET:CE	2.29	0.61
1:E:237:VAL:HG21	1:E:408:TYR:HD1	1.64	0.61
1:A:280:GLN:OE1	1:A:280:GLN:HA	1.99	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:299:LEU:O	1:A:301:ASP:N	2.33	0.60
1:A:281:LEU:HB3	1:A:455:PHE:CE1	2.35	0.60
1:A:321:ARG:NH2	4:A:500:9CR:O1	2.33	0.60
1:E:321:ARG:NH2	4:E:1500:9CR:O2	2.34	0.60
1:E:440:HIS:HE1	2:F:414:GLU:HB2	1.67	0.60
1:A:440:HIS:HE1	2:B:414:GLU:HB2	1.66	0.60
1:E:386:LYS:HG3	1:E:387:GLY:N	2.16	0.60
1:E:237:VAL:HG11	1:E:408:TYR:HD1	1.66	0.60
3:G:644:MET:O	3:G:648:LEU:HB2	2.01	0.60
1:A:288:ALA:O	1:A:291:ILE:HB	2.02	0.60
2:F:411:GLU:O	2:F:412:GLY:O	2.18	0.60
1:A:338:HIS:HD2	1:A:340:ASN:HB2	1.66	0.60
1:A:386:LYS:HG3	1:A:387:GLY:N	2.16	0.60
1:E:280:GLN:HA	1:E:280:GLN:OE1	2.00	0.60
2:B:310:LEU:HB2	2:B:311:PRO:HD3	1.84	0.60
2:F:315:ASP:C	2:F:315:ASP:OD1	2.40	0.59
1:E:402:TYR:CD1	2:F:368:PRO:HB2	2.37	0.59
1:E:346:GLY:O	2:F:415:PRO:HA	2.02	0.59
1:A:241:LEU:HG	1:A:370:THR:HG22	1.84	0.59
2:B:210:ARG:HD3	2:B:291:HIS:CG	2.37	0.59
2:B:315:ASP:C	2:B:315:ASP:OD1	2.40	0.59
1:E:271:THR:HG22	1:E:450:THR:HG23	1.83	0.59
1:E:234:ASP:O	1:E:234:ASP:OD1	2.19	0.59
2:F:211:VAL:HG23	2:F:213:LEU:N	2.16	0.59
2:F:288:THR:HG22	2:F:292:ASN:HD21	1.68	0.59
3:C:644:MET:O	3:C:648:LEU:HB2	2.02	0.59
1:E:241:LEU:HG	1:E:370:THR:HG22	1.85	0.59
1:A:234:ASP:OD1	1:A:234:ASP:O	2.20	0.59
2:F:335:LEU:O	2:F:338:PRO:HD3	2.02	0.59
3:G:641:ASN:ND2	3:G:642:HIS:H	2.00	0.59
1:A:374:CYS:O	1:A:377:ALA:N	2.36	0.59
1:A:399:GLU:OE2	2:B:365:HIS:HD2	1.86	0.59
2:B:392:LYS:HB3	2:B:399:MET:HE3	1.83	0.59
3:C:641:ASN:ND2	3:C:642:HIS:H	2.00	0.59
2:F:413:HIS:N	2:F:413:HIS:ND1	2.51	0.59
1:E:371:GLU:CD	1:E:419:ARG:HH21	2.07	0.59
1:E:399:GLU:OE2	2:F:365:HIS:HD2	1.86	0.59
2:B:184:ILE:HD12	2:B:321:LEU:HD23	1.85	0.58
2:B:211:VAL:HG23	2:B:213:LEU:N	2.17	0.58
2:B:413:HIS:N	2:B:413:HIS:ND1	2.51	0.58
1:A:346:GLY:O	2:B:415:PRO:HA	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:288:THR:HG22	2:B:292:ASN:HD21	1.67	0.58
2:B:335:LEU:O	2:B:338:PRO:HD3	2.04	0.58
1:E:374:CYS:O	1:E:377:ALA:N	2.36	0.58
2:B:227:LYS:HZ3	2:B:227:LYS:HB3	1.68	0.58
1:A:288:ALA:O	1:A:291:ILE:N	2.33	0.58
2:B:391:LEU:O	2:B:393:MET:N	2.36	0.58
1:A:371:GLU:CD	1:A:419:ARG:HH21	2.07	0.58
1:A:320:HIS:HA	1:A:323:ILE:HD11	1.85	0.58
2:B:215:LEU:O	2:B:219:ASP:OD2	2.22	0.58
1:E:405:LEU:HD12	1:E:409:CYS:SG	2.44	0.58
1:A:338:HIS:HD2	1:A:340:ASN:H	1.52	0.58
1:A:237:VAL:HG11	1:A:408:TYR:CD1	2.38	0.58
1:A:271:THR:HG22	1:A:450:THR:HG23	1.85	0.58
1:E:288:ALA:O	1:E:291:ILE:HB	2.03	0.58
2:F:210:ARG:HD3	2:F:291:HIS:CG	2.38	0.58
1:E:281:LEU:HB3	1:E:455:PHE:CD1	2.38	0.57
2:F:310:LEU:HB2	2:F:311:PRO:HD3	1.85	0.57
1:A:399:GLU:HA	1:A:402:TYR:CD2	2.37	0.57
1:E:320:HIS:HA	1:E:323:ILE:HD11	1.85	0.57
2:B:315:ASP:OD1	2:B:317:THR:N	2.38	0.57
1:E:399:GLU:HA	1:E:402:TYR:CD2	2.38	0.57
1:A:235:MET:HG2	1:A:401:VAL:HG22	1.85	0.57
2:F:391:LEU:O	2:F:393:MET:N	2.35	0.57
3:G:641:ASN:HD22	3:G:642:HIS:CD2	2.22	0.57
1:A:402:TYR:CD1	2:B:368:PRO:HB2	2.39	0.57
1:A:431:ARG:NH1	1:A:431:ARG:HG2	2.20	0.57
1:E:268:ASP:OD2	1:E:271:THR:HG23	2.05	0.57
2:F:215:LEU:O	2:F:219:ASP:OD2	2.23	0.57
2:F:337:GLU:O	2:F:338:PRO:C	2.43	0.57
2:B:269:ARG:NH1	2:B:269:ARG:HG3	2.20	0.57
1:E:235:MET:HG2	1:E:401:VAL:HG22	1.86	0.57
2:F:333:GLN:O	2:F:334:ASP:HB2	2.04	0.57
1:A:368:ASP:OD2	1:A:370:THR:OG1	2.22	0.57
1:A:405:LEU:HG	1:A:420:PHE:HE1	1.70	0.57
1:E:292:PRO:O	1:E:293:HIS:HB2	2.05	0.57
2:F:184:ILE:HD12	2:F:321:LEU:HD23	1.86	0.56
2:B:337:GLU:O	2:B:338:PRO:C	2.43	0.56
1:E:338:HIS:HD2	1:E:340:ASN:H	1.52	0.56
1:A:281:LEU:HB3	1:A:455:PHE:CD1	2.40	0.56
3:C:641:ASN:HD22	3:C:642:HIS:CD2	2.23	0.56
1:E:237:VAL:HG11	1:E:408:TYR:CD1	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:333:GLN:O	2:B:334:ASP:HB2	2.05	0.56
1:E:368:ASP:OD2	1:E:370:THR:OG1	2.23	0.56
1:A:292:PRO:O	1:A:293:HIS:HB2	2.04	0.56
1:E:240:ILE:HG23	1:E:291:ILE:CD1	2.36	0.56
1:E:431:ARG:HD3	1:E:431:ARG:O	2.06	0.56
1:A:241:LEU:CD2	1:A:245:LEU:HD23	2.35	0.56
1:A:268:ASP:OD2	1:A:271:THR:HG23	2.06	0.56
3:D:645:LEU:HA	3:D:648:LEU:HD12	1.88	0.56
2:F:250:GLN:NE2	3:H:649:LEU:HD23	2.20	0.56
1:E:288:ALA:O	1:E:291:ILE:N	2.33	0.56
2:B:250:GLN:NE2	3:D:649:LEU:HD23	2.20	0.56
2:B:223:GLU:O	2:B:227:LYS:HG3	2.05	0.55
1:E:241:LEU:CD2	1:E:245:LEU:HD23	2.36	0.55
1:A:405:LEU:HD12	1:A:409:CYS:SG	2.47	0.55
2:B:272:PRO:HG3	2:B:310:LEU:HD11	1.89	0.55
2:F:184:ILE:HD12	2:F:321:LEU:CD2	2.36	0.55
2:F:395:ILE:O	2:F:395:ILE:HG13	2.06	0.55
3:H:647:ASN:O	3:H:650:LYS:HB3	2.06	0.55
2:B:388:VAL:CG2	2:B:407:LEU:HD23	2.37	0.55
2:F:315:ASP:OD1	2:F:317:THR:N	2.40	0.55
1:A:431:ARG:O	1:A:431:ARG:HD3	2.07	0.55
3:H:645:LEU:HA	3:H:648:LEU:HD12	1.89	0.55
2:F:223:GLU:O	2:F:227:LYS:HG3	2.06	0.55
2:F:269:ARG:NH1	2:F:269:ARG:HG3	2.20	0.55
2:B:363:LYS:HB3	2:B:365:HIS:CE1	2.41	0.55
3:D:647:ASN:O	3:D:650:LYS:HB3	2.07	0.54
1:E:431:ARG:HG2	1:E:431:ARG:NH1	2.21	0.54
2:B:184:ILE:HD12	2:B:321:LEU:CD2	2.37	0.54
1:E:368:ASP:OD2	1:E:370:THR:N	2.36	0.54
1:E:244:GLU:OE1	1:E:287:TRP:NE1	2.40	0.54
1:E:405:LEU:HG	1:E:420:PHE:HE1	1.71	0.54
2:B:227:LYS:HA	2:B:230:ILE:HD12	1.88	0.54
2:F:227:LYS:HA	2:F:230:ILE:HD12	1.89	0.54
1:A:244:GLU:OE1	1:A:287:TRP:NE1	2.40	0.54
1:E:398:ARG:HG2	1:E:402:TYR:CE2	2.42	0.54
3:G:641:ASN:ND2	3:G:642:HIS:N	2.55	0.54
2:B:395:ILE:HG13	2:B:395:ILE:O	2.07	0.54
2:F:352:LEU:O	2:F:356:ILE:HG13	2.08	0.54
2:F:388:VAL:CG2	2:F:407:LEU:HD23	2.38	0.54
2:F:414:GLU:HG2	2:F:416:LEU:CD2	2.38	0.54
1:A:282:PHE:O	1:A:284:LEU:N	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:305:LEU:HD21	1:A:394:VAL:HG11	1.89	0.53
3:C:641:ASN:ND2	3:C:642:HIS:N	2.55	0.53
2:F:353:LYS:HD2	2:F:357:ARG:HH12	1.73	0.53
2:B:273:GLU:CD	2:B:273:GLU:H	2.12	0.53
2:B:352:LEU:O	2:B:356:ILE:HG13	2.08	0.53
1:E:287:TRP:CZ3	1:E:380:LEU:HD22	2.44	0.53
1:A:276:ALA:HB1	4:A:500:9CR:O2	2.09	0.53
2:F:189:GLN:HG2	2:F:316:ASP:OD2	2.09	0.53
1:A:372:LEU:O	1:A:376:ARG:HG3	2.09	0.53
2:F:238:ARG:HH11	2:F:238:ARG:HG2	1.73	0.53
1:A:398:ARG:HG2	1:A:402:TYR:CE2	2.43	0.53
1:A:245:LEU:C	1:A:247:VAL:H	2.12	0.53
1:E:445:LYS:NZ	1:E:457:MET:SD	2.82	0.53
1:E:268:ASP:OD1	1:E:269:PRO:HD2	2.09	0.53
2:F:272:PRO:HG3	2:F:310:LEU:HD11	1.91	0.53
1:A:428:PRO:HG3	2:B:375:THR:OG1	2.09	0.53
1:A:268:ASP:OD1	1:A:269:PRO:HD2	2.09	0.52
1:A:302:GLN:HG3	3:C:649:LEU:HD13	1.91	0.52
2:B:346:GLU:N	2:B:347:PRO:HD2	2.24	0.52
1:E:305:LEU:HD21	1:E:394:VAL:HG11	1.89	0.52
2:F:346:GLU:N	2:F:347:PRO:HD2	2.24	0.52
2:F:355:TYR:CD1	2:F:355:TYR:C	2.82	0.52
1:E:276:ALA:HB1	4:E:1500:9CR:O1	2.09	0.52
2:F:273:GLU:CD	2:F:273:GLU:H	2.12	0.52
1:A:291:ILE:HD13	1:A:292:PRO:HD2	1.91	0.52
2:B:214:ASP:C	2:B:214:ASP:OD2	2.47	0.52
2:B:355:TYR:C	2:B:355:TYR:CD1	2.82	0.52
1:E:291:ILE:HD13	1:E:292:PRO:HD2	1.91	0.52
1:E:372:LEU:O	1:E:376:ARG:HG3	2.08	0.52
1:A:368:ASP:OD2	1:A:370:THR:N	2.36	0.52
1:A:408:TYR:HE2	1:A:412:LYS:HD3	1.71	0.52
2:B:189:GLN:HG2	2:B:316:ASP:OD2	2.10	0.52
2:B:414:GLU:HG2	2:B:416:LEU:CD2	2.39	0.52
2:B:266:ILE:HB	4:B:600:9CR:H11	1.92	0.52
1:E:245:LEU:C	1:E:247:VAL:H	2.12	0.52
1:A:240:ILE:HG23	1:A:291:ILE:CD1	2.39	0.52
1:A:445:LYS:NZ	1:A:457:MET:SD	2.82	0.52
1:E:445:LYS:HD3	1:E:446:LEU:CD1	2.40	0.52
2:F:214:ASP:C	2:F:214:ASP:OD2	2.48	0.52
1:A:237:VAL:HG11	1:A:408:TYR:HB2	1.90	0.52
1:A:294:PHE:CZ	1:A:302:GLN:HB2	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:353:LYS:HD2	2:B:357:ARG:HH12	1.74	0.52
1:E:458:GLU:OE2	3:G:644:MET:CG	2.58	0.52
1:A:287:TRP:CZ3	1:A:380:LEU:HD22	2.44	0.52
1:E:431:ARG:C	1:E:431:ARG:HD3	2.30	0.52
1:A:458:GLU:OE2	3:C:644:MET:CG	2.58	0.52
2:F:391:LEU:C	2:F:393:MET:N	2.62	0.52
1:E:237:VAL:HG11	1:E:408:TYR:HB2	1.92	0.51
2:F:363:LYS:HB3	2:F:365:HIS:CE1	2.40	0.51
2:F:227:LYS:HB3	2:F:227:LYS:HZ3	1.73	0.51
1:E:365:MET:CE	1:E:423:LEU:HD13	2.41	0.51
2:B:355:TYR:HE1	2:B:359:ARG:HD3	1.75	0.51
2:B:215:LEU:HD21	2:B:396:PRO:HD2	1.93	0.51
3:G:647:ASN:OD1	3:G:648:LEU:N	2.44	0.51
1:E:302:GLN:HG3	3:G:649:LEU:HD13	1.93	0.51
2:B:238:ARG:HG2	2:B:238:ARG:HH11	1.74	0.51
1:A:445:LYS:HD3	1:A:446:LEU:CD1	2.40	0.51
2:B:373:LYS:CE	2:B:373:LYS:HA	2.41	0.51
1:E:282:PHE:O	1:E:284:LEU:N	2.43	0.51
2:F:193:PRO:HG2	2:F:269:ARG:NH2	2.26	0.51
1:E:428:PRO:HG3	2:F:375:THR:OG1	2.11	0.51
2:F:355:TYR:HE1	2:F:359:ARG:HD3	1.75	0.51
2:F:373:LYS:HA	2:F:373:LYS:CE	2.41	0.51
1:A:353:ARG:NH1	1:A:353:ARG:HG2	2.24	0.50
2:B:331:ASP:O	2:B:332:ARG:C	2.50	0.50
1:A:350:ILE:HD11	1:A:433:ILE:HG23	1.92	0.50
2:B:193:PRO:HG2	2:B:269:ARG:NH2	2.27	0.50
1:E:241:LEU:CD1	1:E:370:THR:HG22	2.41	0.50
1:E:294:PHE:CZ	1:E:302:GLN:HB2	2.46	0.50
1:A:286:GLU:O	1:A:288:ALA:N	2.45	0.50
1:A:294:PHE:CZ	1:A:302:GLN:CB	2.95	0.50
1:E:338:HIS:O	1:E:341:SER:HB3	2.11	0.50
1:A:338:HIS:O	1:A:341:SER:HB3	2.10	0.50
1:A:431:ARG:C	1:A:431:ARG:HD3	2.31	0.50
1:A:449:ASP:OD1	2:F:209:HIS:CB	2.60	0.50
3:C:647:ASN:OD1	3:C:648:LEU:N	2.44	0.50
2:F:227:LYS:HB3	2:F:227:LYS:HZ2	1.74	0.50
1:A:241:LEU:CD1	1:A:370:THR:HG22	2.42	0.50
1:A:310:TRP:NE1	1:A:459:MET:HB3	2.27	0.50
1:A:374:CYS:O	1:A:377:ALA:CB	2.58	0.50
1:E:408:TYR:HE2	1:E:412:LYS:HD3	1.72	0.50
2:F:215:LEU:HD21	2:F:396:PRO:HD2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:280:GLN:OE1	1:A:280:GLN:CA	2.60	0.49
1:A:291:ILE:HD13	1:A:292:PRO:CD	2.42	0.49
2:B:209:HIS:CB	1:E:449:ASP:OD1	2.60	0.49
1:A:368:ASP:C	1:A:368:ASP:OD2	2.51	0.49
2:F:203:THR:HG23	2:F:289:GLN:NE2	2.27	0.49
2:F:266:ILE:HB	4:F:1600:9CR:H11	1.94	0.49
2:B:203:THR:HG23	2:B:289:GLN:NE2	2.28	0.49
1:A:304:ILE:O	1:A:305:LEU:C	2.51	0.49
1:A:411:HIS:HA	1:A:414:PRO:HG3	1.95	0.49
1:E:393:GLU:O	1:E:396:ALA:HB3	2.13	0.49
1:A:365:MET:CE	1:A:423:LEU:HD13	2.43	0.49
2:B:399:MET:HB3	2:B:404:GLN:HE22	1.78	0.49
1:E:368:ASP:C	1:E:368:ASP:OD2	2.50	0.49
1:E:388:LEU:HD23	1:E:391:PRO:HA	1.95	0.49
1:E:411:HIS:HA	1:E:414:PRO:HG3	1.95	0.49
1:E:405:LEU:HG	1:E:420:PHE:CE1	2.47	0.49
1:A:299:LEU:C	1:A:301:ASP:N	2.66	0.49
2:F:406:MET:HE1	3:H:645:LEU:HD21	1.95	0.49
1:A:241:LEU:HD22	1:A:245:LEU:HD23	1.95	0.48
1:A:393:GLU:O	1:A:396:ALA:HB3	2.12	0.48
2:F:331:ASP:O	2:F:332:ARG:C	2.50	0.48
2:F:399:MET:HB3	2:F:404:GLN:HE22	1.77	0.48
1:A:449:ASP:OD1	2:F:209:HIS:HB3	2.13	0.48
1:E:291:ILE:HD13	1:E:292:PRO:CD	2.43	0.48
2:F:203:THR:HG23	2:F:289:GLN:HE22	1.78	0.48
2:F:238:ARG:HG2	2:F:238:ARG:NH1	2.28	0.48
2:F:357:ARG:CG	2:F:357:ARG:NH1	2.64	0.48
1:A:447:ILE:CG2	1:A:447:ILE:O	2.62	0.48
1:E:310:TRP:NE1	1:E:459:MET:HB3	2.28	0.48
1:E:320:HIS:O	1:E:323:ILE:CD1	2.61	0.48
2:F:206:SER:OG	2:F:214:ASP:CB	2.61	0.48
2:F:414:GLU:HG2	2:F:416:LEU:HD23	1.95	0.48
1:E:350:ILE:HD11	1:E:433:ILE:HG23	1.95	0.48
2:F:241:GLY:O	2:F:242:PHE:C	2.51	0.48
2:B:206:SER:OG	2:B:214:ASP:CB	2.61	0.48
2:B:357:ARG:NH1	2:B:357:ARG:CG	2.65	0.48
2:B:394:GLU:HA	2:F:413:HIS:ND1	2.28	0.48
1:E:297:LEU:HD21	1:E:397:LEU:HD12	1.94	0.48
2:F:353:LYS:O	2:F:357:ARG:HG2	2.14	0.48
2:F:354:ILE:O	2:F:358:LYS:HG2	2.12	0.48
1:A:284:LEU:C	1:A:286:GLU:N	2.67	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:304:ILE:HG22	1:A:305:LEU:N	2.27	0.48
1:A:405:LEU:HG	1:A:420:PHE:CE1	2.47	0.48
2:B:391:LEU:C	2:B:393:MET:N	2.62	0.48
1:E:247:VAL:CG1	1:E:283:THR:OG1	2.61	0.48
1:E:304:ILE:HG22	1:E:305:LEU:N	2.28	0.48
1:A:296:GLU:O	1:A:297:LEU:C	2.51	0.48
1:A:388:LEU:HD23	1:A:391:PRO:HA	1.96	0.48
2:B:238:ARG:HG2	2:B:238:ARG:NH1	2.29	0.48
2:B:241:GLY:O	2:B:242:PHE:C	2.50	0.48
1:A:231:ALA:C	1:A:233:GLU:H	2.17	0.48
1:E:294:PHE:CZ	1:E:302:GLN:CB	2.96	0.48
1:E:447:ILE:O	1:E:447:ILE:CG2	2.61	0.48
2:B:353:LYS:O	2:B:357:ARG:HG2	2.14	0.48
2:B:414:GLU:HG2	2:B:416:LEU:HD23	1.96	0.48
1:A:247:VAL:CG1	1:A:283:THR:OG1	2.62	0.48
3:C:641:ASN:HD22	3:C:642:HIS:N	2.10	0.48
1:E:374:CYS:O	1:E:377:ALA:CB	2.59	0.48
1:E:389:SER:O	1:E:390:ASN:HB3	2.14	0.48
2:B:209:HIS:HB3	1:E:449:ASP:OD1	2.14	0.48
2:F:245:LEU:HD21	2:F:341:VAL:HG22	1.96	0.47
1:A:294:PHE:HZ	1:A:302:GLN:HB2	1.79	0.47
1:A:312:GLU:HB3	1:A:430:LEU:HG	1.96	0.47
2:B:354:ILE:HG23	2:B:358:LYS:HE2	1.95	0.47
1:E:284:LEU:C	1:E:286:GLU:N	2.67	0.47
2:F:291:HIS:CD2	2:F:296:GLY:HA2	2.49	0.47
2:F:354:ILE:HG23	2:F:358:LYS:HE2	1.95	0.47
2:B:203:THR:HG23	2:B:289:GLN:HE22	1.78	0.47
2:B:217:LEU:HA	2:B:217:LEU:HD12	1.58	0.47
2:B:291:HIS:CD2	2:B:296:GLY:HA2	2.48	0.47
1:E:286:GLU:O	1:E:288:ALA:N	2.46	0.47
2:F:185:ARG:HG3	2:F:317:THR:CB	2.44	0.47
2:F:246:THR:HG21	2:F:336:GLU:OE1	2.14	0.47
2:B:185:ARG:HG3	2:B:317:THR:CB	2.44	0.47
1:E:299:LEU:C	1:E:301:ASP:H	2.17	0.47
2:B:413:HIS:ND1	2:F:394:GLU:HA	2.28	0.47
1:A:299:LEU:C	1:A:301:ASP:H	2.17	0.47
1:A:338:HIS:CD2	1:A:340:ASN:HB2	2.49	0.47
1:E:445:LYS:HD3	1:E:446:LEU:HD12	1.95	0.47
1:E:299:LEU:C	1:E:301:ASP:N	2.66	0.47
1:E:338:HIS:CD2	1:E:340:ASN:HB2	2.48	0.47
1:E:365:MET:HE1	1:E:423:LEU:HD22	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:395:GLU:O	1:A:399:GLU:HG3	2.13	0.47
1:E:278:ASP:OD2	1:E:453:ASP:HB2	2.14	0.47
1:E:280:GLN:CA	1:E:280:GLN:OE1	2.61	0.47
1:E:304:ILE:O	1:E:305:LEU:C	2.52	0.47
1:E:353:ARG:NH1	1:E:353:ARG:HG2	2.28	0.47
1:E:390:ASN:N	1:E:391:PRO:HD3	2.29	0.47
2:F:177:LEU:O	2:F:177:LEU:HG	2.14	0.47
1:E:312:GLU:HB3	1:E:430:LEU:HG	1.96	0.47
1:A:320:HIS:O	1:A:323:ILE:CD1	2.63	0.47
1:A:452:ILE:CG2	1:A:457:MET:HG2	2.45	0.47
1:E:231:ALA:C	1:E:233:GLU:H	2.17	0.47
1:A:390:ASN:N	1:A:391:PRO:HD3	2.29	0.47
2:B:382:ALA:C	2:B:384:GLY:N	2.68	0.47
3:G:651:ASP:N	3:G:651:ASP:OD1	2.41	0.47
1:A:412:LYS:N	1:A:414:PRO:HD3	2.30	0.47
1:A:365:MET:HE1	1:A:423:LEU:HD22	1.97	0.47
1:A:445:LYS:HD3	1:A:446:LEU:HD12	1.96	0.47
2:B:233:VAL:O	2:B:236:ALA:HB3	2.15	0.47
1:E:241:LEU:HD22	1:E:245:LEU:HD23	1.97	0.47
1:E:296:GLU:O	1:E:297:LEU:C	2.51	0.47
2:B:177:LEU:HG	2:B:177:LEU:O	2.15	0.46
1:A:278:ASP:OD2	1:A:453:ASP:HB2	2.16	0.46
1:A:367:MET:HE2	1:A:423:LEU:HD12	1.97	0.46
1:A:389:SER:O	1:A:390:ASN:HB3	2.15	0.46
1:A:452:ILE:HG22	1:A:457:MET:HG2	1.97	0.46
2:B:239:LEU:HD12	2:B:327:LEU:HD23	1.98	0.46
1:E:314:LEU:HD22	5:E:712:HOH:O	2.14	0.46
1:A:300:ASP:OD2	1:A:300:ASP:N	2.49	0.46
1:E:247:VAL:HG13	1:E:283:THR:OG1	2.16	0.46
1:E:412:LYS:N	1:E:414:PRO:HD3	2.30	0.46
2:B:246:THR:HG21	2:B:336:GLU:OE1	2.15	0.46
2:B:271:THR:HG22	2:B:273:GLU:HG2	1.97	0.46
1:E:296:GLU:O	1:E:297:LEU:O	2.34	0.46
1:E:294:PHE:HZ	1:E:302:GLN:HB2	1.81	0.46
2:F:239:LEU:HD12	2:F:327:LEU:HD23	1.98	0.46
2:F:373:LYS:HA	2:F:373:LYS:HE3	1.97	0.46
1:E:367:MET:HE2	1:E:423:LEU:HD12	1.97	0.46
2:F:233:VAL:O	2:F:236:ALA:HB3	2.16	0.46
1:A:296:GLU:O	1:A:297:LEU:O	2.34	0.46
3:C:648:LEU:O	3:C:648:LEU:HD23	2.16	0.46
1:A:338:HIS:HD2	1:A:340:ASN:CB	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:424:LEU:O	1:A:427:LEU:HB2	2.16	0.46
2:F:183:LYS:HB2	2:F:183:LYS:HE3	1.73	0.46
2:B:419:SER:CB	2:F:215:LEU:HB3	2.46	0.46
3:G:647:ASN:O	3:G:648:LEU:C	2.55	0.46
2:B:247:ILE:HD13	2:B:250:GLN:NE2	2.30	0.46
2:B:373:LYS:HE3	2:B:373:LYS:HA	1.98	0.46
2:B:394:GLU:O	2:B:396:PRO:HD3	2.16	0.46
2:F:394:GLU:O	2:F:396:PRO:HD3	2.16	0.46
2:B:198:LEU:HA	2:B:198:LEU:HD12	1.75	0.45
2:B:245:LEU:HD21	2:B:341:VAL:HG22	1.98	0.45
3:G:641:ASN:HD22	3:G:642:HIS:N	2.10	0.45
2:B:354:ILE:O	2:B:358:LYS:HG2	2.15	0.45
1:E:338:HIS:HD2	1:E:340:ASN:CB	2.28	0.45
2:B:406:MET:CE	3:D:645:LEU:HD21	2.46	0.45
1:E:371:GLU:O	1:E:372:LEU:C	2.55	0.45
1:E:387:GLY:O	1:E:388:LEU:C	2.54	0.45
2:F:406:MET:CE	3:H:645:LEU:HD21	2.47	0.45
2:B:259:LEU:HD11	2:B:384:GLY:HA3	1.99	0.45
2:B:184:ILE:CD1	2:B:321:LEU:HD23	2.47	0.45
2:B:221:PHE:CE1	2:B:295:PHE:HE2	2.35	0.45
2:B:360:ARG:HD2	2:B:363:LYS:HE3	1.98	0.45
1:E:300:ASP:OD2	1:E:300:ASP:N	2.49	0.45
1:A:237:VAL:HG13	1:A:404:SER:HB3	1.99	0.45
1:E:452:ILE:CG2	1:E:457:MET:HG2	2.45	0.45
3:G:648:LEU:O	3:G:648:LEU:HD23	2.17	0.45
1:A:245:LEU:HA	1:A:245:LEU:HD13	1.78	0.45
2:F:200:LYS:HG2	2:F:278:THR:HG21	1.99	0.45
1:E:424:LEU:O	1:E:427:LEU:HB2	2.17	0.45
1:E:452:ILE:HG22	1:E:457:MET:HG2	1.99	0.45
2:B:338:PRO:O	2:B:342:ASP:N	2.49	0.44
1:E:407:ALA:HA	1:E:410:LYS:HD2	1.99	0.44
2:F:221:PHE:CE1	2:F:295:PHE:HE2	2.35	0.44
2:F:389:ILE:C	2:F:391:LEU:H	2.19	0.44
1:A:370:THR:O	1:A:371:GLU:C	2.54	0.44
1:A:387:GLY:O	1:A:388:LEU:C	2.54	0.44
1:E:320:HIS:O	1:E:323:ILE:CG1	2.64	0.44
2:F:271:THR:HG22	2:F:273:GLU:HG2	1.99	0.44
2:F:259:LEU:HD11	2:F:384:GLY:HA3	1.99	0.44
1:A:237:VAL:CG1	1:A:408:TYR:HD1	2.30	0.44
2:B:401:PRO:HG2	2:B:402:LEU:H	1.82	0.44
2:B:389:ILE:C	2:B:391:LEU:H	2.19	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:242:GLU:O	1:E:246:ALA:HB2	2.17	0.44
2:F:236:ALA:CB	2:F:254:LEU:HD21	2.47	0.44
2:F:360:ARG:N	2:F:361:PRO:HD3	2.33	0.44
1:A:323:ILE:HG22	1:A:363:ARG:HB2	1.98	0.44
2:B:405:GLU:OE1	3:D:643:PRO:HD2	2.17	0.44
3:C:651:ASP:OD1	3:C:651:ASP:N	2.40	0.44
2:F:184:ILE:CD1	2:F:321:LEU:HD23	2.47	0.44
1:A:247:VAL:HG13	1:A:283:THR:OG1	2.18	0.44
2:B:360:ARG:N	2:B:361:PRO:HD3	2.33	0.44
1:E:370:THR:O	1:E:371:GLU:C	2.54	0.44
1:E:371:GLU:OE2	1:E:419:ARG:NH2	2.41	0.44
1:E:377:ALA:O	1:E:380:LEU:HB3	2.18	0.44
2:F:360:ARG:HD2	2:F:363:LYS:HE3	1.99	0.44
2:F:382:ALA:C	2:F:384:GLY:N	2.68	0.44
1:A:320:HIS:O	1:A:323:ILE:CG1	2.64	0.44
1:E:395:GLU:O	1:E:399:GLU:HG3	2.15	0.44
2:F:247:ILE:HD13	2:F:250:GLN:NE2	2.32	0.44
1:E:291:ILE:HA	1:E:292:PRO:HD3	1.91	0.44
2:B:210:ARG:HG2	2:B:291:HIS:CG	2.53	0.44
2:B:227:LYS:HZ2	2:B:227:LYS:HB3	1.77	0.44
3:C:647:ASN:O	3:C:648:LEU:C	2.56	0.44
2:F:185:ARG:HG3	2:F:317:THR:CG2	2.46	0.44
2:F:389:ILE:C	2:F:391:LEU:N	2.72	0.44
3:G:641:ASN:HD22	3:G:642:HIS:CG	2.35	0.44
2:B:185:ARG:HG3	2:B:317:THR:CG2	2.47	0.43
2:B:315:ASP:OD1	2:B:317:THR:HG23	2.18	0.43
2:B:392:LYS:HB3	2:B:399:MET:HE2	1.99	0.43
1:E:248:GLU:HA	1:E:249:PRO:HD2	1.78	0.43
2:F:247:ILE:HA	2:F:247:ILE:HD13	1.82	0.43
2:F:338:PRO:O	2:F:342:ASP:N	2.49	0.43
2:B:259:LEU:CD1	2:B:384:GLY:HA3	2.48	0.43
2:F:315:ASP:OD1	2:F:317:THR:HG23	2.18	0.43
3:G:642:HIS:HA	3:G:643:PRO:HD3	1.88	0.43
1:A:438:LEU:HD23	1:A:438:LEU:HA	1.89	0.43
2:B:236:ALA:CB	2:B:254:LEU:HD21	2.48	0.43
2:B:276:THR:HG22	2:B:286:ASN:CA	2.46	0.43
2:B:343:LYS:HG3	2:B:346:GLU:OE2	2.18	0.43
2:B:392:LYS:CB	2:B:399:MET:HE2	2.48	0.43
1:E:350:ILE:HG23	1:E:351:PHE:N	2.33	0.43
1:E:363:ARG:HG2	1:E:364:ASP:OD2	2.19	0.43
1:E:237:VAL:HG13	1:E:404:SER:HB3	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:401:PRO:HG2	2:F:402:LEU:H	1.82	0.43
1:A:242:GLU:O	1:A:246:ALA:HB2	2.18	0.43
1:A:377:ALA:O	1:A:380:LEU:HB3	2.18	0.43
1:E:304:ILE:O	1:E:306:LEU:N	2.51	0.43
1:E:237:VAL:CG2	1:E:408:TYR:HD1	2.31	0.43
2:F:328:ILE:HG22	2:F:345:GLN:HB3	2.01	0.43
1:A:292:PRO:O	1:A:293:HIS:CB	2.67	0.43
1:A:350:ILE:HG23	1:A:351:PHE:N	2.34	0.43
2:B:247:ILE:HD13	2:B:247:ILE:HA	1.83	0.43
2:B:200:LYS:HG2	2:B:278:THR:HG21	2.00	0.43
2:B:302:VAL:HG23	2:B:303:PHE:N	2.34	0.43
2:F:263:ILE:HG12	4:F:1600:9CR:C19	2.49	0.43
1:A:304:ILE:O	1:A:306:LEU:N	2.51	0.43
1:A:318:PHE:C	1:A:318:PHE:CD1	2.92	0.43
2:B:215:LEU:HB3	2:F:419:SER:CB	2.48	0.43
2:F:259:LEU:CD1	2:F:384:GLY:HA3	2.49	0.43
2:F:296:GLY:HA3	2:F:297:PRO:HD3	1.80	0.43
2:F:299:THR:O	2:F:301:LEU:N	2.52	0.43
2:F:414:GLU:CB	2:F:415:PRO:HA	2.42	0.43
1:A:248:GLU:HA	1:A:249:PRO:HD2	1.78	0.43
1:A:237:VAL:CG2	1:A:408:TYR:HD1	2.30	0.43
2:B:325:ILE:O	2:B:325:ILE:HG22	2.19	0.43
2:F:343:LYS:HG3	2:F:346:GLU:OE2	2.19	0.43
1:A:371:GLU:OE2	1:A:419:ARG:NH2	2.42	0.42
1:A:407:ALA:HA	1:A:410:LYS:HD2	2.00	0.42
2:B:221:PHE:CE1	2:B:295:PHE:CE2	3.07	0.42
2:F:360:ARG:HD3	2:F:360:ARG:HA	1.84	0.42
1:A:245:LEU:C	1:A:247:VAL:N	2.73	0.42
1:A:371:GLU:O	1:A:372:LEU:C	2.57	0.42
1:A:399:GLU:OE2	2:B:365:HIS:CD2	2.71	0.42
2:B:353:LYS:CG	2:B:357:ARG:NH1	2.82	0.42
1:E:323:ILE:HG22	1:E:363:ARG:HB2	1.99	0.42
2:F:210:ARG:HG2	2:F:291:HIS:CG	2.53	0.42
2:F:221:PHE:CE1	2:F:295:PHE:CE2	3.08	0.42
1:A:291:ILE:HG22	1:A:294:PHE:CB	2.48	0.42
1:A:353:ARG:HG2	1:A:357:GLU:OE2	2.18	0.42
2:B:407:LEU:N	2:B:407:LEU:HD12	2.35	0.42
1:E:291:ILE:CD1	1:E:292:PRO:HD2	2.49	0.42
1:E:382:ASN:HA	1:E:383:PRO:HD2	1.77	0.42
1:E:450:THR:HA	1:E:451:PRO:HD3	1.92	0.42
1:A:291:ILE:CD1	1:A:292:PRO:HD2	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:449:ASP:OD1	2:F:209:HIS:HB2	2.20	0.42
2:B:389:ILE:C	2:B:391:LEU:N	2.72	0.42
1:E:245:LEU:HA	1:E:245:LEU:HD13	1.79	0.42
2:F:392:LYS:HE3	2:F:408:GLU:OE2	2.19	0.42
1:A:237:VAL:CB	1:A:408:TYR:HD1	2.33	0.42
2:B:177:LEU:HD11	2:B:347:PRO:HB2	2.02	0.42
2:B:404:GLN:HG3	2:B:408:GLU:OE1	2.19	0.42
3:C:641:ASN:HD22	3:C:642:HIS:CG	2.37	0.42
1:E:291:ILE:HG22	1:E:294:PHE:CB	2.49	0.42
1:E:318:PHE:C	1:E:318:PHE:CD1	2.93	0.42
1:E:436:LYS:HD2	1:E:436:LYS:HA	1.78	0.42
2:F:302:VAL:HG23	2:F:303:PHE:N	2.34	0.42
2:B:259:LEU:HA	2:B:259:LEU:HD23	1.86	0.42
2:F:353:LYS:CG	2:F:357:ARG:NH1	2.82	0.42
1:A:321:ARG:O	1:A:321:ARG:HG2	2.20	0.42
1:A:353:ARG:NH2	1:A:432:SER:HB3	2.35	0.42
1:A:364:ASP:OD2	1:A:364:ASP:N	2.51	0.42
2:B:308:GLN:HB3	2:B:373:LYS:HZ3	1.84	0.42
2:B:328:ILE:HG22	2:B:345:GLN:HB3	2.02	0.42
2:B:388:VAL:HG21	2:B:407:LEU:HD23	2.01	0.42
1:E:292:PRO:O	1:E:293:HIS:CB	2.68	0.42
2:B:263:ILE:HG12	4:B:600:9CR:C19	2.49	0.42
2:B:404:GLN:HE21	2:B:404:GLN:HB2	1.50	0.42
1:E:353:ARG:HG2	1:E:357:GLU:OE2	2.20	0.42
2:F:392:LYS:HA	2:F:395:ILE:HG12	2.01	0.42
1:A:312:GLU:O	1:A:430:LEU:HD21	2.20	0.42
1:E:323:ILE:HG23	1:E:363:ARG:CB	2.48	0.42
2:F:308:GLN:HB3	2:F:373:LYS:HZ3	1.85	0.42
2:B:263:ILE:HG12	4:B:600:9CR:H23	2.02	0.42
1:E:419:ARG:HG3	1:E:423:LEU:CD2	2.50	0.42
2:B:299:THR:C	2:B:301:LEU:N	2.74	0.41
2:B:299:THR:O	2:B:301:LEU:N	2.53	0.41
1:E:418:GLY:O	1:E:419:ARG:C	2.57	0.41
1:E:353:ARG:NH2	1:E:432:SER:HB3	2.36	0.41
2:F:217:LEU:HD12	2:F:217:LEU:HA	1.59	0.41
2:F:210:ARG:CD	2:F:291:HIS:CD2	2.98	0.41
2:B:183:LYS:HE3	2:B:183:LYS:HB2	1.73	0.41
2:B:345:GLN:O	2:B:349:LEU:HD13	2.19	0.41
1:E:289:LYS:CD	3:G:649:LEU:O	2.69	0.41
2:F:299:THR:C	2:F:301:LEU:N	2.73	0.41
2:F:355:TYR:CD1	2:F:355:TYR:O	2.73	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:201:TYR:CE1	2:B:283:LEU:HD13	2.55	0.41
2:B:333:GLN:O	2:B:334:ASP:CB	2.68	0.41
2:B:372:MET:CE	2:B:372:MET:HA	2.50	0.41
2:F:345:GLN:O	2:F:349:LEU:HD13	2.20	0.41
1:A:425:LEU:HA	1:A:425:LEU:HD23	1.87	0.41
1:E:245:LEU:C	1:E:247:VAL:N	2.73	0.41
2:F:333:GLN:HG2	2:F:333:GLN:H	1.51	0.41
2:B:392:LYS:HE3	2:B:408:GLU:OE2	2.19	0.41
2:F:333:GLN:O	2:F:334:ASP:CB	2.68	0.41
1:A:282:PHE:C	1:A:284:LEU:H	2.24	0.41
1:E:364:ASP:N	1:E:364:ASP:OD2	2.51	0.41
2:F:177:LEU:HD11	2:F:347:PRO:HB2	2.03	0.41
2:F:404:GLN:HB2	2:F:404:GLN:HE21	1.50	0.41
2:F:407:LEU:N	2:F:407:LEU:HD12	2.35	0.41
2:F:404:GLN:HG3	2:F:408:GLU:OE1	2.20	0.41
1:A:281:LEU:O	1:A:284:LEU:HB3	2.20	0.41
2:B:355:TYR:O	2:B:355:TYR:CD1	2.73	0.41
1:E:281:LEU:O	1:E:284:LEU:HB3	2.20	0.41
1:A:363:ARG:HG2	1:A:364:ASP:OD2	2.21	0.41
1:A:418:GLY:O	1:A:419:ARG:C	2.57	0.41
1:E:280:GLN:HB3	1:E:314:LEU:HD22	2.03	0.41
2:B:209:HIS:HB2	1:E:449:ASP:OD1	2.19	0.41
2:F:211:VAL:HG23	2:F:212:ARG:N	2.36	0.41
2:B:360:ARG:HA	2:B:360:ARG:HD3	1.84	0.41
2:F:263:ILE:HG12	4:F:1600:9CR:H23	2.03	0.41
2:F:246:THR:HG21	2:F:336:GLU:CD	2.41	0.41
2:F:276:THR:HG22	2:F:286:ASN:CA	2.46	0.41
2:F:382:ALA:C	2:F:384:GLY:H	2.25	0.41
2:B:211:VAL:HG23	2:B:212:ARG:N	2.36	0.41
1:E:298:PRO:HB2	1:E:301:ASP:HB2	2.03	0.41
1:E:237:VAL:CG1	1:E:408:TYR:HD1	2.33	0.41
2:F:325:ILE:HG22	2:F:325:ILE:O	2.20	0.41
1:A:306:LEU:C	1:A:308:ALA:N	2.74	0.40
2:B:210:ARG:CD	2:B:291:HIS:CD2	2.97	0.40
2:B:392:LYS:HA	2:B:395:ILE:HG12	2.02	0.40
1:E:405:LEU:CD1	1:E:409:CYS:SG	3.09	0.40
1:A:231:ALA:C	1:A:233:GLU:N	2.75	0.40
1:A:441:LEU:HD11	4:A:500:9CR:H23	2.03	0.40
1:E:235:MET:SD	1:E:292:PRO:HB2	2.61	0.40
1:E:321:ARG:HG2	1:E:321:ARG:O	2.20	0.40
1:A:241:LEU:C	1:A:243:ALA:H	2.24	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:419:ARG:HG3	1:A:423:LEU:CD2	2.51	0.40
2:F:201:TYR:CE1	2:F:283:LEU:HD13	2.55	0.40
2:F:253:LEU:HD21	2:F:341:VAL:HG11	2.03	0.40
1:A:235:MET:SD	1:A:292:PRO:HB2	2.61	0.40
2:B:246:THR:HG21	2:B:336:GLU:CD	2.42	0.40
2:B:414:GLU:CB	2:B:415:PRO:HA	2.42	0.40
3:D:647:ASN:HA	3:D:650:LYS:HE3	2.04	0.40
2:F:384:GLY:O	2:F:387:ARG:N	2.54	0.40
2:B:210:ARG:C	2:B:211:VAL:CG1	2.89	0.40
1:E:282:PHE:C	1:E:284:LEU:H	2.25	0.40
2:F:210:ARG:C	2:F:211:VAL:CG1	2.90	0.40
2:F:405:GLU:OE1	3:H:643:PRO:HD2	2.21	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	213/238 (90%)	165 (78%)	33 (16%)	15 (7%)	1	3
1	E	213/238 (90%)	163 (76%)	34 (16%)	16 (8%)	1	2
2	B	243/303 (80%)	200 (82%)	34 (14%)	9 (4%)	3	13
2	F	243/303 (80%)	202 (83%)	32 (13%)	9 (4%)	3	13
3	C	9/14 (64%)	2 (22%)	2 (22%)	5 (56%)	0	0
3	D	8/14 (57%)	5 (62%)	1 (12%)	2 (25%)	0	0
3	G	9/14 (64%)	2 (22%)	2 (22%)	5 (56%)	0	0
3	H	8/14 (57%)	5 (62%)	1 (12%)	2 (25%)	0	0
All	All	946/1138 (83%)	744 (79%)	139 (15%)	63 (7%)	1	3

All (63) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	238	GLU
1	A	287	TRP
1	A	448	GLY
2	B	412	GLY
3	C	643	PRO
3	C	647	ASN
3	C	648	LEU
3	C	650	LYS
1	E	238	GLU
1	E	448	GLY
2	F	412	GLY
3	G	643	PRO
3	G	647	ASN
3	G	648	LEU
3	G	650	LYS
1	A	237	VAL
1	A	267	ASN
1	A	283	THR
1	A	292	PRO
1	A	298	PRO
1	A	300	ASP
1	A	364	ASP
2	B	392	LYS
3	D	650	LYS
1	E	267	ASN
1	E	287	TRP
1	E	292	PRO
1	E	298	PRO
1	E	300	ASP
1	E	364	ASP
2	F	392	LYS
3	H	650	LYS
1	A	293	HIS
2	B	213	LEU
3	D	643	PRO
1	E	237	VAL
1	E	283	THR
1	E	293	HIS
2	F	213	LEU
3	H	643	PRO
3	C	644	MET
3	G	644	MET
1	A	246	ALA

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Mol	Chain	Res	Type
1	A	297	LEU
1	A	414	PRO
2	B	272	PRO
2	B	292	ASN
2	B	299	THR
2	B	411	GLU
1	E	246	ALA
1	E	297	LEU
1	E	305	LEU
1	E	321	ARG
2	F	272	PRO
2	F	292	ASN
2	F	299	THR
2	F	411	GLU
1	A	305	LEU
2	B	338	PRO
2	B	401	PRO
1	E	414	PRO
2	F	338	PRO
2	F	401	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	184/204 (90%)	161 (88%)	23 (12%)	4	14
1	E	184/204 (90%)	160 (87%)	24 (13%)	4	12
2	B	216/274 (79%)	192 (89%)	24 (11%)	6	19
2	F	216/274 (79%)	192 (89%)	24 (11%)	6	19
3	C	11/13 (85%)	8 (73%)	3 (27%)	0	1
3	D	10/13 (77%)	8 (80%)	2 (20%)	1	4
3	G	11/13 (85%)	8 (73%)	3 (27%)	0	1
3	H	10/13 (77%)	8 (80%)	2 (20%)	1	4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	842/1008 (84%)	737 (88%)	105 (12%)	<b>4</b> <b>14</b>

All (105) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	235	MET
1	A	241	LEU
1	A	242	GLU
1	A	244	GLU
1	A	248	GLU
1	A	271	THR
1	A	280	GLN
1	A	283	THR
1	A	291	ILE
1	A	302	GLN
1	A	318	PHE
1	A	325	VAL
1	A	344	SER
1	A	355	LEU
1	A	366	GLN
1	A	369	LYS
1	A	405	LEU
1	A	431	ARG
1	A	432	SER
1	A	438	LEU
1	A	449	ASP
1	A	455	PHE
1	A	461	GLU
2	B	180	LEU
2	B	194	SER
2	B	198	LEU
2	B	211	VAL
2	B	213	LEU
2	B	217	LEU
2	B	238	ARG
2	B	259	LEU
2	B	273	GLU
2	B	315	ASP
2	B	317	THR
2	B	322	LEU
2	B	333	GLN
2	B	339	THR

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Mol	Chain	Res	Type
2	B	342	ASP
2	B	345	GLN
2	B	357	ARG
2	B	361	PRO
2	B	369	LYS
2	B	376	ASP
2	B	389	ILE
2	B	404	GLN
2	B	413	HIS
2	B	417	THR
3	C	642	HIS
3	C	644	MET
3	C	651	ASP
3	D	645	LEU
3	D	651	ASP
1	E	235	MET
1	E	239	LYS
1	E	241	LEU
1	E	242	GLU
1	E	244	GLU
1	E	248	GLU
1	E	271	THR
1	E	280	GLN
1	E	283	THR
1	E	291	ILE
1	E	302	GLN
1	E	318	PHE
1	E	325	VAL
1	E	344	SER
1	E	355	LEU
1	E	366	GLN
1	E	369	LYS
1	E	405	LEU
1	E	431	ARG
1	E	432	SER
1	E	438	LEU
1	E	449	ASP
1	E	455	PHE
1	E	461	GLU
2	F	180	LEU
2	F	194	SER
2	F	198	LEU

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Mol	Chain	Res	Type
2	F	211	VAL
2	F	213	LEU
2	F	217	LEU
2	F	238	ARG
2	F	259	LEU
2	F	273	GLU
2	F	315	ASP
2	F	317	THR
2	F	322	LEU
2	F	333	GLN
2	F	339	THR
2	F	342	ASP
2	F	345	GLN
2	F	357	ARG
2	F	361	PRO
2	F	369	LYS
2	F	376	ASP
2	F	389	ILE
2	F	404	GLN
2	F	413	HIS
2	F	417	THR
3	G	642	HIS
3	G	644	MET
3	G	651	ASP
3	H	645	LEU
3	H	651	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	302	GLN
1	A	320	HIS
1	A	338	HIS
1	A	366	GLN
2	B	197	GLN
2	B	250	GLN
2	B	365	HIS
3	C	641	ASN
3	D	642	HIS
3	D	647	ASN
1	E	302	GLN
1	E	320	HIS

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Mol	Chain	Res	Type
1	E	338	HIS
1	E	366	GLN
2	F	197	GLN
2	F	250	GLN
2	F	365	HIS
3	G	641	ASN
3	H	647	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

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	$\# Z  > 2$
4	9CR	E	1500	-	19,22,22	2.26	6 (31%)	26,30,30	2.23	7 (26%)
4	9CR	F	1600	-	19,22,22	2.66	4 (21%)	26,30,30	2.32	6 (23%)
4	9CR	B	600	-	19,22,22	2.59	3 (15%)	26,30,30	2.31	7 (26%)
4	9CR	A	500	-	19,22,22	2.31	6 (31%)	26,30,30	2.25	6 (23%)

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	9CR	E	1500	-	-	2/13/32/32	0/1/1/1
4	9CR	F	1600	-	-	2/13/32/32	0/1/1/1
4	9CR	B	600	-	-	2/13/32/32	0/1/1/1
4	9CR	A	500	-	-	2/13/32/32	0/1/1/1

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	1600	9CR	C1-C6	8.35	1.65	1.53
4	B	600	9CR	C1-C6	7.60	1.64	1.53
4	A	500	9CR	C1-C6	6.65	1.62	1.53
4	E	1500	9CR	C1-C6	6.24	1.62	1.53
4	F	1600	9CR	C5-C6	5.43	1.43	1.34
4	B	600	9CR	C5-C6	5.39	1.43	1.34
4	A	500	9CR	C5-C6	4.40	1.42	1.34
4	B	600	9CR	C14-C13	-4.38	1.30	1.35
4	E	1500	9CR	C5-C6	4.03	1.41	1.34
4	E	1500	9CR	C14-C13	-3.88	1.31	1.35
4	F	1600	9CR	C14-C13	-3.78	1.31	1.35
4	A	500	9CR	C14-C13	-3.37	1.31	1.35
4	E	1500	9CR	C8-C9	-3.04	1.39	1.45
4	A	500	9CR	C8-C9	-2.86	1.39	1.45
4	E	1500	9CR	C4-C5	2.38	1.55	1.51
4	A	500	9CR	C4-C5	2.27	1.55	1.51
4	A	500	9CR	C12-C13	2.23	1.50	1.45
4	F	1600	9CR	C12-C13	2.10	1.50	1.45
4	E	1500	9CR	C12-C13	2.00	1.50	1.45

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	1600	9CR	C18-C5-C6	7.16	132.57	124.53
4	B	600	9CR	C18-C5-C6	7.12	132.53	124.53
4	A	500	9CR	C18-C5-C6	6.05	131.33	124.53
4	E	1500	9CR	C18-C5-C6	5.82	131.07	124.53
4	A	500	9CR	C7-C8-C9	5.42	134.43	126.23
4	E	1500	9CR	C7-C8-C9	5.28	134.21	126.23
4	E	1500	9CR	C11-C10-C9	4.31	133.46	127.31
4	E	1500	9CR	C16-C1-C6	4.11	116.97	110.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	500	9CR	C16-C1-C6	4.08	116.91	110.30
4	A	500	9CR	C11-C10-C9	4.07	133.12	127.31
4	B	600	9CR	C7-C8-C9	4.03	132.32	126.23
4	F	1600	9CR	C7-C8-C9	4.01	132.30	126.23
4	F	1600	9CR	C18-C5-C4	-3.94	106.04	113.62
4	B	600	9CR	C18-C5-C4	-3.94	106.06	113.62
4	A	500	9CR	C18-C5-C4	-3.82	106.27	113.62
4	F	1600	9CR	C11-C10-C9	3.70	132.59	127.31
4	E	1500	9CR	C18-C5-C4	-3.70	106.51	113.62
4	B	600	9CR	C11-C10-C9	3.51	132.32	127.31
4	B	600	9CR	C16-C1-C6	3.08	115.29	110.30
4	F	1600	9CR	C16-C1-C6	3.00	115.17	110.30
4	B	600	9CR	C20-C13-C12	2.60	122.17	118.08
4	F	1600	9CR	C20-C13-C12	2.60	122.17	118.08
4	E	1500	9CR	C20-C13-C12	2.25	121.62	118.08
4	A	500	9CR	C20-C13-C12	2.15	121.47	118.08
4	B	600	9CR	C8-C7-C6	2.01	132.85	127.20
4	E	1500	9CR	C3-C4-C5	2.01	117.66	114.08

There are no chirality outliers.

All (8) torsion outliers are listed below:

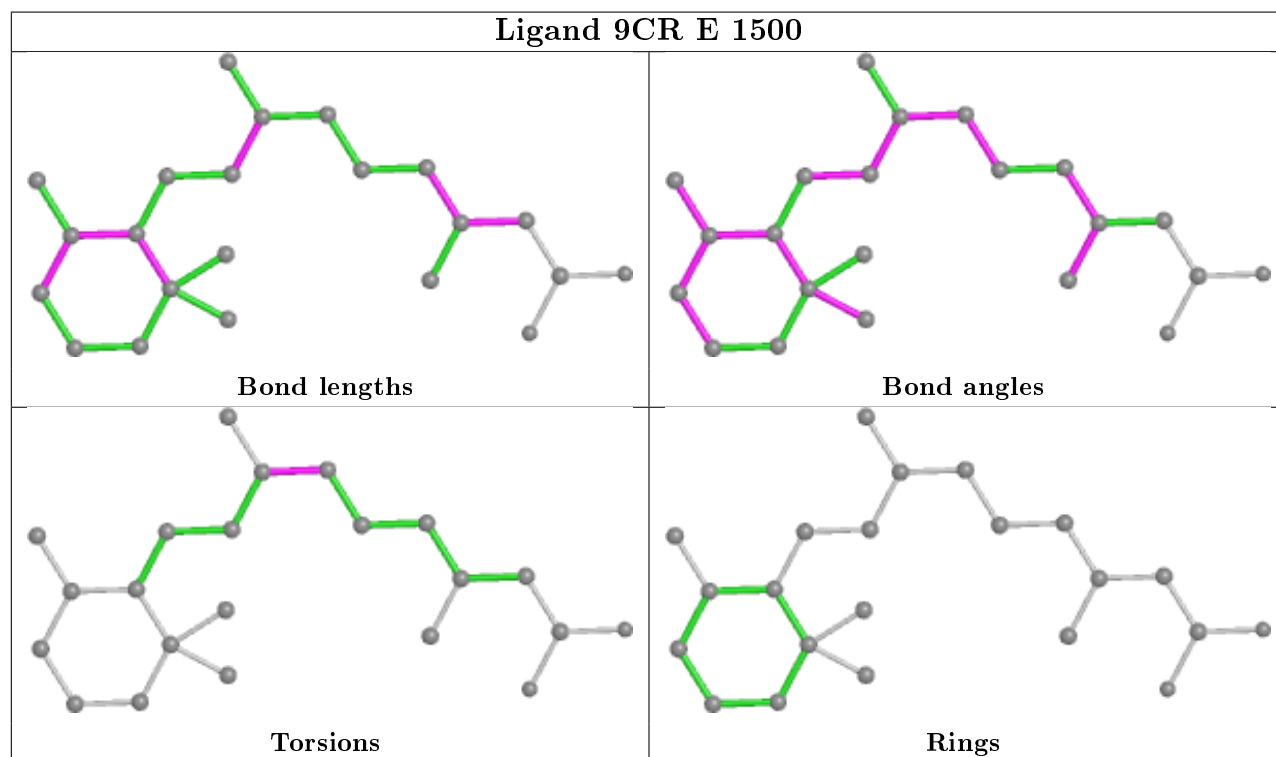
Mol	Chain	Res	Type	Atoms
4	E	1500	9CR	C11-C10-C9-C19
4	F	1600	9CR	C11-C10-C9-C19
4	B	600	9CR	C11-C10-C9-C19
4	A	500	9CR	C11-C10-C9-C19
4	E	1500	9CR	C11-C10-C9-C8
4	F	1600	9CR	C11-C10-C9-C8
4	B	600	9CR	C11-C10-C9-C8
4	A	500	9CR	C11-C10-C9-C8

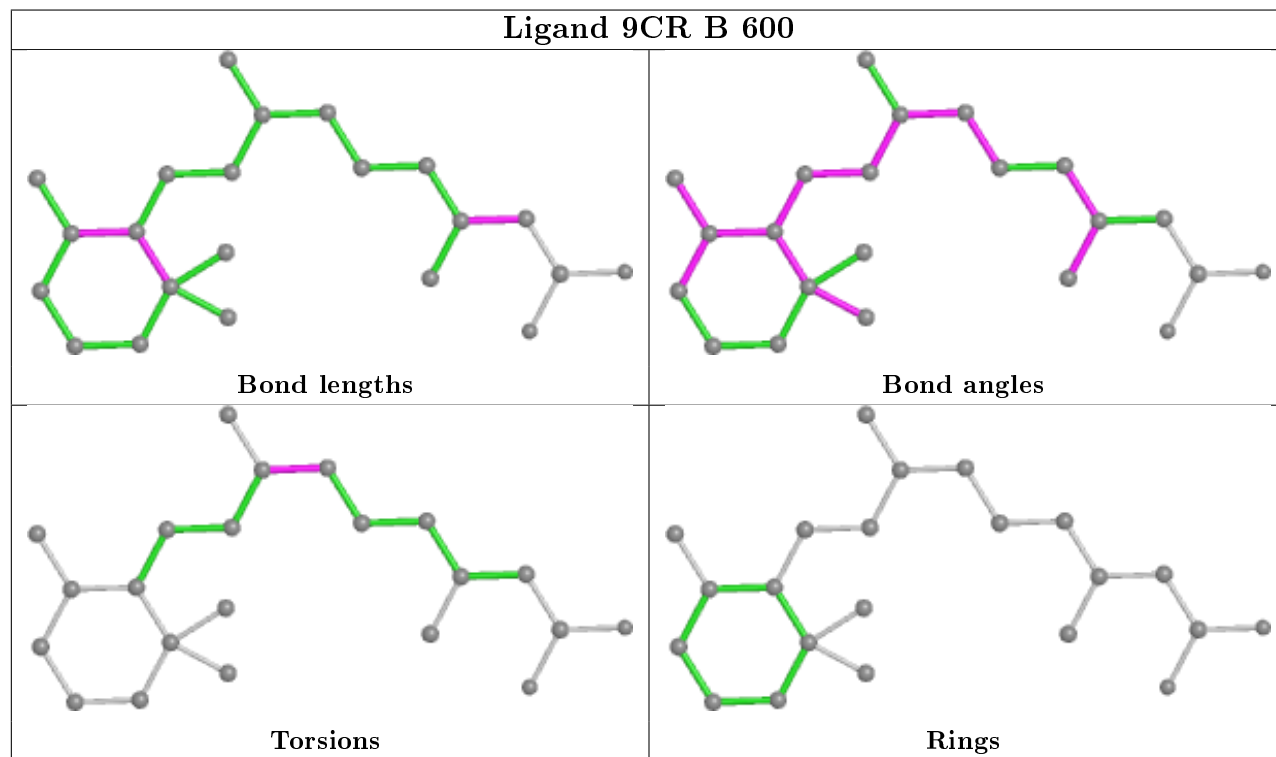
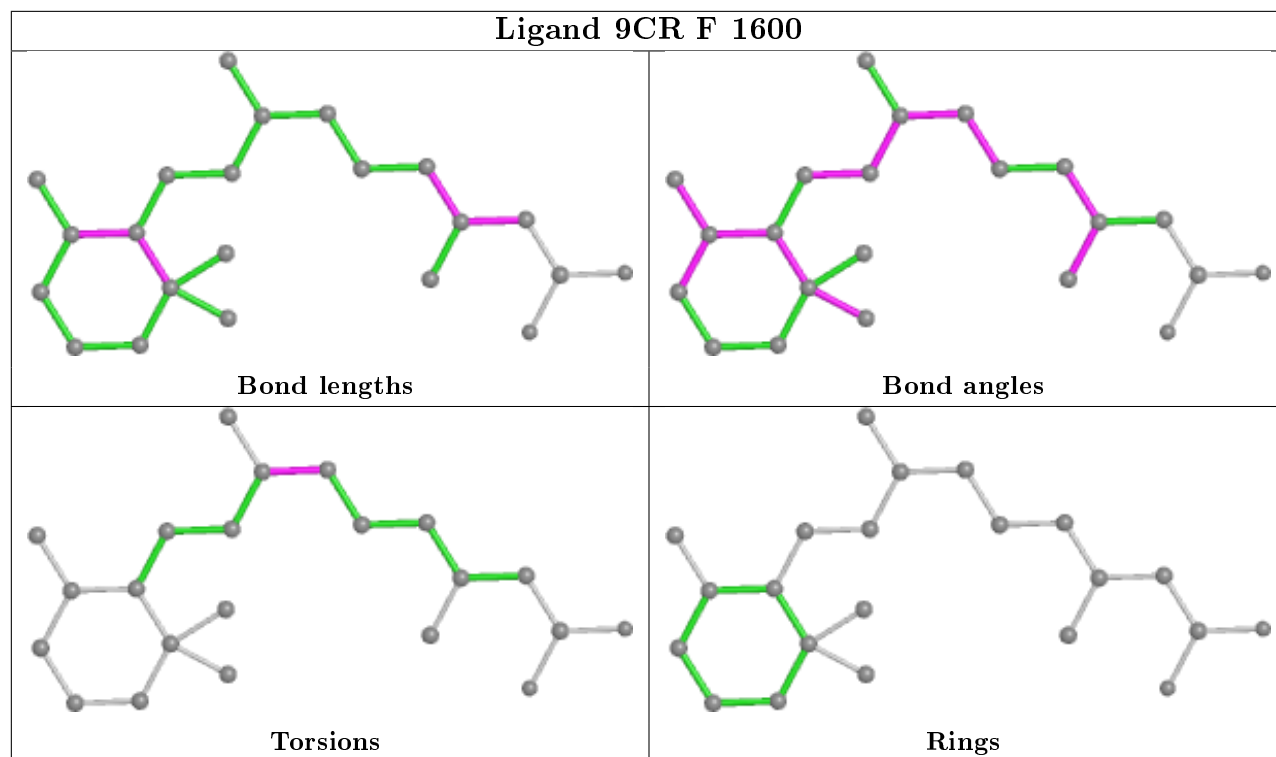
There are no ring outliers.

4 monomers are involved in 11 short contacts:

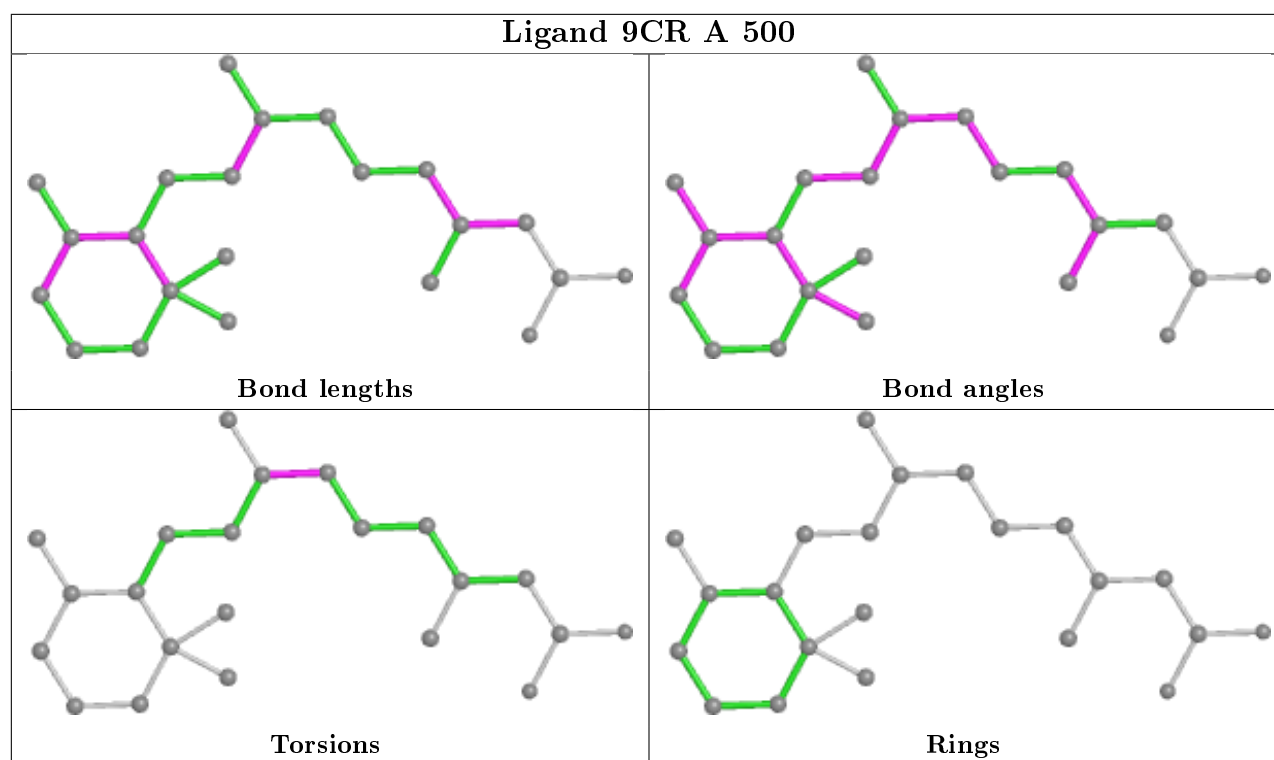
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	1500	9CR	2	0
4	F	1600	9CR	3	0
4	B	600	9CR	3	0
4	A	500	9CR	3	0

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









## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 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	217/238 (91%)	0.56	8 (3%) 41 37	39, 71, 93, 104	0
1	E	217/238 (91%)	0.55	13 (5%) 21 18	40, 71, 92, 105	0
2	B	245/303 (80%)	0.66	15 (6%) 21 17	45, 75, 96, 104	0
2	F	245/303 (80%)	0.68	17 (6%) 16 13	44, 75, 96, 105	0
3	C	11/14 (78%)	1.36	2 (18%) 1 1	91, 96, 102, 103	0
3	D	10/14 (71%)	0.55	0 100 100	91, 96, 101, 106	0
3	G	11/14 (78%)	1.32	4 (36%) 0 0	90, 97, 104, 104	0
3	H	10/14 (71%)	0.58	0 100 100	92, 97, 102, 106	0
All	All	966/1138 (84%)	0.63	59 (6%) 21 17	39, 74, 97, 106	0

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	416	LEU	6.5
2	B	416	LEU	6.0
2	F	413	HIS	5.6
2	F	415	PRO	4.4
2	F	396	PRO	4.4
2	B	412	GLY	4.3
3	C	641	ASN	4.3
2	B	413	HIS	4.2
3	G	641	ASN	4.1
2	B	419	SER	3.6
2	F	213	LEU	3.5
2	B	213	LEU	3.4
1	A	285	VAL	3.4
1	E	388	LEU	3.3
1	E	294	PHE	3.1
2	F	412	GLY	3.1

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Mol	Chain	Res	Type	RSRZ
1	E	246	ALA	3.1
1	A	456	LEU	3.0
3	G	642	HIS	2.9
1	A	240	ILE	2.9
2	B	411	GLU	2.9
1	E	297	LEU	2.9
2	F	393	MET	2.9
2	B	394	GLU	2.7
1	A	408	TYR	2.7
1	E	285	VAL	2.6
1	A	246	ALA	2.6
1	E	303	VAL	2.5
2	F	251	ILE	2.5
2	F	356	ILE	2.5
1	A	463	PRO	2.5
2	B	341	VAL	2.5
2	B	393	MET	2.4
3	G	645	LEU	2.4
1	E	463	PRO	2.4
3	G	646	MET	2.4
1	E	411	HIS	2.4
1	E	231	ALA	2.3
2	F	247	ILE	2.3
2	B	180	LEU	2.3
2	F	285	LEU	2.3
2	B	327	LEU	2.3
3	C	646	MET	2.3
2	F	177	LEU	2.2
2	F	391	LEU	2.2
1	E	247	VAL	2.2
2	B	211	VAL	2.2
2	F	417	THR	2.2
1	A	397	LEU	2.1
1	E	423	LEU	2.1
1	E	305	LEU	2.1
2	B	177	LEU	2.1
1	A	297	LEU	2.1
2	F	206	SER	2.1
2	B	335	LEU	2.1
1	E	329	ILE	2.1
2	B	417	THR	2.1
2	F	215	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
2	F	242	PHE	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](#)

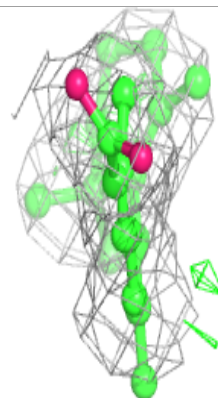
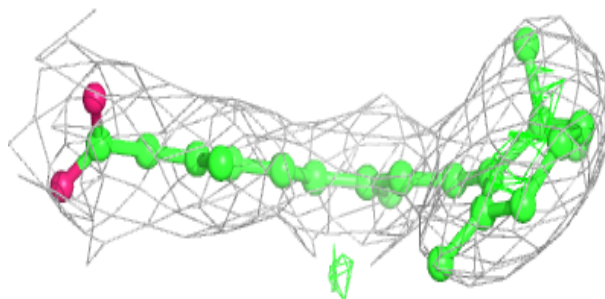
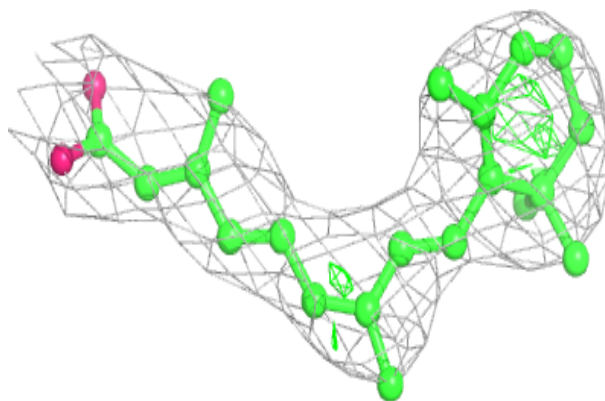
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	9CR	B	600	22/22	0.95	0.40	69,72,76,77	0
4	9CR	F	1600	22/22	0.96	0.40	69,72,75,77	0
4	9CR	E	1500	22/22	0.97	0.29	48,57,69,71	0
4	9CR	A	500	22/22	0.97	0.33	48,57,66,68	0

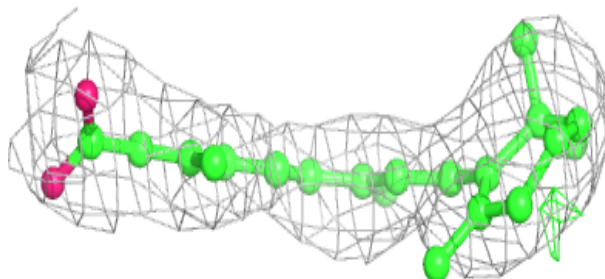
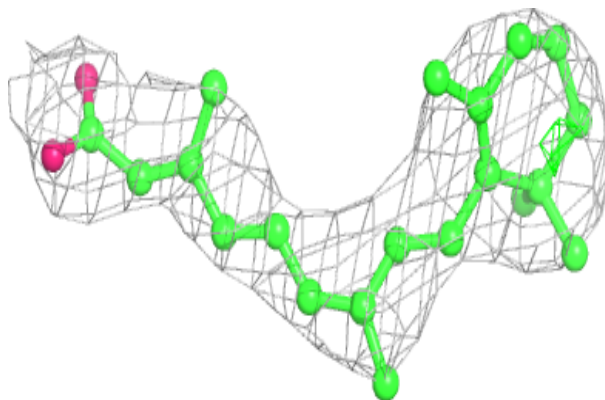
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around 9CR B 600:**

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

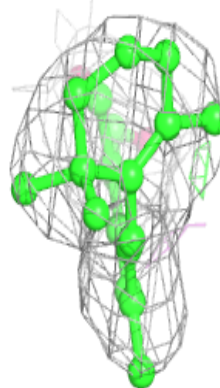
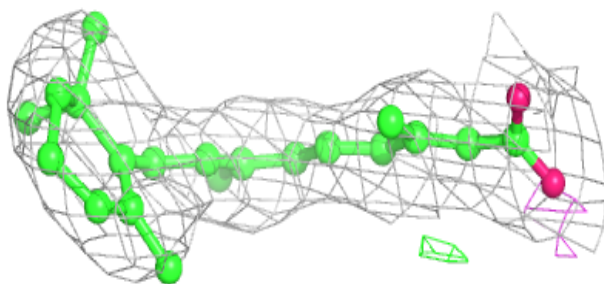
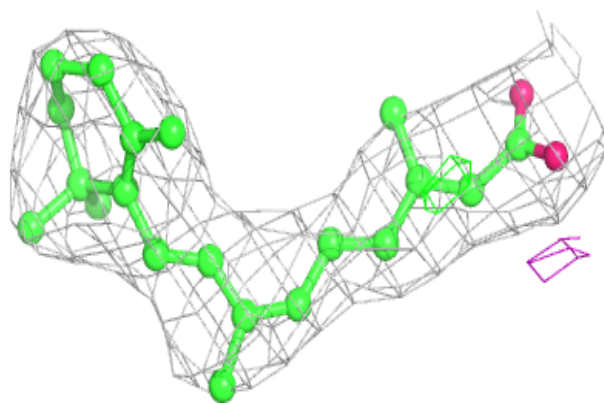
**Electron density around 9CR F 1600:**

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

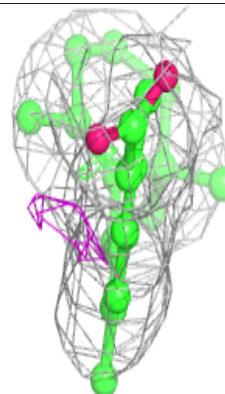
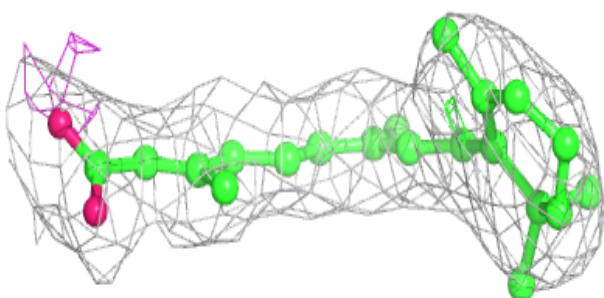
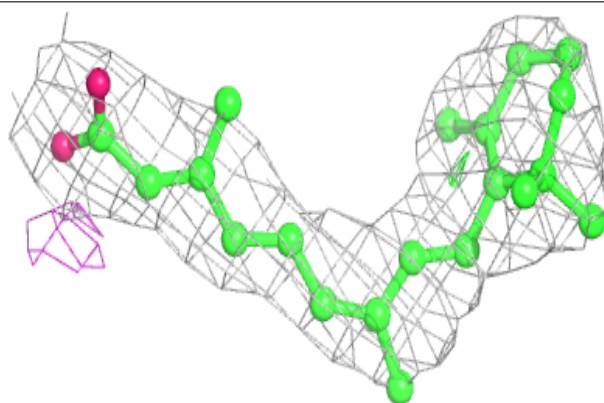


**Electron density around 9CR E 1500:**

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

**Electron density around 9CR A 500:**

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



## 6.5 Other polymers

There are no such residues in this entry.