



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:38 PM GMT

PDB ID : 4YFL
Title : Crystal structure of VH1-46 germline-derived CD4-binding site-directed anti-body 1B2530 in complex with HIV-1 clade A/E 93TH057 gp120
Authors : Acharya, P.; Zhou, T.; Moquin, S.; Kwong, P.D.
Deposited on : 2015-02-25
Resolution : 3.39 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

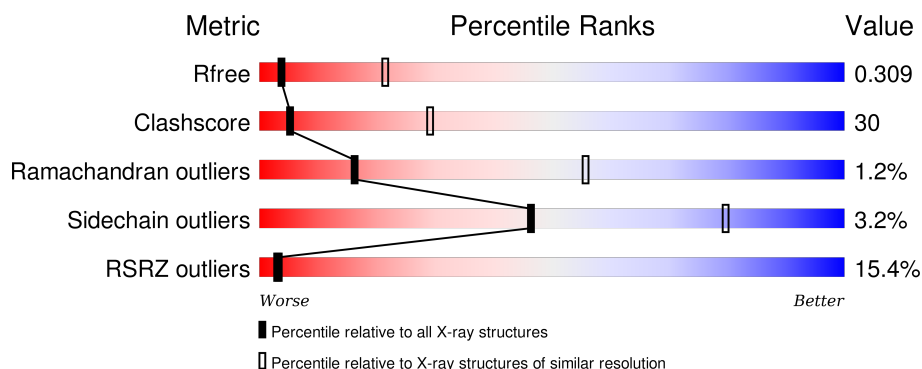
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.39 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	1084 (3.46-3.30)
Clashscore	102246	1158 (3.46-3.30)
Ramachandran outliers	100387	1139 (3.46-3.30)
Sidechain outliers	100360	1138 (3.46-3.30)
RSRZ outliers	91569	1089 (3.46-3.30)

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

Mol	Chain	Length	Quality of chain
1	E	353	<div> <div>11%</div> <div>55%</div> <div>42%</div> <div>..</div> </div>
1	G	353	<div> <div>11%</div> <div>49%</div> <div>47%</div> <div>..</div> </div>
2	F	227	<div> <div>19%</div> <div>42%</div> <div>52%</div> <div>..</div> </div>
2	H	227	<div> <div>15%</div> <div>39%</div> <div>56%</div> <div>..</div> </div>
3	I	215	<div> <div>16%</div> <div>47%</div> <div>44%</div> <div>7%</div> </div>

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Mol	Chain	Length	Quality of chain
3	L	215	<div><div></div><div>22%</div><div>36%</div><div>58%</div><div></div><div></div></div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 23777 atoms, of which 11731 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 Envelope glycoprotein gp160,Envelope glycoprotein gp160,Envelope glycoprotein gp160.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	G	347	Total	C	H	N	O	S	0	0	0
			5360	1700	2647	472	518	23			
1	E	347	Total	C	H	N	O	S	0	0	0
			5356	1700	2643	472	518	23			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	124	GLY	-	linker	UNP Q0ED31
G	198	GLY	-	linker	UNP Q0ED31
G	318	GLY	-	linker	UNP Q0ED31
G	319	GLY	-	linker	UNP Q0ED31
G	320	SER	-	linker	UNP Q0ED31
G	321	GLY	-	linker	UNP Q0ED31
G	322	SER	-	linker	UNP Q0ED31
G	323	GLY	-	linker	UNP Q0ED31
E	124	GLY	-	linker	UNP Q0ED31
E	198	GLY	-	linker	UNP Q0ED31
E	318	GLY	-	linker	UNP Q0ED31
E	319	GLY	-	linker	UNP Q0ED31
E	320	SER	-	linker	UNP Q0ED31
E	321	GLY	-	linker	UNP Q0ED31
E	322	SER	-	linker	UNP Q0ED31
E	323	GLY	-	linker	UNP Q0ED31

- Molecule 2 is a protein called 1B2530 heavy chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	H	223	Total	C	H	N	O	S	0	0	0
			3350	1069	1661	290	322	8			

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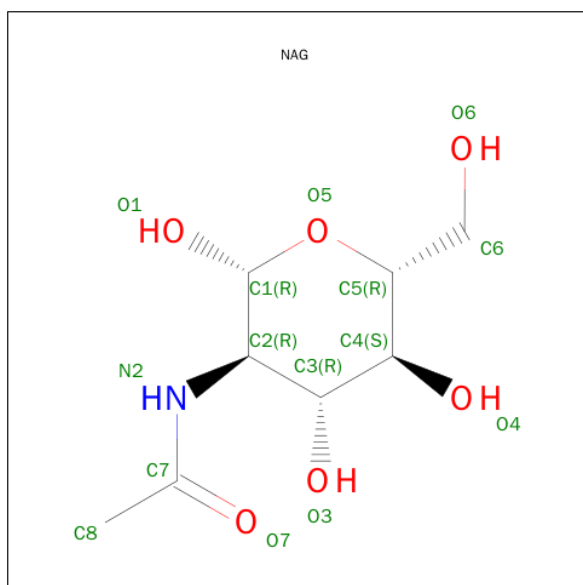
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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	F	221	Total	C	H	N	O	S	0	0	0
			3329	1063	1651	288	319	8			

- Molecule 3 is a protein called 1B2530 Light chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	L	209	Total	C	H	N	O	S	0	0	0
			3020	964	1479	261	312	4			
3	I	200	Total	C	H	N	O	S	0	0	0
			2914	932	1426	251	301	4			

- Molecule 4 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	G	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
4	G	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
4	G	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
4	G	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
4	G	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
4	G	1	Total	C	H	N	O	0	0
			28	8	14	1	5		

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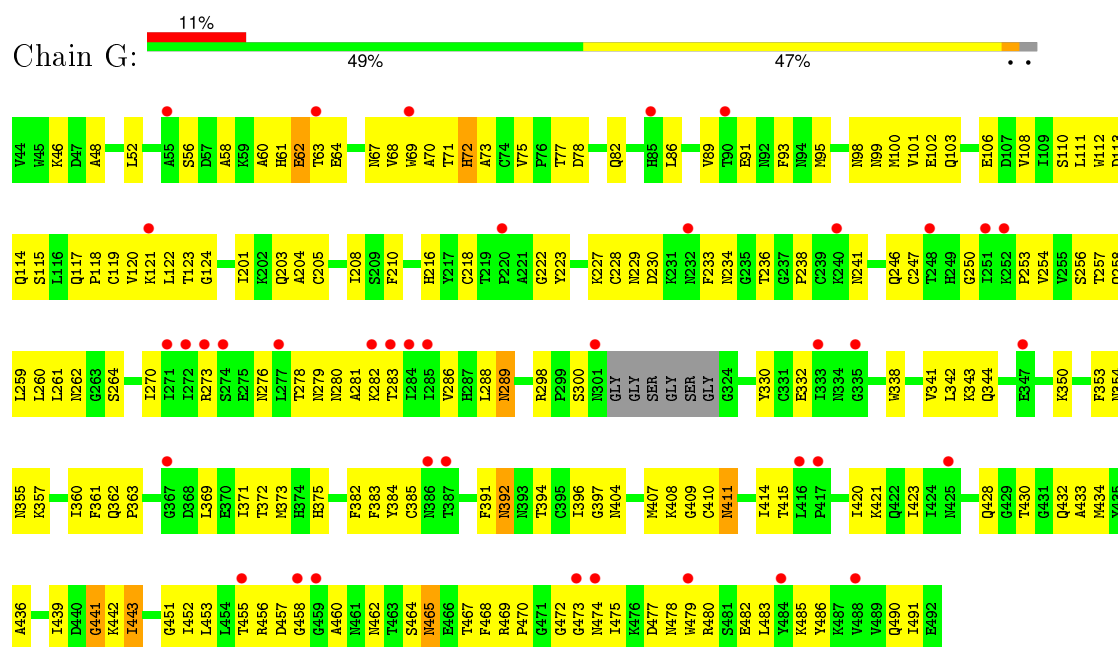
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	E	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
4	E	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
4	E	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
4	E	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
4	E	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
4	E	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
4	E	1	Total	C	H	N	O	0	0
			28	8	14	1	5		
4	E	1	Total	C	H	N	O	0	0
			28	8	14	1	5		

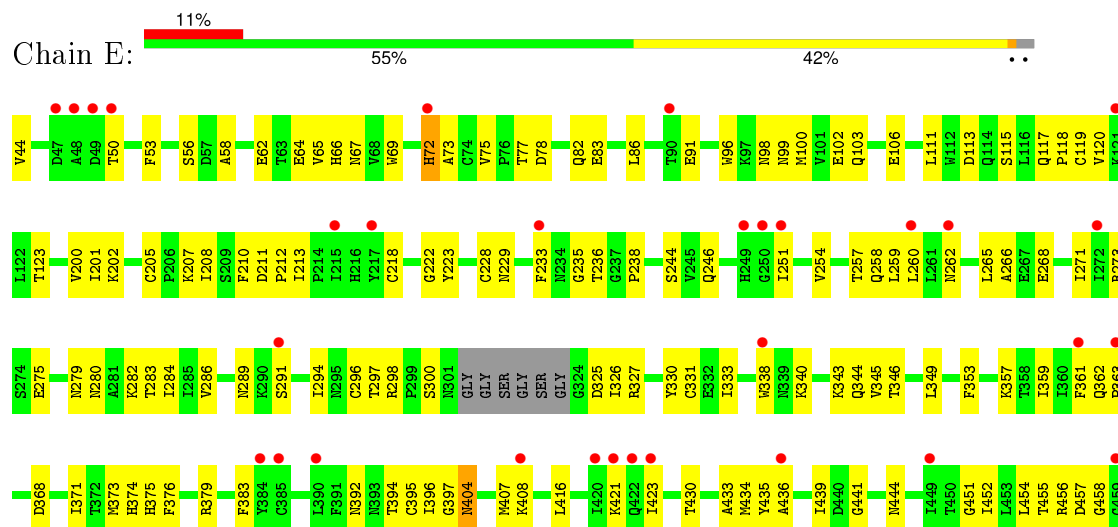
3 Residue-property plots

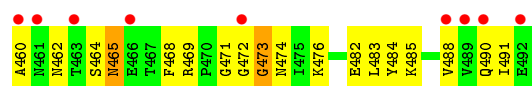
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: Envelope glycoprotein gp160,Envelope glycoprotein gp160,Envelope glycoprotein gp160

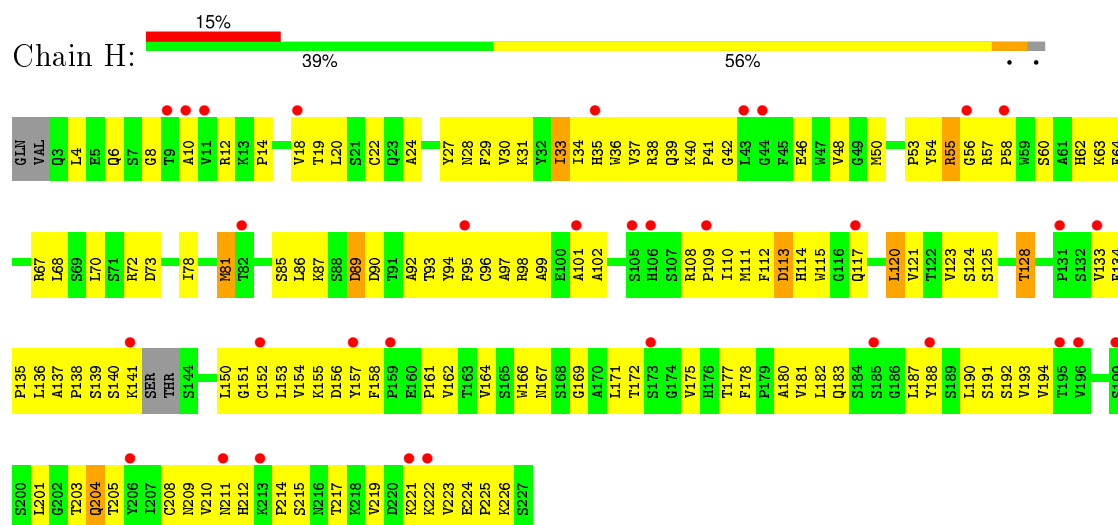


- Molecule 1: Envelope glycoprotein gp160,Envelope glycoprotein gp160,Envelope glycoprotein gp160

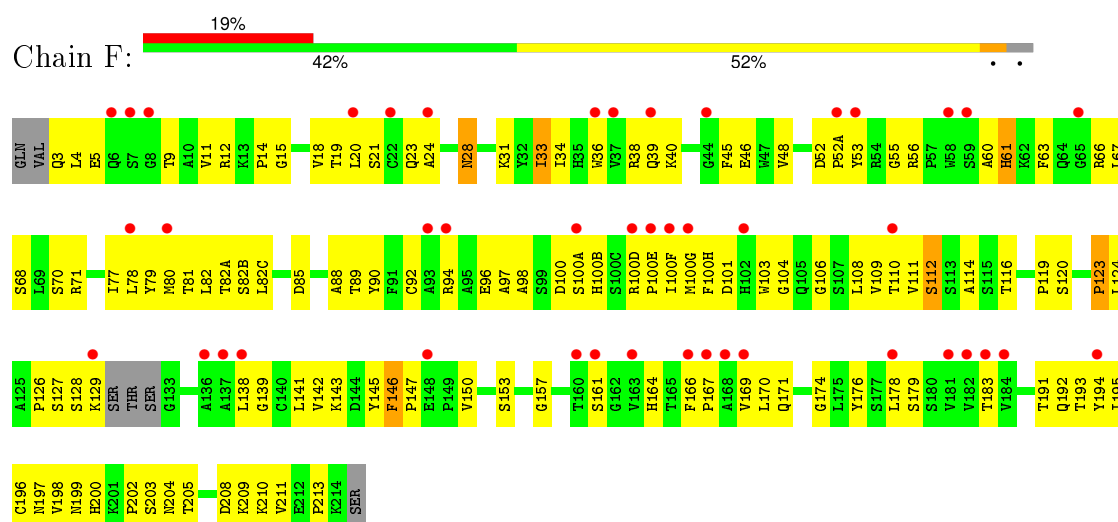




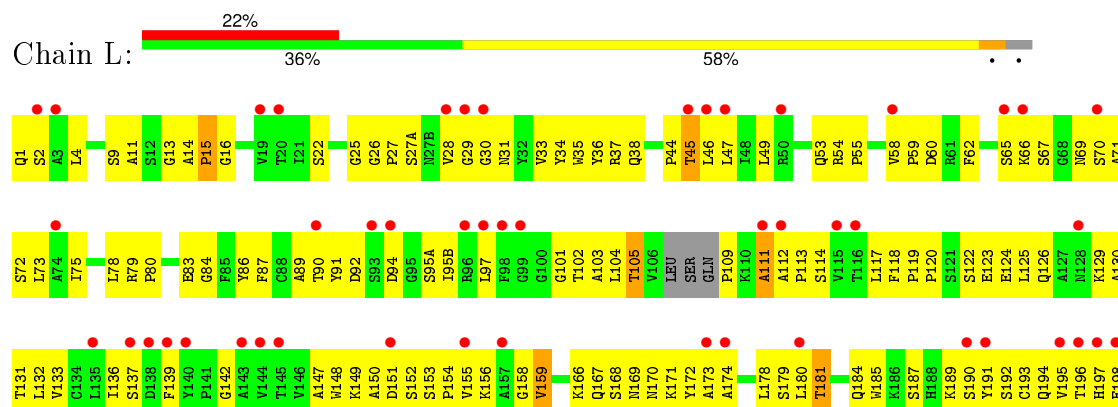
• Molecule 2: 1B2530 heavy chain



• Molecule 2: 1B2530 heavy chain

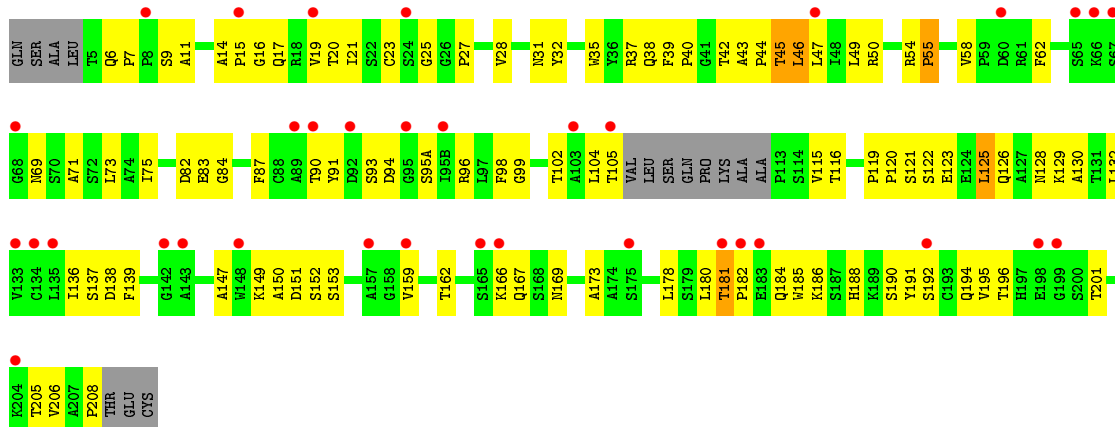


• Molecule 3: 1B2530 Light chain





• Molecule 3: 1B2530 Light chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	66.96Å 57.32Å 254.72Å 90.00° 90.11° 90.00°	Depositor
Resolution (Å)	28.77 – 3.39 28.78 – 3.39	Depositor EDS
% Data completeness (in resolution range)	90.0 (28.77-3.39) 85.2 (28.78-3.39)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.67 (at 3.39Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.268 , 0.326 0.272 , 0.309	Depositor DCC
R_{free} test set	1188 reflections (5.35%)	DCC
Wilson B-factor (Å ²)	113.7	Xtriage
Anisotropy	0.258	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 131.9	EDS
Estimated twinning fraction	0.408 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.24$	Xtriage
Outliers	0 of 24706 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	23777	wwPDB-VP
Average B, all atoms (Å ²)	223.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.73% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	E	0.46	0/2770	0.94	2/3760 (0.1%)
1	G	0.49	0/2770	0.96	6/3760 (0.2%)
2	F	0.41	0/1722	0.70	0/2341
2	H	0.46	0/1733	0.78	0/2355
3	I	0.40	0/1527	0.72	0/2083
3	L	0.46	0/1580	0.79	1/2157 (0.0%)
All	All	0.46	0/12102	0.85	9/16456 (0.1%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L	109	PRO	N-CA-CB	6.82	111.48	103.30
1	G	62	GLU	N-CA-C	-5.74	95.50	111.00
1	G	441	GLY	N-CA-C	5.70	127.34	113.10
1	G	411	ASN	N-CA-C	5.48	125.80	111.00
1	E	483	LEU	CA-CB-CG	5.40	127.72	115.30
1	G	420	ILE	N-CA-C	5.24	125.14	111.00
1	G	443	ILE	N-CA-C	5.20	125.03	111.00
1	G	382	PHE	N-CA-C	5.19	125.00	111.00
1	E	86	LEU	N-CA-C	5.11	124.79	111.00

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	E	2713	2643	2644	117	0
1	G	2713	2647	2647	148	1
2	F	1678	1651	1651	125	0
2	H	1689	1661	1661	135	22
3	I	1488	1426	1426	92	0
3	L	1541	1479	1473	132	17
4	E	140	140	130	11	0
4	G	84	84	78	11	0
All	All	12046	11731	11710	723	24

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 30.

All (723) 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:F:3:GLN:N	2:F:24:ALA:HA	1.37	1.36
2:F:3:GLN:N	2:F:24:ALA:CA	2.17	1.08
1:E:113:ASP:O	1:E:117:GLN:NE2	2.01	0.93
2:F:5:GLU:OE2	2:F:23:GLN:OE1	1.88	0.92
2:F:5:GLU:CG	2:F:23:GLN:HB3	2.01	0.91
3:L:151:ASP:OD2	3:L:190:SER:HB2	1.71	0.90
2:H:182:LEU:HA	2:H:188:TYR:HA	1.52	0.90
3:L:150:ALA:N	3:L:153:SER:O	2.04	0.89
2:F:28:ASN:OD1	2:F:94:ARG:NH1	2.08	0.86
3:L:153:SER:OG	3:L:154:PRO:HD2	1.78	0.84
1:G:98:ASN:ND2	1:G:100:MET:SD	2.51	0.84
2:H:226:LYS:NZ	3:L:120:PRO:O	2.14	0.81
3:I:166:LYS:NZ	3:I:167:GLN:O	2.12	0.81
3:I:14:ALA:O	3:I:16:GLY:N	2.14	0.81
3:L:111:ALA:HB1	3:L:112:ALA:HB2	1.63	0.80
3:L:90:THR:OG1	3:L:97:LEU:N	2.15	0.80
3:L:46:LEU:HD23	3:L:47:LEU:N	1.97	0.79
2:H:20:LEU:HD12	2:H:81:MET:SD	2.22	0.79
2:H:55:ARG:O	2:H:72:ARG:NH2	2.16	0.78
3:L:124:GLU:OE2	3:L:131:THR:OG1	2.02	0.78
1:G:58:ALA:HB2	1:G:70:ALA:HB3	1.66	0.78
1:G:229:ASN:CG	4:G:501:NAG:H82	2.03	0.78
4:E:510:NAG:H83	4:E:510:NAG:H3	1.67	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:52:LEU:HD11	1:G:100:MET:HG2	1.67	0.77
1:E:455:THR:OG1	1:E:471:GLY:O	2.03	0.76
2:F:124:LEU:HD21	2:F:141:LEU:CD2	2.15	0.76
1:G:254:VAL:CG1	4:G:502:NAG:H81	2.16	0.76
2:H:6:GLN:OE1	2:H:96:CYS:N	2.19	0.75
2:H:54:TYR:O	2:H:56:GLY:N	2.19	0.75
3:L:111:ALA:HB1	3:L:112:ALA:CB	2.17	0.74
2:H:6:GLN:O	2:H:117:GLN:NE2	2.22	0.73
3:I:138:ASP:OD1	3:I:169:ASN:ND2	2.22	0.72
1:E:102:GLU:OE2	1:E:476:LYS:NZ	2.21	0.72
2:H:101:ALA:N	2:H:109:PRO:O	2.22	0.72
2:F:68:SER:OG	2:F:81:THR:OG1	2.01	0.71
1:E:465:ASN:OD1	1:E:465:ASN:N	2.20	0.71
2:H:139:SER:O	2:H:141:LYS:NZ	2.23	0.71
3:L:46:LEU:HD23	3:L:47:LEU:H	1.55	0.71
3:I:167:GLN:HG2	3:I:173:ALA:HB2	1.72	0.70
2:F:209:LYS:NZ	2:F:210:LYS:O	2.24	0.70
3:L:1:GLN:N	3:L:95(A):SER:O	2.24	0.70
2:F:39:GLN:O	2:F:88:ALA:HB1	1.91	0.70
3:I:11:ALA:HB3	3:I:19:VAL:HG23	1.73	0.70
1:E:340:LYS:NZ	1:E:344:GLN:OE1	2.24	0.70
2:H:150:LEU:HD13	2:H:223:VAL:HG11	1.72	0.69
2:F:60:ALA:HB3	2:F:63:PHE:CD1	2.27	0.69
3:I:123:GLU:OE1	3:I:123:GLU:N	2.25	0.69
2:F:124:LEU:HD21	2:F:141:LEU:HD22	1.73	0.69
3:L:193:CYS:N	3:L:203:GLU:OE2	2.26	0.69
3:I:159:VAL:HG22	3:I:178:LEU:CD1	2.23	0.69
1:G:410:CYS:SG	4:G:506:NAG:O6	2.49	0.69
3:I:25:GLY:N	3:I:69:ASN:OD1	2.27	0.68
2:H:33:ILE:HD12	2:H:50:MET:HB2	1.75	0.68
3:L:147:ALA:O	3:L:194:GLN:N	2.27	0.68
3:L:189:LYS:HZ3	3:L:207:ALA:HB1	1.57	0.67
3:L:111:ALA:CB	3:L:112:ALA:HB2	2.23	0.67
3:L:117:LEU:HD12	3:L:133:VAL:O	1.95	0.67
1:E:279:ASN:ND2	3:I:94:ASP:OD2	2.27	0.67
3:L:184:GLN:HA	3:L:187:SER:HB3	1.75	0.67
1:E:119:CYS:N	1:E:434:MET:O	2.28	0.67
1:E:421:LYS:NZ	1:E:423:ILE:O	2.24	0.67
1:G:396:ILE:O	1:G:404:ASN:N	2.26	0.67
1:E:283:THR:OG1	1:E:473:GLY:N	2.22	0.66
1:E:69:TRP:CG	1:E:111:LEU:HD12	2.30	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:460:ALA:HB1	3:L:1:GLN:NE2	2.10	0.66
3:L:166:LYS:NZ	3:L:167:GLN:O	2.28	0.66
1:G:262:ASN:ND2	4:G:502:NAG:O7	2.29	0.66
2:H:38:ARG:NE	2:H:46:GLU:OE1	2.22	0.66
1:G:408:LYS:O	4:G:506:NAG:O6	2.12	0.66
1:G:369:LEU:HD22	1:G:373:MET:SD	2.36	0.66
3:I:27:PRO:O	3:I:69:ASN:ND2	2.28	0.66
1:E:64:GLU:HG3	1:E:211:ASP:H	1.61	0.66
2:F:5:GLU:OE2	2:F:23:GLN:HB3	1.95	0.65
2:H:150:LEU:HD13	2:H:223:VAL:CG1	2.26	0.65
1:G:60:ALA:HB2	1:G:71:THR:HG21	1.79	0.65
1:G:61:HIS:HB3	2:F:79:TYR:HB2	1.78	0.65
3:L:54:ARG:NH2	3:L:62:PHE:O	2.30	0.64
1:G:278:THR:O	1:G:456:ARG:NH2	2.30	0.64
3:L:167:GLN:HG2	3:L:173:ALA:HB2	1.79	0.64
1:E:119:CYS:SG	1:E:436:ALA:N	2.70	0.64
3:L:111:ALA:HB1	3:L:112:ALA:CA	2.28	0.64
1:G:58:ALA:HB1	1:G:67:ASN:O	1.99	0.63
1:G:362:GLN:N	1:G:468:PHE:O	2.30	0.63
2:H:221:LYS:NZ	2:H:222:LYS:O	2.32	0.63
2:F:200:HIS:ND1	2:F:203:SER:OG	2.19	0.63
3:I:54:ARG:NH2	3:I:62:PHE:O	2.32	0.63
1:G:254:VAL:HG13	4:G:502:NAG:H81	1.79	0.63
3:L:54:ARG:NE	3:L:59:PRO:O	2.31	0.62
1:E:363:PRO:O	1:E:469:ARG:NH1	2.32	0.62
1:G:276:ASN:HB3	1:G:282:LYS:HG3	1.81	0.62
2:H:212:HIS:ND1	2:H:215:SER:OG	2.22	0.62
3:L:151:ASP:CG	3:L:190:SER:HB2	2.19	0.62
1:G:371:ILE:HG21	2:H:55:ARG:HB3	1.81	0.62
1:E:373:MET:SD	4:E:508:NAG:H81	2.40	0.62
1:G:52:LEU:CD1	1:G:100:MET:HG2	2.29	0.62
2:F:4:LEU:N	2:F:23:GLN:O	2.33	0.62
2:F:5:GLU:HG3	2:F:23:GLN:HB3	1.82	0.62
2:H:4:LEU:HD23	2:H:24:ALA:HB2	1.82	0.61
1:E:357:LYS:NZ	1:E:465:ASN:O	2.32	0.61
1:G:465:ASN:N	1:G:465:ASN:OD1	2.32	0.61
2:H:14:PRO:HB3	2:H:87:LYS:HA	1.82	0.61
2:F:20:LEU:HD12	2:F:80:MET:SD	2.41	0.61
2:F:124:LEU:HD21	2:F:141:LEU:HD23	1.81	0.61
4:E:503:NAG:O7	4:E:503:NAG:O3	2.14	0.61
1:E:254:VAL:HG21	1:E:262:ASN:HB2	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:28:VAL:O	3:L:66:LYS:NZ	2.20	0.61
1:G:113:ASP:O	1:G:117:GLN:NE2	2.34	0.61
1:G:86:LEU:O	1:G:89:VAL:HG12	2.01	0.61
1:G:110:SER:O	1:G:114:GLN:HG2	2.01	0.60
2:F:38:ARG:NH2	2:F:46:GLU:OE1	2.34	0.60
1:E:257:THR:O	1:E:259:LEU:N	2.30	0.60
3:L:181:THR:O	3:L:185:TRP:N	2.31	0.60
3:I:159:VAL:HG13	3:I:178:LEU:HD13	1.84	0.60
3:L:9:SER:O	3:L:103:ALA:N	2.35	0.60
2:F:3:GLN:N	2:F:24:ALA:CB	2.65	0.60
2:F:5:GLU:HG2	2:F:23:GLN:HB3	1.82	0.60
3:I:150:ALA:O	3:I:152:SER:N	2.34	0.60
1:E:64:GLU:CG	1:E:211:ASP:H	2.15	0.59
2:F:200:HIS:O	2:F:204:ASN:N	2.35	0.59
1:G:48:ALA:CB	1:G:490:GLN:HB2	2.32	0.59
3:L:153:SER:OG	3:L:154:PRO:CD	2.50	0.59
2:F:9:THR:O	2:F:12:ARG:NH2	2.35	0.59
2:F:96:GLU:HA	2:F:100:ASP:HB3	1.84	0.59
3:L:123:GLU:OE1	3:L:123:GLU:N	2.32	0.59
3:I:37:ARG:NE	3:I:45:THR:HB	2.18	0.59
3:I:46:LEU:HD12	3:I:47:LEU:H	1.68	0.59
2:F:97:ALA:N	2:F:100(E):PRO:O	2.35	0.58
1:E:56:SER:N	1:E:75:VAL:O	2.31	0.58
2:H:14:PRO:HA	2:H:86:LEU:HB2	1.84	0.58
2:H:101:ALA:HA	2:H:110:ILE:HG22	1.86	0.58
4:E:504:NAG:O3	4:E:504:NAG:O7	2.21	0.58
3:I:122:SER:O	3:I:125:LEU:N	2.36	0.58
2:H:182:LEU:O	2:H:182:LEU:HD12	2.03	0.57
3:I:150:ALA:HB3	3:I:153:SER:HB3	1.86	0.57
1:E:404:ASN:O	1:E:404:ASN:ND2	2.37	0.57
3:L:34:TYR:HB3	3:L:46:LEU:HD21	1.86	0.57
1:G:298:ARG:NH2	1:G:441:GLY:O	2.29	0.57
2:F:124:LEU:HD22	3:I:121:SER:H	1.69	0.57
1:E:62:GLU:HG3	1:E:64:GLU:HB3	1.86	0.57
1:E:457:ASP:OD2	1:E:469:ARG:NE	2.36	0.57
2:H:180:ALA:HB2	2:H:190:LEU:HD12	1.86	0.57
4:E:510:NAG:C8	4:E:510:NAG:H3	2.34	0.57
2:F:195:ILE:HG12	2:F:210:LYS:HA	1.86	0.57
2:F:116:THR:HA	2:F:146:PHE:CD1	2.40	0.57
3:I:181:THR:OG1	3:I:184:GLN:N	2.34	0.57
1:E:275:GLU:OE2	2:F:100(D):ARG:NH2	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:83:GLU:HG2	3:L:105:THR:HA	1.86	0.57
2:F:96:GLU:O	2:F:100:ASP:N	2.38	0.56
1:G:298:ARG:HB3	1:G:443:ILE:HB	1.87	0.56
3:L:14:ALA:O	3:L:16:GLY:N	2.38	0.56
3:L:117:LEU:HD23	3:L:205:THR:HA	1.86	0.56
1:E:64:GLU:OE2	1:E:66:HIS:ND1	2.35	0.56
1:G:260:LEU:O	1:G:451:GLY:N	2.37	0.56
3:L:181:THR:OG1	3:L:184:GLN:N	2.32	0.56
3:L:148:TRP:CD1	3:L:159:VAL:HG11	2.41	0.56
1:G:119:CYS:N	1:G:434:MET:O	2.38	0.56
1:E:260:LEU:HB2	1:E:451:GLY:CA	2.36	0.56
1:G:258:GLN:NE2	1:G:372:THR:O	2.39	0.56
3:I:14:ALA:HB3	3:I:17:GLN:HG3	1.88	0.56
3:L:9:SER:HB3	3:L:11:ALA:HB2	1.88	0.56
1:G:260:LEU:HB2	1:G:451:GLY:HA3	1.88	0.56
1:E:257:THR:O	1:E:374:HIS:ND1	2.37	0.56
3:I:122:SER:O	3:I:126:GLN:N	2.39	0.55
3:L:122:SER:O	3:L:126:GLN:N	2.38	0.55
2:H:139:SER:OG	2:H:141:LYS:NZ	2.35	0.55
2:F:60:ALA:HB3	2:F:63:PHE:HD1	1.71	0.55
2:F:11:VAL:HG11	2:F:147:PRO:CB	2.37	0.55
3:L:15:PRO:HA	3:L:78:LEU:HD22	1.88	0.55
1:G:350:LYS:HB3	1:G:355:ASN:HA	1.88	0.55
1:G:300:SER:HB3	1:G:442:LYS:HB2	1.87	0.55
1:E:282:LYS:NZ	2:F:98:ALA:O	2.40	0.55
1:G:279:ASN:ND2	3:L:94:ASP:OD2	2.38	0.55
2:H:182:LEU:CA	2:H:188:TYR:HA	2.32	0.55
2:F:124:LEU:HD22	3:I:120:PRO:HA	1.89	0.55
1:E:62:GLU:HG3	1:E:64:GLU:CB	2.37	0.55
2:F:103:TRP:HB2	3:I:43:ALA:HB1	1.88	0.54
3:L:46:LEU:HD22	3:L:49:LEU:HD23	1.90	0.54
1:E:396:ILE:O	1:E:404:ASN:N	2.34	0.54
3:L:27:PRO:O	3:L:69:ASN:ND2	2.40	0.54
2:H:73:ASP:N	2:H:78:ILE:O	2.41	0.54
2:F:60:ALA:HB3	2:F:63:PHE:CE1	2.42	0.54
3:L:184:GLN:O	3:L:191:TYR:OH	2.25	0.54
3:I:167:GLN:CG	3:I:173:ALA:HB2	2.38	0.54
1:G:60:ALA:CB	1:G:71:THR:HG21	2.37	0.54
1:G:62:GLU:HG3	1:G:64:GLU:CB	2.37	0.54
2:H:182:LEU:HB3	2:H:188:TYR:CZ	2.42	0.54
1:G:205:CYS:SG	1:G:436:ALA:HB2	2.48	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:189:LYS:NZ	3:L:207:ALA:HB1	2.23	0.54
1:E:53:PHE:CE2	1:E:218:CYS:HB2	2.42	0.54
1:E:111:LEU:HD23	1:E:115:SER:HB2	1.89	0.53
2:F:171:GLN:O	2:F:174:GLY:N	2.41	0.53
3:L:111:ALA:HB1	3:L:112:ALA:HA	1.89	0.53
1:G:407:MET:SD	4:G:506:NAG:H62	2.49	0.53
1:E:98:ASN:OD1	1:E:100:MET:HG3	2.08	0.53
2:H:178:PHE:N	2:H:191:SER:O	2.41	0.53
2:H:215:SER:CB	2:H:217:THR:HG1	2.19	0.53
1:E:257:THR:OG1	1:E:375:HIS:N	2.32	0.53
2:H:178:PHE:HB2	2:H:191:SER:HB2	1.91	0.53
1:E:298:ARG:NH2	1:E:441:GLY:O	2.35	0.53
1:E:268:GLU:O	1:E:289:ASN:ND2	2.33	0.53
2:H:182:LEU:HA	2:H:188:TYR:CA	2.32	0.53
2:H:98:ARG:NE	2:H:113:ASP:OD2	2.41	0.53
2:F:5:GLU:CD	2:F:23:GLN:HB3	2.28	0.53
2:H:162:VAL:HB	2:H:190:LEU:HD13	1.91	0.53
2:H:108:ARG:N	2:H:109:PRO:HD3	2.24	0.53
1:G:421:LYS:NZ	1:G:423:ILE:O	2.32	0.53
2:F:33:ILE:HG13	2:F:34:ILE:N	2.23	0.53
3:I:159:VAL:HG22	3:I:178:LEU:HD13	1.89	0.53
1:G:62:GLU:HG3	1:G:64:GLU:HB3	1.90	0.53
1:G:343:LYS:HD3	1:G:396:ILE:HG23	1.91	0.53
3:L:4:LEU:HA	3:L:25:GLY:HA2	1.91	0.53
1:E:120:VAL:HB	1:E:434:MET:HB3	1.91	0.53
1:E:118:PRO:HB3	1:E:435:TYR:CE1	2.44	0.52
1:G:428:GLN:OE1	1:G:428:GLN:N	2.36	0.52
2:H:157:TYR:CZ	2:H:188:TYR:HB2	2.45	0.52
1:G:91:GLU:O	1:G:238:PRO:HA	2.10	0.52
2:H:203:THR:HG23	2:H:204:GLN:OE1	2.09	0.52
2:H:182:LEU:HB3	2:H:188:TYR:CE2	2.44	0.52
2:H:134:PHE:HB2	2:H:153:LEU:HD23	1.92	0.52
2:F:197:ASN:ND2	2:F:208:ASP:OD1	2.37	0.52
2:F:55:GLY:HA3	2:F:71:ARG:NE	2.24	0.52
3:L:36:TYR:O	3:L:86:TYR:HA	2.10	0.52
1:G:230:ASP:OD1	1:G:241:ASN:N	2.41	0.52
3:L:35:TRP:CD2	3:L:73:LEU:HD22	2.44	0.52
2:H:139:SER:H	3:L:118:PHE:HE1	1.57	0.52
1:G:253:PRO:HA	1:G:479:TRP:CZ3	2.44	0.51
1:E:325:ASP:OD2	1:E:327:ARG:NH1	2.44	0.51
3:L:91:TYR:O	3:L:94:ASP:N	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:32:TYR:CD2	3:I:50:ARG:HG2	2.45	0.51
2:F:142:VAL:HG12	2:F:145:TYR:CE1	2.45	0.51
2:H:6:GLN:HG2	2:H:22:CYS:SG	2.50	0.51
2:H:14:PRO:HD2	2:H:125:SER:HA	1.92	0.51
1:E:91:GLU:O	1:E:238:PRO:HA	2.10	0.51
1:G:218:CYS:HA	1:G:247:CYS:HA	1.93	0.51
3:L:124:GLU:CD	3:L:131:THR:HG1	2.07	0.51
3:L:167:GLN:CG	3:L:173:ALA:HB2	2.41	0.51
1:G:56:SER:N	1:G:75:VAL:O	2.40	0.51
1:G:423:ILE:HA	1:G:433:ALA:O	2.11	0.51
1:E:343:LYS:O	1:E:346:THR:OG1	2.22	0.51
1:E:283:THR:CG2	1:E:472:GLY:HA3	2.41	0.51
1:G:276:ASN:ND2	1:G:279:ASN:HB2	2.26	0.51
2:F:100(G):MET:SD	3:I:49:LEU:HD22	2.51	0.51
2:H:156:ASP:HA	2:H:187:LEU:HD13	1.93	0.51
3:L:54:ARG:HB2	3:L:58:VAL:HG11	1.93	0.51
1:E:407:MET:HG2	1:E:408:LYS:N	2.25	0.51
3:I:20:THR:HA	3:I:73:LEU:O	2.11	0.51
3:L:142:GLY:HA3	3:L:172:TYR:CG	2.46	0.50
2:H:86:LEU:C	2:H:87:LYS:HG3	2.31	0.50
1:E:223:TYR:CE2	1:E:490:GLN:HG3	2.46	0.50
2:F:100(A):SER:OG	2:F:100(B):HIS:N	2.43	0.50
2:H:164:VAL:HG11	2:H:192:SER:CB	2.41	0.50
1:G:61:HIS:HA	2:F:70:SER:CB	2.41	0.50
2:F:96:GLU:CA	2:F:100:ASP:HB3	2.42	0.50
2:F:178:LEU:HD23	2:F:179:SER:N	2.26	0.50
2:H:111:MET:SD	3:L:49:LEU:HD22	2.52	0.50
3:L:148:TRP:NE1	3:L:159:VAL:HG11	2.26	0.50
3:I:39:PHE:HB3	3:I:40:PRO:HD2	1.93	0.50
2:F:61:HIS:N	2:F:61:HIS:CD2	2.78	0.50
1:E:297:THR:OG1	1:E:444:ASN:OD1	2.26	0.50
1:G:330:TYR:CD1	1:G:415:THR:HG23	2.46	0.50
1:G:82:GLN:O	1:G:246:GLN:NE2	2.45	0.50
2:F:145:TYR:CZ	2:F:176:TYR:HB3	2.47	0.50
1:G:375:HIS:ND1	1:G:383:PHE:O	2.36	0.50
2:H:124:SER:HB2	2:H:158:PHE:CE1	2.47	0.50
2:F:112:SER:OG	2:F:114:ALA:O	2.29	0.50
1:G:222:GLY:O	1:G:491:ILE:N	2.34	0.50
2:F:70:SER:OG	2:F:79:TYR:O	2.29	0.50
1:E:294:ILE:HD12	1:E:333:ILE:HD11	1.92	0.50
3:I:119:PRO:HA	3:I:132:LEU:HD23	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:46:LEU:HD12	3:I:47:LEU:N	2.27	0.49
1:G:475:ILE:CG2	1:G:479:TRP:CZ2	2.95	0.49
3:L:54:ARG:CZ	3:L:60:ASP:HA	2.42	0.49
1:G:257:THR:O	1:G:259:LEU:N	2.42	0.49
3:I:19:VAL:CG1	3:I:75:ILE:HB	2.42	0.49
1:G:392:ASN:OD1	4:G:506:NAG:H2	2.11	0.49
2:H:212:HIS:HB3	2:H:217:THR:HB	1.95	0.49
2:H:182:LEU:HB3	2:H:188:TYR:CE1	2.47	0.49
3:L:26:GLY:N	3:L:27:PRO:HD2	2.27	0.49
3:L:2:SER:CB	3:L:27:PRO:HD3	2.42	0.49
2:F:169:VAL:HB	3:I:162:THR:HG22	1.94	0.49
1:E:266:ALA:HB3	1:E:289:ASN:HB3	1.94	0.49
2:H:36:TRP:O	2:H:48:VAL:HG22	2.12	0.49
2:F:150:VAL:HG13	2:F:198:VAL:CG1	2.43	0.49
1:E:423:ILE:HG12	1:E:434:MET:HB2	1.93	0.49
4:E:503:NAG:C7	4:E:503:NAG:HO3	2.22	0.49
2:H:60:SER:HB3	2:H:68:LEU:HD21	1.94	0.49
1:G:453:LEU:HD21	1:G:477:ASP:HB3	1.94	0.49
3:L:33:VAL:HG12	3:L:35:TRP:CD1	2.47	0.49
2:H:20:LEU:HB2	2:H:81:MET:HG2	1.94	0.49
1:G:260:LEU:N	1:G:451:GLY:O	2.40	0.49
3:L:91:TYR:HD1	3:L:91:TYR:H	1.60	0.49
3:L:198:GLU:O	3:L:200:SER:N	2.43	0.49
1:E:208:ILE:HD12	1:E:210:PHE:HB2	1.93	0.49
2:H:137:ALA:HB1	2:H:225:PRO:HA	1.94	0.49
1:G:61:HIS:CB	2:F:79:TYR:HB2	2.42	0.49
2:H:4:LEU:HD12	2:H:114:HIS:ND1	2.28	0.49
3:L:75:ILE:HG21	3:L:78:LEU:HA	1.93	0.49
2:F:15:GLY:H	2:F:82(C):LEU:HB2	1.77	0.49
3:L:29:GLY:HA2	3:L:31:ASN:N	2.27	0.49
2:H:180:ALA:HA	2:H:190:LEU:HA	1.95	0.49
2:F:169:VAL:O	2:F:171:GLN:N	2.46	0.49
2:F:119:PRO:HB3	2:F:145:TYR:HB3	1.94	0.49
3:I:196:THR:HA	3:I:201:THR:HA	1.95	0.49
2:F:5:GLU:HG2	2:F:23:GLN:O	2.12	0.49
2:F:200:HIS:HB3	2:F:205:THR:HB	1.95	0.49
3:I:37:ARG:NH2	3:I:46:LEU:O	2.46	0.49
2:H:102:ALA:HA	2:H:108:ARG:HB3	1.95	0.49
2:H:178:PHE:HE1	2:H:193:VAL:HG12	1.78	0.49
3:I:21:ILE:HD11	3:I:73:LEU:HD23	1.94	0.49
1:E:251:ILE:HD13	1:E:482:GLU:HB3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:137:ALA:HB3	2:H:226:LYS:HE3	1.96	0.48
2:H:153:LEU:HD11	3:L:131:THR:HG21	1.95	0.48
1:G:58:ALA:CB	1:G:70:ALA:HB3	2.39	0.48
3:I:32:TYR:CG	3:I:50:ARG:HG2	2.48	0.48
1:G:228:CYS:SG	1:G:233:PHE:CG	3.07	0.48
2:H:167:ASN:CG	2:H:171:LEU:HB2	2.33	0.48
2:F:97:ALA:HA	2:F:100(F):ILE:HG22	1.95	0.48
1:G:120:VAL:HB	1:G:434:MET:HB3	1.94	0.48
3:I:205:THR:HG22	3:I:206:VAL:H	1.77	0.48
1:G:280:ASN:HB3	1:G:456:ARG:CZ	2.44	0.48
3:I:23:CYS:HB3	3:I:71:ALA:HB3	1.95	0.48
1:G:363:PRO:O	1:G:469:ARG:NH1	2.41	0.48
2:F:166:PHE:HB2	2:F:179:SER:HB2	1.95	0.48
3:I:90:THR:O	3:I:96:ARG:NE	2.47	0.48
1:G:123:THR:OG1	1:G:430:THR:O	2.16	0.48
1:E:205:CYS:SG	1:E:436:ALA:HB2	2.54	0.48
3:L:67:SER:O	3:L:70:SER:OG	2.17	0.48
2:F:89:THR:HA	2:F:108:LEU:HA	1.95	0.48
3:L:125:LEU:HD23	3:L:129:LYS:O	2.13	0.48
3:L:69:ASN:O	3:L:71:ALA:N	2.47	0.48
1:G:475:ILE:HA	1:G:478:ASN:OD1	2.13	0.48
2:F:18:VAL:HG22	2:F:19:THR:N	2.28	0.48
3:L:83:GLU:HG2	3:L:105:THR:HB	1.95	0.48
3:I:39:PHE:CD1	3:I:84:GLY:HA3	2.49	0.48
1:G:72:HIS:CE1	1:G:73:ALA:HB2	2.48	0.48
3:I:167:GLN:HG2	3:I:173:ALA:CB	2.40	0.48
1:G:464:SER:OG	1:G:465:ASN:OD1	2.24	0.48
2:F:100(F):ILE:HG13	2:F:100(F):ILE:O	2.14	0.48
2:F:145:TYR:OH	2:F:178:LEU:HB2	2.14	0.48
2:F:198:VAL:HG12	2:F:199:ASN:N	2.29	0.48
1:G:283:THR:HG23	1:G:472:GLY:HA3	1.96	0.48
2:F:52:ASP:O	2:F:55:GLY:HA2	2.14	0.48
1:E:296:CYS:HA	1:E:331:CYS:HA	1.95	0.48
1:G:477:ASP:HA	1:G:480:ARG:HB2	1.95	0.48
2:F:138:LEU:HD12	2:F:138:LEU:C	2.34	0.48
1:E:69:TRP:HA	1:E:72:HIS:CD2	2.49	0.47
1:E:469:ARG:HB3	2:F:56:ARG:NH2	2.28	0.47
1:G:279:ASN:OD1	1:G:281:ALA:HB3	2.14	0.47
3:L:148:TRP:CZ3	3:L:178:LEU:HB2	2.48	0.47
2:H:166:TRP:HB3	2:H:171:LEU:HD23	1.96	0.47
3:I:32:TYR:CE2	3:I:91:TYR:HB3	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:453:LEU:HB3	1:G:472:GLY:HA3	1.95	0.47
1:G:99:ASN:O	1:G:103:GLN:N	2.46	0.47
3:I:195:VAL:O	3:I:201:THR:HA	2.15	0.47
2:F:153:SER:HB2	2:F:157:GLY:HA2	1.96	0.47
1:E:120:VAL:HG22	1:E:202:LYS:HG2	1.97	0.47
2:F:161:SER:O	2:F:183:THR:N	2.44	0.47
2:H:156:ASP:HA	2:H:187:LEU:HB3	1.97	0.47
3:L:87:PHE:CE2	3:L:101:GLY:HA3	2.50	0.47
2:F:66:ARG:HE	2:F:82(B):SER:HB3	1.79	0.47
3:L:33:VAL:CG1	3:L:34:TYR:N	2.78	0.47
1:G:408:LYS:CG	1:G:409:GLY:N	2.77	0.47
3:L:11:ALA:O	3:L:13:GLY:N	2.45	0.47
2:H:67:ARG:NH2	2:H:85:SER:HB3	2.29	0.47
1:E:474:ASN:OD1	1:E:474:ASN:N	2.47	0.47
1:E:362:GLN:N	1:E:468:PHE:O	2.41	0.47
1:G:122:LEU:HB2	1:G:432:GLN:HB2	1.96	0.47
2:F:21:SER:HB2	2:F:77:ILE:HD11	1.96	0.47
1:G:279:ASN:OD1	1:G:281:ALA:N	2.42	0.47
2:H:124:SER:HB2	2:H:158:PHE:CZ	2.50	0.47
2:F:138:LEU:HD12	2:F:139:GLY:N	2.29	0.47
2:H:182:LEU:HB3	2:H:188:TYR:CD2	2.50	0.47
1:G:63:THR:HG21	2:F:68:SER:HB3	1.97	0.47
2:H:172:THR:HA	2:H:175:VAL:HB	1.97	0.47
2:H:121:VAL:CG1	2:H:123:VAL:HG23	2.44	0.47
2:H:154:VAL:HG12	2:H:157:TYR:CE1	2.50	0.47
3:L:149:LYS:CA	3:L:155:VAL:HG23	2.45	0.47
2:H:29:PHE:O	2:H:53:PRO:HB2	2.15	0.47
2:H:135:PRO:HA	2:H:223:VAL:HG22	1.97	0.46
1:G:396:ILE:HD12	1:G:396:ILE:N	2.30	0.46
2:H:212:HIS:CE1	2:H:214:PRO:HG2	2.50	0.46
3:I:147:ALA:HB3	3:I:194:GLN:HB2	1.96	0.46
2:H:89:ASP:N	2:H:89:ASP:OD1	2.47	0.46
2:F:123:PRO:HG3	2:F:209:LYS:HZ2	1.80	0.46
2:H:178:PHE:HE1	2:H:193:VAL:CG1	2.28	0.46
1:G:391:PHE:HE2	1:G:470:PRO:HG3	1.81	0.46
2:F:164:HIS:NE2	3:I:167:GLN:HG2	2.29	0.46
1:G:63:THR:HG21	2:F:68:SER:CB	2.46	0.46
1:G:408:LYS:HG2	1:G:409:GLY:N	2.29	0.46
2:F:94:ARG:O	2:F:100(H):PHE:HA	2.16	0.46
1:G:101:VAL:HG22	1:G:483:LEU:CD1	2.45	0.46
2:H:10:ALA:O	2:H:12:ARG:NH2	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:67:LEU:HG	2:F:68:SER:N	2.30	0.46
2:H:128:THR:HA	2:H:158:PHE:HD2	1.80	0.46
1:E:207:LYS:NZ	1:E:439:ILE:HG23	2.31	0.46
2:F:82:LEU:HD12	2:F:82(A):THR:H	1.80	0.46
3:I:184:GLN:O	3:I:191:TYR:CZ	2.69	0.46
1:G:120:VAL:HA	1:G:201:ILE:O	2.16	0.46
3:L:119:PRO:HA	3:L:132:LEU:HD23	1.97	0.46
3:L:189:LYS:NZ	3:L:190:SER:OG	2.41	0.46
4:E:504:NAG:O6	3:I:32:TYR:OH	2.17	0.46
3:L:159:VAL:HG22	3:L:178:LEU:HD13	1.98	0.46
1:E:58:ALA:HB1	1:E:67:ASN:O	2.15	0.46
2:F:31:LYS:HE3	2:F:100:ASP:HA	1.97	0.46
4:E:504:NAG:H5	3:I:93:SER:HA	1.98	0.46
2:H:210:VAL:HG12	2:H:211:ASN:N	2.30	0.46
3:I:82:ASP:O	3:I:84:GLY:N	2.48	0.46
1:G:77:THR:CG2	1:G:78:ASP:N	2.78	0.46
2:F:101:ASP:HA	3:I:46:LEU:HD23	1.98	0.46
3:I:139:PHE:CE2	3:I:173:ALA:HA	2.51	0.46
3:L:78:LEU:HD23	3:L:79:ARG:N	2.31	0.46
2:F:166:PHE:HZ	3:I:137:SER:HB3	1.81	0.46
1:G:208:ILE:HD12	1:G:210:PHE:HB2	1.98	0.46
1:G:95:MET:HG2	1:G:236:THR:HG22	1.98	0.46
1:E:361:PHE:HE1	1:E:454:LEU:HD11	1.81	0.46
1:G:407:MET:O	1:G:411:ASN:ND2	2.49	0.45
3:L:66:LYS:HG2	3:L:67:SER:N	2.31	0.45
2:F:61:HIS:CD2	2:F:61:HIS:H	2.33	0.45
2:F:193:THR:HB	2:F:210:LYS:HE2	1.99	0.45
1:G:439:ILE:HD11	1:G:443:ILE:HG12	1.99	0.45
3:L:122:SER:O	3:L:125:LEU:N	2.49	0.45
1:E:210:PHE:CE1	1:E:212:PRO:HD3	2.50	0.45
2:F:36:TRP:HE1	2:F:78:LEU:CD2	2.28	0.45
3:I:136:ILE:HG22	3:I:139:PHE:CE2	2.50	0.45
3:L:111:ALA:HA	3:L:197:HIS:HD1	1.81	0.45
2:F:195:ILE:HG21	2:F:208:ASP:HB3	1.97	0.45
1:G:457:ASP:HB2	1:G:467:THR:HB	1.98	0.45
2:H:164:VAL:HG11	2:H:192:SER:OG	2.17	0.45
3:I:39:PHE:CE2	3:I:82:ASP:HA	2.52	0.45
1:G:72:HIS:ND1	1:G:72:HIS:C	2.69	0.45
1:E:284:ILE:HB	1:E:454:LEU:HB2	1.97	0.45
2:H:224:GLU:HG2	2:H:225:PRO:O	2.17	0.45
3:L:205:THR:HG22	3:L:206:VAL:H	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:411:ASN:N	1:G:411:ASN:OD1	2.47	0.45
3:L:149:LYS:C	3:L:155:VAL:HG23	2.37	0.45
1:E:120:VAL:HA	1:E:201:ILE:O	2.16	0.45
1:E:283:THR:HG23	1:E:472:GLY:HA3	1.99	0.45
1:G:280:ASN:HD22	1:G:458:GLY:CA	2.29	0.45
1:E:210:PHE:CD1	1:E:379:ARG:HA	2.50	0.45
1:G:286:VAL:HB	1:G:452:ILE:HB	1.98	0.45
3:L:151:ASP:OD1	3:L:190:SER:HB2	2.16	0.45
1:E:258:GLN:NE2	1:E:373:MET:C	2.70	0.45
1:G:48:ALA:HB3	1:G:490:GLN:HB2	1.98	0.45
2:F:116:THR:HG22	2:F:147:PRO:HD3	1.98	0.45
3:I:19:VAL:HG13	3:I:75:ILE:HB	1.98	0.45
1:E:423:ILE:HA	1:E:433:ALA:O	2.17	0.45
1:G:373:MET:HE2	1:G:385:CYS:C	2.36	0.45
3:L:30:GLY:O	3:L:66:LYS:NZ	2.47	0.45
2:F:127:SER:O	2:F:129:LYS:NZ	2.48	0.45
2:H:30:VAL:HG13	2:H:31:LYS:CG	2.47	0.45
3:L:169:ASN:C	3:L:171:LYS:H	2.20	0.45
2:F:67:LEU:HD13	2:F:82:LEU:HD13	1.99	0.45
1:E:457:ASP:CG	1:E:469:ARG:HE	2.19	0.45
1:E:374:HIS:CD2	1:E:376:PHE:CD1	3.05	0.45
2:F:100(F):ILE:O	2:F:100(G):MET:HB3	2.16	0.45
1:E:100:MET:HE3	1:E:488:VAL:CG2	2.46	0.45
1:G:230:ASP:HB2	1:G:233:PHE:HB2	1.97	0.45
1:E:228:CYS:O	1:E:485:LYS:HB2	2.17	0.45
1:E:235:GLY:N	1:E:273:ARG:NH1	2.65	0.45
3:L:117:LEU:CD2	3:L:205:THR:HA	2.46	0.45
1:E:118:PRO:HB3	1:E:435:TYR:CZ	2.52	0.45
1:G:354:ASN:HB2	1:G:357:LYS:HG3	1.98	0.45
3:L:65:SER:O	3:L:72:SER:OG	2.30	0.45
1:G:408:LYS:CG	1:G:409:GLY:H	2.30	0.45
1:E:65:VAL:O	1:E:69:TRP:CB	2.65	0.45
1:E:123:THR:OG1	1:E:430:THR:O	2.16	0.45
2:H:181:VAL:O	2:H:183:GLN:N	2.50	0.45
2:H:133:VAL:HG21	2:H:219:VAL:HG11	1.99	0.45
2:H:33:ILE:HD11	2:H:35:HIS:NE2	2.32	0.44
3:I:54:ARG:HB2	3:I:58:VAL:HG11	1.99	0.44
3:L:136:ILE:CG2	3:L:195:VAL:HG11	2.47	0.44
1:G:475:ILE:O	1:G:478:ASN:HB2	2.17	0.44
1:G:396:ILE:CD1	1:G:396:ILE:N	2.80	0.44
3:L:9:SER:O	3:L:102:THR:HB	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:73:ASP:HB3	2:H:78:ILE:HG22	1.98	0.44
1:E:330:TYR:HB2	1:E:416:LEU:O	2.18	0.44
1:E:96:TRP:HE1	1:E:236:THR:HG22	1.82	0.44
3:L:113:PRO:HB3	3:L:139:PHE:HB3	1.99	0.44
1:G:455:THR:OG1	2:H:57:ARG:NH1	2.50	0.44
2:F:100(H):PHE:O	2:F:103:TRP:NE1	2.44	0.44
2:H:55:ARG:H	2:H:55:ARG:HH11	1.64	0.44
1:G:227:LYS:HG3	1:G:486:TYR:CE1	2.53	0.44
1:E:229:ASN:ND2	4:E:503:NAG:H62	2.32	0.44
3:I:9:SER:CB	3:I:21:ILE:HG22	2.47	0.44
3:I:38:GLN:C	3:I:39:PHE:HD1	2.20	0.44
1:G:216:HIS:CE1	1:G:250:GLY:N	2.86	0.44
3:I:6:GLN:HE21	3:I:102:THR:HG23	1.83	0.44
3:L:46:LEU:HD22	3:L:49:LEU:CD2	2.47	0.44
2:H:20:LEU:O	2:H:81:MET:N	2.51	0.44
2:F:203:SER:CB	2:F:205:THR:HG1	2.31	0.44
1:E:286:VAL:O	1:E:451:GLY:HA2	2.17	0.44
2:H:90:ASP:HB2	2:H:123:VAL:HG21	2.00	0.44
2:F:90:TYR:HE1	2:F:109:VAL:HG21	1.83	0.44
3:I:188:HIS:HB2	3:I:191:TYR:CZ	2.53	0.44
1:G:121:LYS:HB3	1:G:201:ILE:HB	2.00	0.44
2:H:166:TRP:O	2:H:169:GLY:N	2.50	0.44
2:H:137:ALA:CB	2:H:226:LYS:HG3	2.47	0.44
2:H:37:VAL:HG23	2:H:95:PHE:HB2	2.00	0.44
3:I:39:PHE:HB2	3:I:42:THR:HG21	2.00	0.44
1:E:222:GLY:HA2	1:E:491:ILE:HD12	2.00	0.44
1:E:77:THR:CG2	1:E:78:ASP:N	2.80	0.44
2:H:137:ALA:CB	2:H:225:PRO:HA	2.48	0.44
3:L:117:LEU:HD23	3:L:205:THR:CA	2.47	0.44
1:G:258:GLN:NE2	1:G:373:MET:HA	2.33	0.44
1:G:456:ARG:HD3	1:G:468:PHE:HE2	1.83	0.44
3:L:15:PRO:HA	3:L:78:LEU:CD2	2.48	0.44
3:L:4:LEU:HD23	3:L:25:GLY:HA2	2.00	0.44
4:E:509:NAG:H82	4:E:509:NAG:C1	2.48	0.44
2:H:108:ARG:N	2:H:109:PRO:CD	2.81	0.44
2:F:18:VAL:O	2:F:81:THR:HG22	2.18	0.44
2:F:166:PHE:HB3	2:F:167:PRO:HD2	2.00	0.44
1:E:67:ASN:HA	1:E:213:ILE:HD13	2.00	0.44
1:G:453:LEU:HD21	1:G:477:ASP:CB	2.47	0.44
2:H:121:VAL:HG12	2:H:123:VAL:HG23	2.00	0.44
1:E:349:LEU:HD22	1:E:353:PHE:HE2	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:94:ARG:HE	2:F:101:ASP:HB2	1.82	0.43
2:H:38:ARG:NH2	2:H:40:LYS:HE2	2.33	0.43
3:I:9:SER:HB2	3:I:21:ILE:HG22	2.00	0.43
3:I:6:GLN:HG3	3:I:99:GLY:HA3	1.99	0.43
1:G:460:ALA:H	3:L:95(B):ILE:HG23	1.83	0.43
3:L:193:CYS:H	3:L:203:GLU:CD	2.21	0.43
2:H:10:ALA:HA	2:H:120:LEU:HD13	2.00	0.43
3:L:136:ILE:HB	3:L:174:ALA:HB3	2.01	0.43
2:F:90:TYR:O	2:F:106:GLY:HA2	2.18	0.43
3:L:120:PRO:HB3	3:L:130:ALA:HA	2.00	0.43
3:L:27(A):SER:C	3:L:69:ASN:HB2	2.38	0.43
1:G:453:LEU:HB3	1:G:472:GLY:CA	2.48	0.43
1:E:69:TRP:O	1:E:73:ALA:N	2.49	0.43
1:G:223:TYR:CD2	1:G:490:GLN:HA	2.53	0.43
1:E:265:LEU:HD13	1:E:291:SER:N	2.33	0.43
1:E:82:GLN:HB3	1:E:246:GLN:HE22	1.84	0.43
3:L:84:GLY:O	3:L:103:ALA:HA	2.18	0.43
3:L:80:PRO:O	3:L:83:GLU:HG3	2.18	0.43
1:E:300:SER:HA	1:E:441:GLY:O	2.18	0.43
2:H:166:TRP:CB	2:H:171:LEU:HB3	2.48	0.43
1:E:359:ILE:HG23	1:E:468:PHE:HE2	1.84	0.43
2:H:92:ALA:H	2:H:121:VAL:HB	1.83	0.43
1:E:280:ASN:HB3	1:E:456:ARG:CZ	2.49	0.43
1:G:260:LEU:HD22	1:G:478:ASN:CG	2.38	0.43
3:L:35:TRP:CE3	3:L:73:LEU:HD22	2.54	0.43
2:H:134:PHE:HB2	2:H:153:LEU:HB3	1.99	0.43
2:H:4:LEU:CD1	2:H:114:HIS:HB3	2.49	0.43
2:H:64:PHE:O	2:H:67:ARG:N	2.47	0.43
2:H:8:GLY:O	2:H:120:LEU:HD11	2.19	0.43
2:F:194:TYR:HB2	2:F:211:VAL:HB	2.01	0.43
3:I:178:LEU:CD2	3:I:180:LEU:HD21	2.48	0.43
3:L:166:LYS:HD2	3:L:170:ASN:HA	1.99	0.43
2:H:27:TYR:O	2:H:30:VAL:HG12	2.19	0.43
4:E:509:NAG:H2	4:E:509:NAG:C6	2.49	0.43
1:E:280:ASN:HB2	1:E:456:ARG:HB3	2.01	0.43
2:H:99:ALA:HB1	2:H:111:MET:H	1.83	0.43
2:H:111:MET:HB3	3:L:34:TYR:CZ	2.54	0.43
3:L:117:LEU:HD12	3:L:118:PHE:H	1.83	0.43
1:G:373:MET:SD	1:G:384:TYR:HB3	2.59	0.43
3:L:114:SER:O	3:L:137:SER:OG	2.35	0.43
2:F:20:LEU:O	2:F:79:TYR:HA	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:62:GLU:O	1:G:68:VAL:HG23	2.19	0.43
1:E:210:PHE:CD1	1:E:210:PHE:C	2.92	0.43
2:H:92:ALA:O	2:H:121:VAL:HB	2.18	0.43
2:H:138:PRO:HD2	2:H:225:PRO:N	2.33	0.42
1:G:254:VAL:O	1:G:478:ASN:ND2	2.46	0.42
2:F:68:SER:OG	2:F:81:THR:O	2.37	0.42
1:G:474:ASN:O	1:G:477:ASP:HB2	2.18	0.42
3:I:190:SER:HB2	3:I:205:THR:HG22	2.01	0.42
1:G:254:VAL:HG11	1:G:261:LEU:HB2	2.01	0.42
2:F:200:HIS:CE1	2:F:202:PRO:HG2	2.54	0.42
3:L:16:GLY:N	3:L:78:LEU:HD22	2.34	0.42
3:L:4:LEU:HD23	3:L:25:GLY:CA	2.50	0.42
1:E:50:THR:HG21	1:E:223:TYR:CD2	2.54	0.42
3:I:205:THR:HG22	3:I:206:VAL:N	2.34	0.42
1:G:341:VAL:O	1:G:344:GLN:HB2	2.19	0.42
2:H:154:VAL:HB	2:H:190:LEU:O	2.19	0.42
2:F:161:SER:OG	2:F:183:THR:O	2.22	0.42
3:L:33:VAL:HG13	3:L:89:ALA:H	1.84	0.42
2:H:34:ILE:CG2	2:H:96:CYS:HB2	2.49	0.42
1:E:102:GLU:O	1:E:106:GLU:HG3	2.19	0.42
1:E:258:GLN:NE2	1:E:371:ILE:O	2.52	0.42
3:I:49:LEU:HD21	3:I:55:PRO:CG	2.49	0.42
1:G:270:ILE:HG13	1:G:289:ASN:ND2	2.34	0.42
1:G:270:ILE:HG12	1:G:288:LEU:HA	2.02	0.42
1:E:233:PHE:O	1:E:271:ILE:HG21	2.19	0.42
2:H:182:LEU:HB3	2:H:188:TYR:CD1	2.53	0.42
3:L:54:ARG:HB2	3:L:58:VAL:CG1	2.48	0.42
2:F:45:PHE:HB2	3:I:98:PHE:CD2	2.55	0.42
3:L:38:GLN:HA	3:L:44:PRO:HA	2.00	0.42
2:H:58:PRO:HB2	2:H:70:LEU:HD12	2.02	0.42
1:E:83:GLU:HA	1:E:244:SER:O	2.20	0.42
3:L:158:GLY:O	3:L:179:SER:N	2.51	0.42
1:G:69:TRP:HA	1:G:72:HIS:CD2	2.54	0.42
2:H:39:GLN:N	2:H:93:THR:O	2.41	0.42
2:H:102:ALA:HA	2:H:108:ARG:CA	2.49	0.42
2:F:40:LYS:CG	2:F:88:ALA:HB2	2.49	0.42
3:L:27(A):SER:HA	3:L:69:ASN:HB2	2.02	0.42
1:E:273:ARG:NH2	1:E:484:TYR:CD2	2.88	0.42
1:G:354:ASN:N	1:G:354:ASN:OD1	2.52	0.42
1:E:82:GLN:O	1:E:246:GLN:NE2	2.52	0.42
3:L:196:THR:HG23	3:L:199:GLY:HA2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:37:ARG:HB2	3:L:45:THR:OG1	2.19	0.42
2:H:18:VAL:HG22	2:H:19:THR:N	2.35	0.42
1:E:99:ASN:OD1	1:E:103:GLN:NE2	2.49	0.42
3:L:150:ALA:HB3	3:L:153:SER:HB3	2.01	0.42
3:L:149:LYS:HB2	3:L:194:GLN:HE22	1.84	0.42
1:E:374:HIS:CD2	1:E:376:PHE:CE1	3.07	0.42
1:E:376:PHE:CZ	1:E:383:PHE:HB3	2.54	0.42
3:I:188:HIS:N	3:I:191:TYR:OH	2.44	0.42
1:E:260:LEU:HB2	1:E:451:GLY:HA3	1.98	0.42
3:L:22:SER:OG	3:L:71:ALA:HB3	2.20	0.42
2:H:164:VAL:CG2	2:H:177:THR:HG23	2.50	0.42
2:F:150:VAL:HG13	2:F:198:VAL:HG13	2.01	0.42
3:I:115:VAL:CG1	3:I:116:THR:N	2.82	0.42
1:G:332:GLU:HA	1:G:414:ILE:O	2.19	0.42
2:H:182:LEU:CB	2:H:188:TYR:CE1	3.03	0.42
1:G:227:LYS:HD3	1:G:229:ASN:HD21	1.84	0.42
2:H:152:CYS:SG	2:H:223:VAL:CG2	3.08	0.42
2:F:33:ILE:CG1	2:F:34:ILE:N	2.82	0.42
2:F:55:GLY:HA3	2:F:71:ARG:CZ	2.50	0.42
1:G:69:TRP:O	1:G:73:ALA:N	2.51	0.42
2:H:115:TRP:HB3	3:L:44:PRO:HD2	2.02	0.42
1:E:111:LEU:O	1:E:115:SER:N	2.53	0.42
3:I:21:ILE:HG13	3:I:35:TRP:CZ3	2.54	0.42
1:E:345:VAL:HG12	1:E:349:LEU:CD1	2.50	0.42
1:E:280:ASN:ND2	1:E:458:GLY:CA	2.83	0.42
1:G:234:ASN:C	1:G:273:ARG:NH1	2.73	0.42
2:F:67:LEU:HD12	2:F:68:SER:H	1.84	0.41
1:G:280:ASN:HB2	1:G:456:ARG:O	2.20	0.41
1:G:360:ILE:HD12	1:G:465:ASN:HB2	2.02	0.41
3:L:87:PHE:N	3:L:87:PHE:CD1	2.87	0.41
1:G:361:PHE:CD1	1:G:391:PHE:CD1	3.08	0.41
3:L:132:LEU:CD1	3:L:180:LEU:HD11	2.50	0.41
1:G:63:THR:CG2	2:F:68:SER:HB2	2.50	0.41
3:L:83:GLU:CG	3:L:105:THR:HA	2.50	0.41
2:H:178:PHE:CB	2:H:191:SER:HB2	2.50	0.41
2:F:120:SER:O	2:F:143:LYS:HB2	2.20	0.41
2:H:152:CYS:N	2:H:208:CYS:SG	2.93	0.41
1:E:65:VAL:O	1:E:69:TRP:HB3	2.20	0.41
1:G:204:ALA:C	1:G:205:CYS:SG	2.98	0.41
1:E:280:ASN:HD22	1:E:458:GLY:N	2.18	0.41
1:G:108:VAL:O	1:G:112:TRP:CD1	2.73	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:92:CYS:O	2:F:104:GLY:N	2.52	0.41
1:E:338:TRP:CH2	1:E:452:ILE:HD11	2.55	0.41
1:G:338:TRP:CE2	1:G:342:LEU:HD22	2.55	0.41
3:I:125:LEU:HD23	3:I:125:LEU:N	2.36	0.41
1:G:423:ILE:HG12	1:G:434:MET:HB2	2.02	0.41
1:G:93:PHE:HB2	1:G:233:PHE:HZ	1.84	0.41
1:E:460:ALA:HB2	3:I:95(A):SER:OG	2.20	0.41
2:H:182:LEU:HB3	2:H:188:TYR:CG	2.56	0.41
3:I:23:CYS:HB2	3:I:35:TRP:CZ2	2.56	0.41
3:I:7:PRO:O	3:I:102:THR:HG22	2.20	0.41
2:F:103:TRP:CZ3	3:I:44:PRO:HG2	2.56	0.41
3:L:149:LYS:HB2	3:L:192:SER:HB2	2.02	0.41
3:L:184:GLN:HA	3:L:187:SER:CB	2.46	0.41
2:F:38:ARG:HA	2:F:89:THR:O	2.20	0.41
2:F:100(D):ARG:N	2:F:100(E):PRO:CD	2.84	0.41
3:L:83:GLU:HG2	3:L:105:THR:CB	2.51	0.41
1:E:294:ILE:HD11	1:E:331:CYS:HB3	2.03	0.41
2:H:171:LEU:HD21	2:H:194:VAL:HG21	2.03	0.41
1:G:264:SER:N	1:G:482:GLU:OE2	2.45	0.41
2:H:137:ALA:HB3	2:H:226:LYS:CE	2.50	0.41
3:L:166:LYS:HG2	3:L:167:GLN:N	2.36	0.41
1:E:298:ARG:NH1	1:E:326:ILE:HB	2.36	0.41
2:F:52:ASP:HB3	2:F:52(A):PRO:HD2	2.02	0.41
2:F:14:PRO:HG3	2:F:111:VAL:CG1	2.50	0.41
3:I:186:LYS:HG2	3:I:208:PRO:HG2	2.03	0.41
1:E:462:ASN:O	1:E:464:SER:N	2.53	0.41
3:I:130:ALA:N	3:I:180:LEU:O	2.54	0.41
2:F:11:VAL:HG23	2:F:110:THR:CG2	2.50	0.41
1:G:118:PRO:HB2	1:G:434:MET:O	2.20	0.41
2:F:21:SER:HA	2:F:78:LEU:O	2.20	0.41
1:G:353:PHE:O	1:G:357:LYS:HB2	2.20	0.41
3:I:128:ASN:HA	3:I:182:PRO:HG2	2.02	0.41
2:H:109:PRO:HB2	2:H:111:MET:HE2	2.02	0.41
1:G:254:VAL:HG13	4:G:502:NAG:C8	2.48	0.41
2:H:34:ILE:HG21	2:H:96:CYS:HB2	2.03	0.41
3:L:95(A):SER:HA	3:L:95(B):ILE:HA	1.80	0.41
2:H:150:LEU:HD12	2:H:151:GLY:N	2.35	0.41
3:I:49:LEU:HG	3:I:55:PRO:HG3	2.03	0.41
3:L:16:GLY:CA	3:L:78:LEU:HB3	2.51	0.41
1:G:119:CYS:O	1:G:203:GLN:N	2.54	0.41
2:F:145:TYR:CE2	2:F:176:TYR:HB3	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:45:PHE:HE1	3:I:87:PHE:CG	2.39	0.41
1:G:108:VAL:HG12	1:G:112:TRP:CD1	2.56	0.41
1:G:102:GLU:O	1:G:106:GLU:HG3	2.20	0.41
2:F:126:PRO:HG2	2:F:213:PRO:HB3	2.03	0.41
1:G:362:GLN:HG3	1:G:467:THR:HG21	2.01	0.41
3:I:28:VAL:HG22	3:I:31:ASN:ND2	2.36	0.41
2:H:64:PHE:HB2	2:H:68:LEU:HB2	2.03	0.41
1:G:111:LEU:O	1:G:115:SER:N	2.54	0.41
4:G:504:NAG:O7	4:G:504:NAG:O3	2.33	0.41
2:H:97:ALA:HB1	2:H:112:PHE:HB3	2.02	0.41
2:H:182:LEU:CB	2:H:188:TYR:CD1	3.04	0.40
2:H:136:LEU:HD21	2:H:153:LEU:HB2	2.02	0.40
1:E:283:THR:HG1	1:E:473:GLY:H	1.59	0.40
2:H:40:LYS:O	2:H:42:GLY:N	2.54	0.40
3:L:91:TYR:CG	3:L:92:ASP:N	2.89	0.40
1:E:368:ASP:O	1:E:371:ILE:HG12	2.21	0.40
2:H:4:LEU:HD12	2:H:114:HIS:HB3	2.02	0.40
3:I:188:HIS:ND1	3:I:191:TYR:OH	2.45	0.40
3:L:80:PRO:O	3:L:83:GLU:N	2.50	0.40
1:G:256:SER:H	1:G:475:ILE:CD1	2.34	0.40
1:E:120:VAL:O	1:E:434:MET:N	2.53	0.40
1:E:72:HIS:CE1	1:E:73:ALA:HB2	2.56	0.40
2:H:4:LEU:CD2	2:H:24:ALA:HB2	2.51	0.40
3:I:31:ASN:HB2	3:I:91:TYR:CZ	2.56	0.40
3:I:129:LYS:HA	3:I:182:PRO:HD3	2.03	0.40
1:E:392:ASN:HB3	1:E:395:CYS:HB2	2.01	0.40
3:I:149:LYS:HB2	3:I:192:SER:HB2	2.02	0.40
2:H:102:ALA:HA	2:H:108:ARG:HA	2.02	0.40
1:G:229:ASN:ND2	4:G:501:NAG:H82	2.35	0.40
3:I:49:LEU:HD21	3:I:55:PRO:HG2	2.02	0.40
3:I:185:TRP:CZ3	3:I:206:VAL:HB	2.56	0.40
3:I:37:ARG:CD	3:I:47:LEU:HD21	2.51	0.40
2:H:138:PRO:HD2	2:H:225:PRO:CD	2.51	0.40
2:F:124:LEU:HD13	3:I:120:PRO:HA	2.03	0.40
3:L:117:LEU:HD12	3:L:118:PHE:N	2.36	0.40
1:G:407:MET:HG2	1:G:408:LYS:N	2.36	0.40
3:L:178:LEU:HD12	3:L:179:SER:H	1.85	0.40
2:H:156:ASP:CB	2:H:187:LEU:HD13	2.52	0.40
2:H:94:TYR:CE1	2:H:121:VAL:HG21	2.57	0.40
1:E:67:ASN:HA	1:E:213:ILE:CD1	2.52	0.40
2:F:85:ASP:N	2:F:85:ASP:OD1	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:227:LYS:HA	1:G:485:LYS:O	2.21	0.40
2:H:37:VAL:HA	2:H:46:GLU:O	2.22	0.40
3:I:6:GLN:HE22	3:I:87:PHE:HA	1.86	0.40

All (24) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:63:LYS:C	3:L:152:SER:OG[2_656]	1.03	1.17
2:H:63:LYS:HA	3:L:152:SER:HG[2_656]	0.62	0.98
2:H:140:SER:HB2	2:H:182:LEU:HD12[2_646]	0.90	0.70
2:H:63:LYS:O	3:L:152:SER:OG[2_656]	1.62	0.58
2:H:63:LYS:CA	3:L:152:SER:HG[2_656]	1.06	0.54
2:H:63:LYS:HA	3:L:152:SER:OG[2_656]	1.21	0.39
2:H:140:SER:HB2	2:H:182:LEU:CD1[2_646]	1.21	0.39
2:H:63:LYS:O	3:L:152:SER:CB[2_656]	1.84	0.36
2:H:140:SER:CB	2:H:182:LEU:HD12[2_646]	1.28	0.32
2:H:140:SER:HG	2:H:182:LEU:O[2_646]	1.32	0.28
2:H:63:LYS:C	3:L:152:SER:CB[2_656]	1.95	0.25
2:H:155:LYS:NZ	2:H:201:LEU:O[2_656]	1.96	0.24
2:H:38:ARG:NH2	3:L:189:LYS:O[2_656]	1.98	0.22
2:H:205:THR:O	3:L:179:SER:HG[2_646]	1.41	0.19
2:H:140:SER:CB	2:H:182:LEU:CD1[2_646]	2.03	0.17
2:H:205:THR:O	3:L:179:SER:OG[2_646]	2.07	0.13
2:H:64:PHE:N	3:L:152:SER:OG[2_656]	2.08	0.12
3:L:53:GLN:OE1	3:L:168:SER:OG[2_556]	2.09	0.11
2:H:63:LYS:O	3:L:152:SER:HB3[2_656]	1.53	0.07
2:H:205:THR:OG1	3:L:158:GLY:O[2_646]	2.14	0.06
2:H:140:SER:OG	2:H:182:LEU:O[2_646]	2.15	0.05
1:G:46:LYS:HZ2	3:L:196:THR:OG1[2_556]	1.56	0.04
2:H:209:ASN:HD21	3:L:156:LYS:O[2_646]	1.58	0.02
2:H:90:ASP:OD1	3:L:207:ALA:H[2_656]	1.58	0.02

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	E	343/353 (97%)	323 (94%)	18 (5%)	2 (1%)	30	71
1	G	343/353 (97%)	325 (95%)	15 (4%)	3 (1%)	21	63
2	F	217/227 (96%)	184 (85%)	31 (14%)	2 (1%)	21	63
2	H	219/227 (96%)	180 (82%)	35 (16%)	4 (2%)	11	47
3	I	196/215 (91%)	171 (87%)	21 (11%)	4 (2%)	9	45
3	L	205/215 (95%)	172 (84%)	29 (14%)	4 (2%)	9	45
All	All	1523/1590 (96%)	1355 (89%)	149 (10%)	19 (1%)	16	56

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	473	GLY
2	H	55	ARG
3	L	199	GLY
1	E	473	GLY
1	G	397	GLY
3	L	15	PRO
1	E	397	GLY
2	F	170	LEU
3	I	15	PRO
3	L	111	ALA
3	I	83	GLU
3	I	55	PRO
2	H	113	ASP
3	L	55	PRO
3	I	151	ASP
1	G	124	GLY
2	F	123	PRO
2	H	41	PRO
2	H	161	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	E	309/311 (99%)	303 (98%)	6 (2%)	65	86
1	G	309/311 (99%)	303 (98%)	6 (2%)	65	86
2	F	188/194 (97%)	177 (94%)	11 (6%)	24	63
2	H	190/194 (98%)	182 (96%)	8 (4%)	36	73
3	I	165/177 (93%)	159 (96%)	6 (4%)	42	77
3	L	168/177 (95%)	163 (97%)	5 (3%)	48	80
All	All	1329/1364 (97%)	1287 (97%)	42 (3%)	46	80

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	72	HIS
1	G	289	ASN
1	G	392	ASN
1	G	394	THR
1	G	462	ASN
1	G	465	ASN
2	H	28	ASN
2	H	33	ILE
2	H	62	HIS
2	H	81	MET
2	H	89	ASP
2	H	120	LEU
2	H	128	THR
2	H	204	GLN
3	L	45	THR
3	L	104	LEU
3	L	105	THR
3	L	159	VAL
3	L	181	THR
1	E	44	VAL
1	E	72	HIS
1	E	200	VAL
1	E	394	THR
1	E	404	ASN
1	E	465	ASN
2	F	28	ASN
2	F	33	ILE
2	F	48	VAL

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Mol	Chain	Res	Type
2	F	53	TYR
2	F	61	HIS
2	F	112	SER
2	F	128	SER
2	F	146	PHE
2	F	191	THR
2	F	192	GLN
2	F	196	CYS
3	I	45	THR
3	I	46	LEU
3	I	104	LEU
3	I	105	THR
3	I	125	LEU
3	I	181	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	F	23	GLN
3	I	6	GLN

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](#)

16 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	NAG	E	501	-	14,14,15	0.22	0	15,19,21	0.81	1 (6%)
4	NAG	E	502	1	14,14,15	0.41	0	15,19,21	0.59	1 (6%)
4	NAG	E	503	1	14,14,15	0.70	1 (7%)	15,19,21	0.42	0
4	NAG	E	504	1	14,14,15	0.80	1 (7%)	15,19,21	0.78	1 (6%)
4	NAG	E	505	1	14,14,15	0.27	0	15,19,21	0.96	1 (6%)
4	NAG	E	506	1	14,14,15	0.47	0	15,19,21	0.77	0
4	NAG	E	507	1	14,14,15	0.46	0	15,19,21	0.58	0
4	NAG	E	508	1	14,14,15	0.32	0	15,19,21	0.69	1 (6%)
4	NAG	E	509	1	14,14,15	0.37	0	15,19,21	1.77	2 (13%)
4	NAG	E	510	1	14,14,15	0.39	0	15,19,21	1.18	1 (6%)
4	NAG	G	501	1	14,14,15	0.53	0	15,19,21	0.97	1 (6%)
4	NAG	G	502	1	14,14,15	0.19	0	15,19,21	1.04	1 (6%)
4	NAG	G	503	1	14,14,15	0.67	1 (7%)	15,19,21	0.93	1 (6%)
4	NAG	G	504	1	14,14,15	0.47	0	15,19,21	0.33	0
4	NAG	G	505	1	14,14,15	0.49	0	15,19,21	0.48	0
4	NAG	G	506	1	14,14,15	0.45	0	15,19,21	0.70	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
4	NAG	E	501	-	-	0/6/23/26	0/1/1/1
4	NAG	E	502	1	-	0/6/23/26	0/1/1/1
4	NAG	E	503	1	-	0/6/23/26	0/1/1/1
4	NAG	E	504	1	-	0/6/23/26	0/1/1/1
4	NAG	E	505	1	-	0/6/23/26	0/1/1/1
4	NAG	E	506	1	-	0/6/23/26	0/1/1/1
4	NAG	E	507	1	-	0/6/23/26	0/1/1/1
4	NAG	E	508	1	-	0/6/23/26	0/1/1/1
4	NAG	E	509	1	-	0/6/23/26	0/1/1/1
4	NAG	E	510	1	-	0/6/23/26	0/1/1/1
4	NAG	G	501	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	G	502	1	-	0/6/23/26	0/1/1/1
4	NAG	G	503	1	-	0/6/23/26	0/1/1/1
4	NAG	G	504	1	-	0/6/23/26	0/1/1/1
4	NAG	G	505	1	-	0/6/23/26	0/1/1/1
4	NAG	G	506	1	-	0/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	503	NAG	O5-C1	2.12	1.47	1.43
4	E	503	NAG	C1-C2	2.28	1.55	1.52
4	E	504	NAG	C1-C2	2.88	1.56	1.52

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	504	NAG	C1-O5-C5	2.11	114.92	112.25
4	E	502	NAG	C1-O5-C5	2.14	114.96	112.25
4	E	508	NAG	C1-O5-C5	2.33	115.21	112.25
4	E	501	NAG	C1-O5-C5	2.94	115.98	112.25
4	E	505	NAG	C1-O5-C5	3.42	116.59	112.25
4	G	503	NAG	C1-O5-C5	3.52	116.72	112.25
4	G	501	NAG	C1-O5-C5	3.66	116.90	112.25
4	G	502	NAG	C1-O5-C5	3.74	116.99	112.25
4	E	510	NAG	C2-N2-C7	3.97	128.15	123.04
4	E	509	NAG	C2-N2-C7	4.35	128.63	123.04
4	E	509	NAG	C1-O5-C5	4.83	118.38	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	503	NAG	3	0
4	E	504	NAG	3	0
4	E	508	NAG	1	0
4	E	509	NAG	2	0
4	E	510	NAG	2	0
4	G	501	NAG	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	G	502	NAG	4	0
4	G	504	NAG	1	0
4	G	506	NAG	4	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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	E	347/353 (98%)	0.50	40 (11%) 6 7	71, 165, 396, 660	0
1	G	347/353 (98%)	0.38	39 (11%) 7 7	66, 154, 341, 695	0
2	F	221/227 (97%)	1.16	44 (19%) 1 2	94, 191, 520, 722	0
2	H	223/227 (98%)	0.51	33 (14%) 3 3	75, 173, 465, 632	0
3	I	200/215 (93%)	0.72	35 (17%) 2 2	91, 177, 486, 709	0
3	L	209/215 (97%)	1.18	48 (22%) 1 1	91, 183, 587, 723	0
All	All	1547/1590 (97%)	0.69	239 (15%) 3 3	66, 170, 481, 723	0

All (239) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	184	VAL	21.8
1	G	283	THR	21.7
2	F	182	VAL	19.8
3	L	97	LEU	18.4
3	I	134	CYS	16.6
3	L	116	THR	15.6
1	E	48	ALA	15.3
3	L	98	PHE	13.5
1	G	285	ILE	13.2
1	G	284	ILE	13.0
3	L	195	VAL	12.8
3	L	115	VAL	12.5
2	F	138	LEU	12.4
3	L	2	SER	12.2
2	F	181	VAL	11.9
3	L	144	VAL	11.4
3	L	197	HIS	11.3
3	L	140	TYR	11.1
1	G	273	ARG	11.1

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Mol	Chain	Res	Type	RSRZ
3	I	89	ALA	10.8
1	G	387	THR	10.4
2	H	157	TYR	10.4
3	I	135	LEU	10.4
1	G	272	ILE	10.3
2	F	7	SER	10.1
3	L	46	LEU	10.1
2	H	58	PRO	10.0
3	I	133	VAL	10.0
1	E	49	ASP	9.9
2	F	100(E)	PRO	9.8
2	F	52(A)	PRO	9.7
1	G	455	THR	9.6
1	G	367	GLY	9.4
2	F	163	VAL	9.0
3	I	143	ALA	9.0
3	I	92	ASP	8.9
1	E	489	VAL	8.8
2	H	195	THR	8.7
1	E	260	LEU	8.6
1	E	251	ILE	8.6
2	F	194	TYR	8.6
1	G	458	GLY	8.5
3	I	65	SER	8.4
1	E	215	ILE	8.4
1	E	422	GLN	8.2
2	F	53	TYR	8.2
3	L	173	ALA	8.1
2	H	221	LYS	7.7
2	F	100(G)	MET	7.7
1	E	72	HIS	7.5
1	G	271	ILE	7.5
1	E	272	ILE	7.5
1	E	436	ALA	7.5
3	L	137	SER	7.5
3	L	3	ALA	7.5
3	I	68	GLY	7.4
1	E	250	GLY	7.4
2	H	196	VAL	7.4
2	F	167	PRO	7.3
2	F	110	THR	7.3
3	L	47	LEU	7.2

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Mol	Chain	Res	Type	RSRZ
3	L	65	SER	7.1
2	H	35	HIS	7.1
3	L	139	PHE	7.1
2	F	20	LEU	6.9
1	E	420	ILE	6.8
3	L	180	LEU	6.8
2	F	36	TRP	6.7
3	L	20	THR	6.7
1	E	385	CYS	6.7
2	H	9	THR	6.5
3	I	8	PRO	6.5
1	E	423	ILE	6.5
3	L	190	SER	6.4
2	H	159	PRO	6.2
1	E	461	ASN	6.2
3	L	45	THR	6.1
2	F	8	GLY	6.1
3	I	60	ASP	6.1
2	H	185	SER	6.0
1	G	479	TRP	5.9
1	G	333	ILE	5.7
2	F	100(D)	ARG	5.7
1	E	472	GLY	5.6
2	F	80	MET	5.5
2	F	166	PHE	5.4
1	E	384	TYR	5.4
2	H	133	VAL	5.4
2	H	10	ALA	5.4
2	F	6	GLN	5.4
2	F	137	ALA	5.3
1	E	490	GLN	5.3
1	E	488	VAL	5.2
3	L	66	LYS	5.2
3	L	74	ALA	5.2
2	F	58	TRP	5.2
1	E	90	THR	5.1
3	I	90	THR	5.1
3	L	196	THR	5.1
1	G	301	ASN	5.1
1	G	274	SER	5.1
1	G	335	GLY	5.0
3	I	182	PRO	5.0

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Mol	Chain	Res	Type	RSRZ
3	L	191	TYR	5.0
1	E	459	GLY	5.0
2	H	82	THR	4.9
1	E	463	THR	4.9
3	I	15	PRO	4.9
3	I	166	LYS	4.8
2	F	39	GLN	4.8
3	I	157	ALA	4.7
1	E	121	LYS	4.7
2	H	222	LYS	4.7
3	L	112	ALA	4.6
2	H	11	VAL	4.6
3	L	111	ALA	4.5
1	G	474	ASN	4.5
2	H	173	SER	4.5
3	I	47	LEU	4.5
3	I	159	VAL	4.5
3	I	198	GLU	4.5
2	H	117	GLN	4.4
3	I	67	SER	4.3
3	L	99	GLY	4.3
3	I	105	THR	4.2
3	I	66	LYS	4.2
2	F	160	THR	4.1
3	I	183	GLU	4.1
2	H	141	LYS	4.1
2	H	206	TYR	4.1
1	E	421	LYS	4.1
3	L	93	SER	4.1
2	H	109	PRO	4.1
3	L	28	VAL	4.0
3	I	199	GLY	4.0
3	I	24	SER	4.0
2	H	106	HIS	4.0
2	F	59	SER	3.9
1	E	47	ASP	3.8
1	G	69	TRP	3.8
3	I	142	GLY	3.8
2	H	18	VAL	3.8
2	F	37	VAL	3.7
3	L	145	THR	3.7
1	G	55	ALA	3.7

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Mol	Chain	Res	Type	RSRZ
3	L	135	LEU	3.7
1	E	390	LEU	3.7
2	F	183	THR	3.6
3	L	30	GLY	3.6
2	F	100(A)	SER	3.6
2	F	94	ARG	3.5
1	E	408	LYS	3.5
1	G	121	LYS	3.5
1	E	249	HIS	3.4
1	E	492	GLU	3.4
2	H	131	PRO	3.4
2	H	199	SER	3.4
2	F	168	ALA	3.4
2	H	211	ASN	3.4
2	F	24	ALA	3.4
3	I	103	ALA	3.4
3	L	151	ASP	3.3
2	H	43	LEU	3.3
2	H	105	SER	3.3
3	L	58	VAL	3.3
2	F	44	GLY	3.3
1	G	252	LYS	3.2
1	G	282	LYS	3.2
2	F	100(F)	ILE	3.1
3	I	204	LYS	3.1
3	L	157	ALA	3.1
3	L	143	ALA	3.0
2	H	152	CYS	3.0
3	I	95(B)	ILE	3.0
1	G	240	LYS	3.0
1	G	90	THR	2.9
3	I	165	SER	2.9
2	F	129	LYS	2.9
3	I	19	VAL	2.9
1	G	425	ASN	2.9
2	F	22	CYS	2.9
3	I	95	GLY	2.9
1	G	85	HIS	2.9
1	G	277	LEU	2.8
3	I	175	SER	2.8
2	H	188	TYR	2.8
3	I	148	TRP	2.8

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Mol	Chain	Res	Type	RSRZ
3	L	19	VAL	2.8
1	G	386	ASN	2.8
3	L	174	ALA	2.8
1	G	473	GLY	2.7
1	G	248	THR	2.7
2	H	213	LYS	2.6
2	F	136	ALA	2.6
2	H	56	GLY	2.6
2	F	93	ALA	2.6
3	L	50	ARG	2.6
2	F	78	LEU	2.6
1	E	291	SER	2.5
1	G	484	TYR	2.5
3	L	94	ASP	2.5
2	F	102	HIS	2.5
1	G	63	THR	2.5
2	H	95	PHE	2.4
2	F	148	GLU	2.4
3	L	70	SER	2.4
3	I	192	SER	2.3
1	E	50	THR	2.3
1	E	466	GLU	2.3
1	G	251	ILE	2.3
1	E	460	ALA	2.3
1	E	233	PHE	2.3
1	E	363	PRO	2.3
1	G	416	LEU	2.3
1	G	232	ASN	2.2
3	L	29	GLY	2.2
3	L	155	VAL	2.2
1	G	459	GLY	2.2
1	G	488	VAL	2.2
3	L	128	ASN	2.2
1	G	347	GLU	2.2
3	L	96	ARG	2.2
2	F	169	VAL	2.2
1	E	262	ASN	2.1
1	G	220	PRO	2.1
3	L	138	ASP	2.1
3	L	90	THR	2.1
2	F	161	SER	2.1
2	F	65	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
2	F	178	LEU	2.1
1	E	217	TYR	2.1
3	I	181	THR	2.1
2	H	44	GLY	2.0
2	H	101	ALA	2.0
1	G	417	PRO	2.0
3	L	198	GLU	2.0
1	E	338	TRP	2.0
1	E	449	ILE	2.0
1	E	361	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	NAG	G	502	14/15	0.83	0.25	0.31	81,133,246,246	0
4	NAG	G	506	14/15	0.95	0.21	0.29	96,186,232,279	0
4	NAG	G	501	14/15	0.79	0.28	0.27	98,157,226,334	0
4	NAG	G	504	14/15	0.89	0.22	0.11	98,144,250,250	0
4	NAG	E	508	14/15	0.83	0.21	0.05	97,126,157,181	0
4	NAG	E	501	14/15	0.92	0.24	0.02	71,103,199,199	0
4	NAG	G	503	14/15	0.90	0.28	-0.06	100,140,214,237	0
4	NAG	E	510	14/15	0.78	0.20	-0.16	74,153,204,223	0
4	NAG	E	507	14/15	0.89	0.17	-0.18	88,116,149,179	0
4	NAG	E	505	14/15	0.79	0.16	-0.49	117,155,206,210	0
4	NAG	E	502	14/15	0.93	0.18	-0.54	94,127,225,267	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	NAG	E	506	14/15	0.92	0.18	-0.60	117,150,180,183	0
4	NAG	G	505	14/15	0.89	0.13	-0.66	84,139,189,227	0
4	NAG	E	504	14/15	0.80	0.14	-0.69	98,148,184,193	0
4	NAG	E	509	14/15	0.92	0.15	-0.72	57,73,118,127	0
4	NAG	E	503	14/15	0.94	0.14	-	73,114,157,193	0

6.5 Other polymers [i](#)

There are no such residues in this entry.