



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 04:34 PM UTC

PDB ID : 2J42 / pdb_00002j42
Title : low quality crystal structure of the transport component C2-II of the C2-toxin from Clostridium botulinum
Authors : Schleberger, C.; Hochmann, H.; Barth, H.; Aktories, K.; Schulz, G.E.
Deposited on : 2006-08-24
Resolution : 3.13 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

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

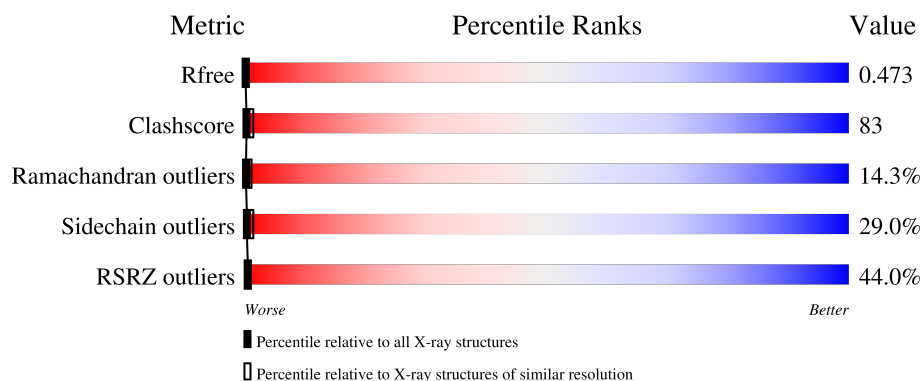
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.13 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}	180053	2351 (3.18-3.10)
Clashscore	190562	2452 (3.18-3.10)
Ramachandran outliers	187476	2324 (3.18-3.10)
Sidechain outliers	187428	2324 (3.18-3.10)
RSRZ outliers	180081	2351 (3.18-3.10)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 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	721	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3948 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 C2 TOXIN COMPONENT-II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	505	3948	2493	654	786	15	0	0	1

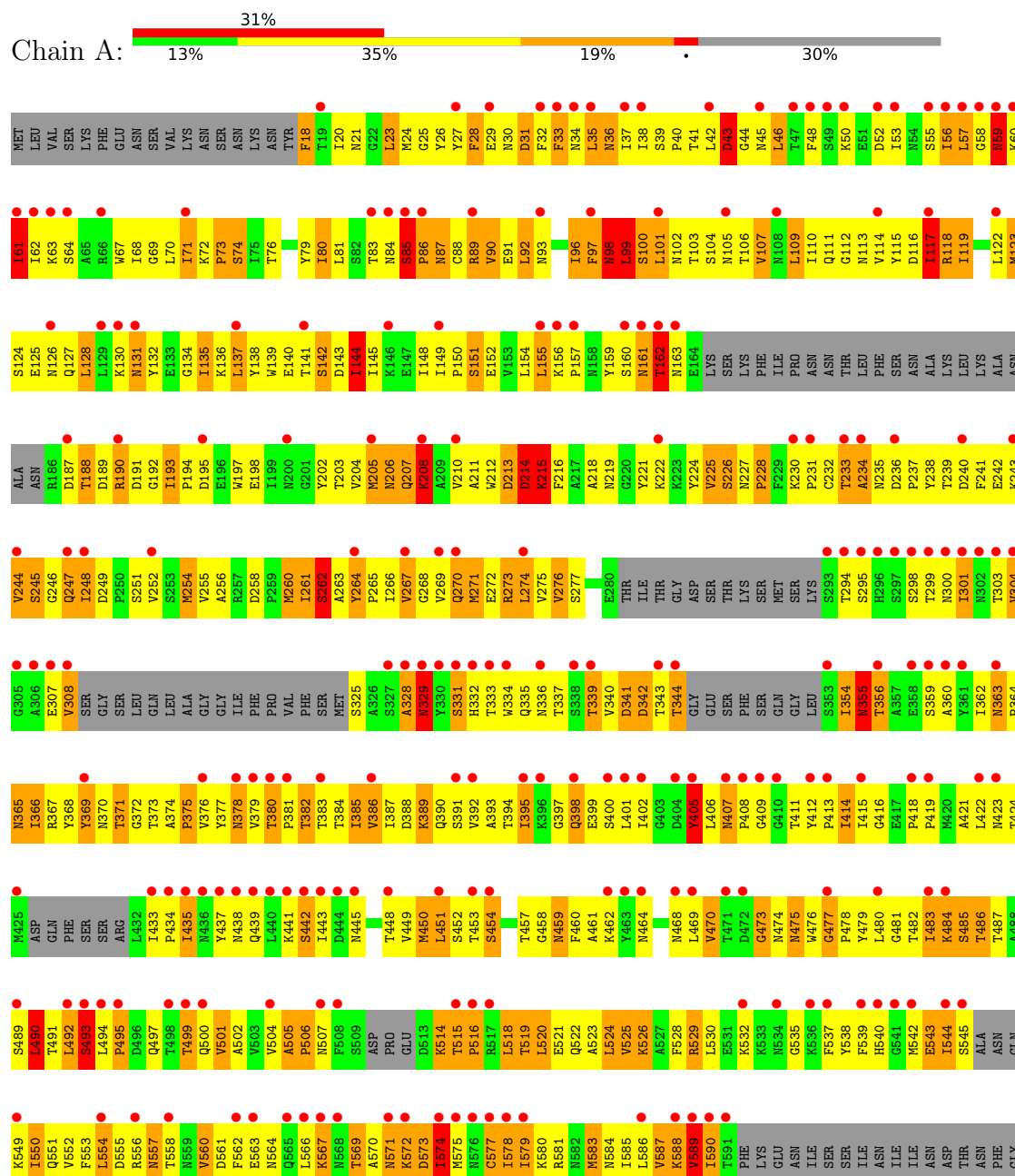
There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	357	ALA	GLY	conflict	UNP O86171
A	494	LEU	PHE	conflict	UNP O86171
A	495	PRO	SER	conflict	UNP O86171
A	496	ASP	GLY	conflict	UNP O86171
A	517	ARG	LYS	conflict	UNP O86171
A	529	ARG	ALA	conflict	UNP O86171
A	542	MET	LEU	conflict	UNP O86171
A	556	ARG	SER	conflict	UNP O86171
A	560	VAL	ASN	conflict	UNP O86171
A	571	ASN	ASP	conflict	UNP O86171
A	576	ASN	HIS	conflict	UNP O86171

3 Residue-property plots

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

• Molecule 1: C2 TOXIN COMPONENT-II



VAL	GLU	SER	MET	THR	GLY	LEU	SER	LYS	ARG	ILE	TYR	LYS	GLY	ASN	ASP	GLY	ILE	TYR	ARG	ALA	SER	THR	LYS	SER	PHE	SER	PHE	PHE	LYS	SER	SER	LYS	GLU	ILE	LYS	TYR	PRO	GLU	GLY	PHE	PHE	TYR	ARG	MET	ARG	PHE	VAL	ILE	GLN	SER	TYR	GLU	PRO	PHE	THR	CYS	ASN	PHE	LYS	LEU	PHE	ASN	ASN
LEU	ILE	TYR	SER	ASN	SER	PHE	ASP	ILE	GLY	TYR	TYR	ASP	GLU	PHE	PHE	TYR	PHE	TYR	CYS	ASN	GLY	SER	LYS	SER	PHE	PHE	ASP	ILE	ILE	SER	SER	CYS	ASP	ILE	ILE	ASN	ASN	ARG	LEU	SER	GLY	VAL	PHE	PHE	LEU	ILE	GLN	SER	GLU	LEU	ASP	LYS	LEU	ILE	ILE								

4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	104.40Å 104.40Å 153.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 3.13 30.00 – 3.13	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-3.13) 99.5 (30.00-3.13)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.99 (at 3.13Å)	Xtriage
Refinement program	TNT BUSTER/TNT	Depositor
R, R_{free}	0.413 , 0.433 0.447 , 0.473	Depositor DCC
R_{free} test set	775 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	84.0	Xtriage
Anisotropy	0.159	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 54.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.64	EDS
Total number of atoms	3948	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.68% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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	0.32	1/4019 (0.0%)	0.81	4/5461 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	590	ILE	C-N	-5.70	1.25	1.33

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	85	SER	C-N-CD	-19.14	46.52	125.00
1	A	395	ILE	N-CA-C	6.03	112.66	106.21
1	A	374	ALA	C-N-CD	-5.31	103.23	125.00
1	A	97	PHE	N-CA-C	5.13	115.31	108.23

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3948	0	3888	652	0
All	All	3948	0	3888	652	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 83.

All (652) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:83:THR:HG23	1:A:98:ASN:HD21	1.10	1.16
1:A:586:LEU:HD21	1:A:588:LYS:HE2	1.31	1.11
1:A:507:ASN:HB2	1:A:581:ARG:HD2	1.36	1.08
1:A:461:ALA:HB1	1:A:470:VAL:HG13	1.36	1.07
1:A:528:PHE:HB2	1:A:530:LEU:HD11	1.38	1.04
1:A:337:THR:HG22	1:A:339:THR:HG23	1.38	1.02
1:A:414:ILE:HG23	1:A:416:GLY:H	1.21	1.02
1:A:70:LEU:HD13	1:A:114:VAL:HG11	1.41	1.01
1:A:543:GLU:HB2	1:A:549:LYS:HE3	1.44	1.00
1:A:267:VAL:HG12	1:A:268:GLY:H	1.28	0.99
1:A:554:LEU:HD23	1:A:585:ILE:HG12	1.44	0.99
1:A:386:VAL:HG13	1:A:391:SER:HA	1.43	0.98
1:A:492:LEU:HD13	1:A:587:VAL:HG12	1.45	0.98
1:A:379:VAL:HB	1:A:458:GLY:N	1.79	0.98
1:A:236:ASP:HB2	1:A:237:PRO:HD2	1.46	0.98
1:A:379:VAL:H	1:A:458:GLY:HA3	1.26	0.97
1:A:271:MET:HE1	1:A:274:LEU:HB3	1.46	0.97
1:A:204:VAL:HG12	1:A:208:LYS:HG2	1.47	0.96
1:A:23:LEU:HG	1:A:154:LEU:HD22	1.47	0.95
1:A:586:LEU:HD12	1:A:587:VAL:H	1.30	0.95
1:A:28:PHE:HD2	1:A:35:LEU:H	1.15	0.94
1:A:274:LEU:HD23	1:A:274:LEU:H	1.33	0.93
1:A:580:LYS:H	1:A:583:MET:HE3	1.32	0.92
1:A:298:SER:HB2	1:A:334:TRP:CZ2	2.04	0.92
1:A:328:ALA:HB3	1:A:484:LYS:HE2	1.52	0.92
1:A:335:GLN:HG2	1:A:336:ASN:H	1.33	0.92
1:A:462:LYS:HE3	1:A:473:GLY:HA3	1.51	0.91
1:A:260:MET:HE1	1:A:526:LYS:NZ	1.87	0.90
1:A:30:ASN:HB2	1:A:34:ASN:HD22	1.38	0.89
1:A:53:ILE:HD11	1:A:130:LYS:HG2	1.55	0.89
1:A:238:TYR:CD2	1:A:248:ILE:HD11	2.09	0.88
1:A:29:GLU:HB2	1:A:36:ASN:ND2	1.89	0.88
1:A:580:LYS:N	1:A:583:MET:HE3	1.89	0.87
1:A:366:ILE:HD13	1:A:422:LEU:HD21	1.54	0.87
1:A:71:ILE:HD11	1:A:92:LEU:HD21	1.56	0.87
1:A:83:THR:HG23	1:A:98:ASN:ND2	1.91	0.86
1:A:23:LEU:CG	1:A:154:LEU:HD22	2.05	0.86
1:A:586:LEU:HD21	1:A:588:LYS:CE	2.04	0.86
1:A:461:ALA:HB1	1:A:470:VAL:CG1	2.06	0.86
1:A:354:ILE:HD12	1:A:437:TYR:HE1	1.40	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:23:LEU:HD11	1:A:117:ILE:HD12	1.58	0.85
1:A:70:LEU:HD22	1:A:114:VAL:HG12	1.56	0.85
1:A:363:ASN:ND2	1:A:423:ASN:HB2	1.91	0.85
1:A:334:TRP:CD1	1:A:449:VAL:HG22	2.12	0.85
1:A:494:LEU:HD23	1:A:589:VAL:HG21	1.59	0.84
1:A:386:VAL:HG13	1:A:391:SER:CA	2.08	0.83
1:A:529:ARG:HH21	1:A:529:ARG:HG3	1.43	0.83
1:A:70:LEU:HB2	1:A:155:LEU:HG	1.61	0.82
1:A:276:VAL:HG13	1:A:362:ILE:HB	1.60	0.82
1:A:276:VAL:HG13	1:A:362:ILE:CB	2.10	0.82
1:A:72:LYS:HB3	1:A:114:VAL:HG22	1.62	0.81
1:A:387:ILE:CD1	1:A:449:VAL:HG12	2.10	0.81
1:A:136:LYS:HE2	1:A:148:ILE:HD11	1.60	0.81
1:A:343:THR:HG23	1:A:344:THR:HG22	1.61	0.81
1:A:365:ASN:HA	1:A:421:ALA:HA	1.60	0.81
1:A:125:GLU:HB3	1:A:127:GLN:NE2	1.96	0.81
1:A:79:TYR:CD1	1:A:109:LEU:HB2	2.16	0.81
1:A:234:ALA:HB1	1:A:262:SER:HA	1.62	0.81
1:A:558:THR:HA	1:A:561:ASP:HB2	1.63	0.81
1:A:71:ILE:CD1	1:A:92:LEU:HD21	2.11	0.80
1:A:276:VAL:HG13	1:A:362:ILE:CG1	2.11	0.80
1:A:563:GLU:O	1:A:567:LYS:HB2	1.81	0.80
1:A:26:TYR:CD2	1:A:38:ILE:HG12	2.17	0.79
1:A:265:PRO:HD3	1:A:476:TRP:CH2	2.17	0.79
1:A:407:ASN:N	1:A:407:ASN:ND2	2.29	0.79
1:A:407:ASN:ND2	1:A:407:ASN:H	1.79	0.79
1:A:117:ILE:HG22	1:A:118:ARG:H	1.47	0.79
1:A:79:TYR:HD1	1:A:109:LEU:HB2	1.46	0.78
1:A:407:ASN:N	1:A:407:ASN:HD22	1.82	0.78
1:A:530:LEU:HD22	1:A:537:PHE:CZ	2.18	0.78
1:A:232:CYS:SG	1:A:239:THR:HA	2.23	0.78
1:A:387:ILE:HD11	1:A:449:VAL:HG12	1.66	0.78
1:A:328:ALA:HB3	1:A:484:LYS:CE	2.12	0.78
1:A:328:ALA:HB3	1:A:484:LYS:CD	2.13	0.77
1:A:328:ALA:HB3	1:A:484:LYS:HD3	1.66	0.77
1:A:38:ILE:HB	1:A:208:LYS:NZ	1.99	0.77
1:A:86:PRO:HB3	1:A:123:MET:SD	2.24	0.77
1:A:411:THR:OG1	1:A:414:ILE:HA	1.85	0.76
1:A:232:CYS:SG	1:A:239:THR:HG22	2.24	0.76
1:A:80:ILE:HG13	1:A:140:GLU:O	1.84	0.76
1:A:493:SER:HA	1:A:497:GLN:O	1.85	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:335:GLN:HG2	1:A:336:ASN:N	2.01	0.76
1:A:439:GLN:O	1:A:443:ILE:HG13	1.85	0.76
1:A:494:LEU:HD13	1:A:539:PHE:CD2	2.20	0.76
1:A:269:VAL:HG11	1:A:366:ILE:HD12	1.66	0.76
1:A:225:VAL:HG23	1:A:260:MET:HE3	1.68	0.75
1:A:379:VAL:N	1:A:458:GLY:HA3	1.99	0.75
1:A:67:TRP:CH2	1:A:135:ILE:HG21	2.21	0.75
1:A:414:ILE:HG23	1:A:416:GLY:N	1.99	0.75
1:A:155:LEU:HD13	1:A:468:ASN:OD1	1.87	0.75
1:A:459:ASN:HD22	1:A:459:ASN:N	1.84	0.75
1:A:149:ILE:HG21	1:A:154:LEU:HG	1.69	0.75
1:A:24:MET:HE3	1:A:247:GLN:NE2	2.01	0.75
1:A:379:VAL:HB	1:A:458:GLY:CA	2.17	0.75
1:A:492:LEU:HD13	1:A:587:VAL:CG1	2.15	0.75
1:A:125:GLU:HB3	1:A:127:GLN:HE21	1.51	0.74
1:A:386:VAL:C	1:A:387:ILE:HD13	2.12	0.74
1:A:380:THR:HB	1:A:397:GLY:HA3	1.70	0.74
1:A:224:TYR:CE2	1:A:244:VAL:HB	2.23	0.74
1:A:386:VAL:O	1:A:387:ILE:HD13	1.86	0.73
1:A:128:LEU:HB2	1:A:131:ASN:OD1	1.88	0.73
1:A:271:MET:HB3	1:A:334:TRP:CZ3	2.24	0.73
1:A:71:ILE:HG23	1:A:117:ILE:HD11	1.70	0.73
1:A:28:PHE:CD2	1:A:33:PHE:HA	2.23	0.73
1:A:543:GLU:HB2	1:A:549:LYS:CE	2.16	0.73
1:A:204:VAL:HG11	1:A:244:VAL:CG2	2.18	0.73
1:A:520:LEU:HB3	1:A:577:CYS:HB2	1.71	0.72
1:A:494:LEU:CD2	1:A:589:VAL:HG21	2.19	0.72
1:A:57:LEU:HG	1:A:58:GLY:H	1.53	0.72
1:A:99:LEU:N	1:A:99:LEU:HD13	2.05	0.72
1:A:76:THR:OG1	1:A:110:ILE:HG23	1.90	0.72
1:A:110:ILE:HB	1:A:113:ASN:HD22	1.54	0.72
1:A:494:LEU:HB2	1:A:495:PRO:HD3	1.70	0.72
1:A:256:ALA:HB2	1:A:373:THR:HB	1.71	0.71
1:A:354:ILE:HD12	1:A:437:TYR:CE1	2.24	0.71
1:A:532:LYS:HE3	1:A:535:GLY:HA2	1.72	0.71
1:A:44:GLY:HA3	1:A:148:ILE:HG23	1.72	0.71
1:A:519:THR:CG2	1:A:578:ILE:HD12	2.21	0.71
1:A:252:VAL:CG1	1:A:256:ALA:HB3	2.20	0.71
1:A:337:THR:CG2	1:A:339:THR:HG23	2.20	0.70
1:A:492:LEU:CG	1:A:493:SER:H	2.04	0.70
1:A:70:LEU:HB3	1:A:114:VAL:CG1	2.20	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:393:ALA:HB2	1:A:433:ILE:HG12	1.72	0.70
1:A:90:VAL:CG2	1:A:98:ASN:HB2	2.21	0.70
1:A:343:THR:HG23	1:A:344:THR:CG2	2.20	0.70
1:A:155:LEU:HD12	1:A:156:LYS:O	1.92	0.70
1:A:519:THR:HA	1:A:578:ILE:HA	1.72	0.70
1:A:53:ILE:CD1	1:A:130:LYS:HG2	2.22	0.69
1:A:98:ASN:C	1:A:99:LEU:HD22	2.16	0.69
1:A:492:LEU:CD1	1:A:587:VAL:HG12	2.20	0.69
1:A:50:LYS:HG2	1:A:132:TYR:CE2	2.27	0.69
1:A:373:THR:CG2	1:A:501:VAL:HG22	2.23	0.69
1:A:202:TYR:O	1:A:224:TYR:HB2	1.91	0.69
1:A:71:ILE:O	1:A:114:VAL:HA	1.91	0.69
1:A:385:ILE:HD11	1:A:395:ILE:CD1	2.23	0.69
1:A:109:LEU:HD23	1:A:115:TYR:CD2	2.27	0.69
1:A:518:LEU:O	1:A:578:ILE:HG13	1.93	0.69
1:A:29:GLU:O	1:A:63:LYS:HG3	1.93	0.69
1:A:383:THR:HG21	1:A:451:LEU:HD23	1.76	0.68
1:A:266:ILE:CD1	1:A:372:GLY:HA2	2.24	0.68
1:A:204:VAL:HG11	1:A:244:VAL:HG23	1.74	0.68
1:A:30:ASN:CB	1:A:34:ASN:HD22	2.06	0.68
1:A:248:ILE:HG23	1:A:249:ASP:N	2.07	0.68
1:A:225:VAL:HG23	1:A:260:MET:CE	2.23	0.68
1:A:70:LEU:HD12	1:A:155:LEU:HD11	1.76	0.67
1:A:460:PHE:CZ	1:A:462:LYS:HG2	2.29	0.67
1:A:23:LEU:CD2	1:A:154:LEU:HD22	2.22	0.67
1:A:59:ASN:OD1	1:A:59:ASN:N	2.22	0.67
1:A:507:ASN:CB	1:A:581:ARG:HD2	2.21	0.67
1:A:24:MET:HG2	1:A:159:TYR:OH	1.95	0.67
1:A:35:LEU:HG	1:A:194:PRO:HG3	1.76	0.67
1:A:160:SER:N	1:A:242:GLU:OE2	2.28	0.67
1:A:219:ASN:HD22	1:A:221:TYR:HE2	1.41	0.67
1:A:243:LYS:NZ	1:A:261:ILE:O	2.28	0.67
1:A:276:VAL:O	1:A:294:THR:N	2.28	0.67
1:A:379:VAL:H	1:A:458:GLY:CA	2.04	0.67
1:A:329:ASN:H	1:A:329:ASN:ND2	1.92	0.66
1:A:266:ILE:HD12	1:A:372:GLY:HA2	1.77	0.66
1:A:492:LEU:HD12	1:A:493:SER:N	2.11	0.66
1:A:300:ASN:OD1	1:A:301:ILE:N	2.29	0.66
1:A:359:SER:OG	1:A:360:ALA:N	2.29	0.65
1:A:487:THR:HG22	1:A:504:VAL:HA	1.76	0.65
1:A:90:VAL:HG23	1:A:98:ASN:HB2	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:492:LEU:HD12	1:A:493:SER:H	1.62	0.65
1:A:401:LEU:HD12	1:A:401:LEU:O	1.97	0.65
1:A:101:LEU:HD22	1:A:102:ASN:H	1.62	0.65
1:A:118:ARG:O	1:A:119:ILE:HG13	1.95	0.65
1:A:398:GLN:HG3	1:A:401:LEU:HD21	1.77	0.65
1:A:343:THR:HG23	1:A:344:THR:N	2.12	0.64
1:A:556:ARG:HG2	1:A:556:ARG:HH21	1.62	0.64
1:A:117:ILE:O	1:A:118:ARG:HB2	1.95	0.64
1:A:255:VAL:O	1:A:261:ILE:HG21	1.96	0.64
1:A:363:ASN:HD22	1:A:423:ASN:HB2	1.61	0.64
1:A:93:ASN:HD22	1:A:115:TYR:HB3	1.61	0.64
1:A:271:MET:HG2	1:A:366:ILE:HG22	1.77	0.64
1:A:490:LEU:HD21	1:A:524:LEU:CD1	2.28	0.64
1:A:520:LEU:N	1:A:577:CYS:O	2.29	0.64
1:A:70:LEU:HD23	1:A:116:ASP:HA	1.79	0.64
1:A:46:LEU:HD23	1:A:46:LEU:N	2.12	0.64
1:A:89:ARG:HG2	1:A:90:VAL:N	2.12	0.64
1:A:269:VAL:HG11	1:A:366:ILE:CD1	2.27	0.64
1:A:61:ILE:HG22	1:A:126:ASN:HB3	1.78	0.64
1:A:264:TYR:CE1	1:A:266:ILE:HD11	2.33	0.64
1:A:70:LEU:CD1	1:A:114:VAL:HG11	2.24	0.64
1:A:227:ASN:ND2	1:A:514:LYS:O	2.31	0.64
1:A:462:LYS:CE	1:A:473:GLY:HA3	2.27	0.64
1:A:260:MET:CE	1:A:526:LYS:HD2	2.28	0.63
1:A:507:ASN:HB2	1:A:581:ARG:CD	2.23	0.63
1:A:459:ASN:N	1:A:459:ASN:ND2	2.45	0.63
1:A:89:ARG:NE	1:A:96:ILE:HG13	2.14	0.63
1:A:205:MET:O	1:A:207:GLN:N	2.29	0.63
1:A:365:ASN:OD1	1:A:365:ASN:N	2.30	0.63
1:A:551:GLN:HE21	1:A:590:ILE:HD13	1.63	0.63
1:A:492:LEU:CD1	1:A:493:SER:H	2.12	0.63
1:A:188:THR:HG22	1:A:189:ASP:N	2.12	0.63
1:A:26:TYR:HD2	1:A:38:ILE:HG12	1.64	0.62
1:A:260:MET:HE2	1:A:526:LYS:HD2	1.82	0.62
1:A:328:ALA:CB	1:A:484:LYS:HE2	2.26	0.62
1:A:477:GLY:C	1:A:479:TYR:H	2.08	0.62
1:A:524:LEU:O	1:A:530:LEU:HD13	1.98	0.62
1:A:544:ILE:CD1	1:A:550:ILE:HD13	2.29	0.62
1:A:56:ILE:O	1:A:60:LYS:HE3	2.00	0.62
1:A:266:ILE:HD12	1:A:372:GLY:CA	2.30	0.62
1:A:385:ILE:HD12	1:A:393:ALA:O	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:586:LEU:HD12	1:A:587:VAL:N	2.09	0.62
1:A:375:PRO:HB3	1:A:408:PRO:HD3	1.81	0.62
1:A:483:ILE:HG22	1:A:484:LYS:N	2.15	0.62
1:A:276:VAL:CG1	1:A:362:ILE:HB	2.29	0.62
1:A:490:LEU:HD12	1:A:528:PHE:HZ	1.65	0.62
1:A:529:ARG:HG3	1:A:529:ARG:NH2	2.14	0.62
1:A:93:ASN:ND2	1:A:115:TYR:HB3	2.15	0.61
1:A:491:THR:HG22	1:A:492:LEU:N	2.16	0.61
1:A:530:LEU:HD22	1:A:537:PHE:HZ	1.64	0.61
1:A:543:GLU:CB	1:A:549:LYS:HE3	2.25	0.61
1:A:71:ILE:HD13	1:A:117:ILE:HD13	1.82	0.61
1:A:387:ILE:HD12	1:A:449:VAL:HG12	1.82	0.61
1:A:70:LEU:HB2	1:A:155:LEU:CG	2.30	0.61
1:A:44:GLY:HA3	1:A:148:ILE:CG2	2.31	0.61
1:A:387:ILE:CD1	1:A:449:VAL:HA	2.30	0.61
1:A:225:VAL:CG2	1:A:260:MET:HE3	2.29	0.61
1:A:70:LEU:HB3	1:A:114:VAL:HG13	1.82	0.60
1:A:260:MET:HE1	1:A:526:LYS:HZ2	1.62	0.60
1:A:494:LEU:HD13	1:A:539:PHE:CG	2.36	0.60
1:A:206:ASN:O	1:A:207:GLN:HG2	2.01	0.60
1:A:328:ALA:CB	1:A:484:LYS:HD3	2.32	0.60
1:A:515:THR:HG22	1:A:516:PRO:HD2	1.83	0.60
1:A:109:LEU:HD23	1:A:115:TYR:CE2	2.36	0.60
1:A:492:LEU:HG	1:A:493:SER:H	1.65	0.60
1:A:38:ILE:HB	1:A:208:LYS:HZ1	1.64	0.60
1:A:53:ILE:HD12	1:A:60:LYS:HB3	1.84	0.60
1:A:71:ILE:HD11	1:A:92:LEU:CD2	2.29	0.59
1:A:235:ASN:HD22	1:A:482:THR:HB	1.67	0.59
1:A:434:PRO:O	1:A:435:ILE:HG23	2.01	0.59
1:A:219:ASN:HB2	1:A:221:TYR:CE2	2.38	0.59
1:A:81:LEU:HD11	1:A:92:LEU:CD1	2.33	0.59
1:A:197:TRP:HZ3	1:A:208:LYS:NZ	2.00	0.59
1:A:204:VAL:HG12	1:A:208:LYS:CG	2.26	0.59
1:A:583:MET:O	1:A:585:ILE:HG13	2.02	0.59
1:A:492:LEU:HD21	1:A:494:LEU:HD12	1.83	0.59
1:A:215:LYS:O	1:A:215:LYS:NZ	2.36	0.59
1:A:586:LEU:CD1	1:A:587:VAL:H	2.10	0.59
1:A:260:MET:HE1	1:A:526:LYS:CE	2.33	0.58
1:A:378:ASN:HB3	1:A:458:GLY:HA3	1.85	0.58
1:A:487:THR:HG22	1:A:504:VAL:CA	2.32	0.58
1:A:162:THR:OG1	1:A:163:ASN:N	2.35	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:383:THR:CG2	1:A:451:LEU:HD23	2.33	0.58
1:A:580:LYS:H	1:A:583:MET:CE	2.13	0.58
1:A:264:TYR:CZ	1:A:266:ILE:HD11	2.39	0.58
1:A:492:LEU:HD11	1:A:494:LEU:HG	1.84	0.58
1:A:551:GLN:NE2	1:A:590:ILE:HD13	2.18	0.58
1:A:246:GLY:O	1:A:248:ILE:N	2.37	0.58
1:A:255:VAL:HG12	1:A:529:ARG:HG3	1.85	0.58
1:A:530:LEU:HD22	1:A:537:PHE:CE2	2.39	0.58
1:A:303:THR:HG21	1:A:331:SER:CB	2.34	0.58
1:A:28:PHE:HD2	1:A:34:ASN:H	1.50	0.58
1:A:235:ASN:HB3	1:A:482:THR:OG1	2.04	0.58
1:A:233:THR:C	1:A:235:ASN:H	2.12	0.57
1:A:373:THR:HG21	1:A:501:VAL:HG22	1.86	0.57
1:A:558:THR:O	1:A:562:PHE:HB2	2.04	0.57
1:A:458:GLY:O	1:A:476:TRP:N	2.36	0.57
1:A:57:LEU:HG	1:A:58:GLY:N	2.19	0.57
1:A:480:LEU:O	1:A:483:ILE:HB	2.05	0.57
1:A:276:VAL:HG13	1:A:362:ILE:HG13	1.87	0.57
1:A:70:LEU:HD22	1:A:114:VAL:CG1	2.29	0.57
1:A:76:THR:HG23	1:A:110:ILE:CG1	2.35	0.57
1:A:143:ASP:C	1:A:145:ILE:H	2.12	0.57
1:A:141:THR:OG1	1:A:142:SER:N	2.38	0.57
1:A:369:TYR:HD2	1:A:370:ASN:N	2.02	0.57
1:A:387:ILE:HD12	1:A:449:VAL:HA	1.85	0.57
1:A:68:ILE:HG23	1:A:157:PRO:HG3	1.87	0.57
1:A:71:ILE:H	1:A:114:VAL:HG13	1.69	0.57
1:A:572:LYS:H	1:A:572:LYS:HD2	1.68	0.57
1:A:308:VAL:HG23	1:A:556:ARG:HD3	1.86	0.56
1:A:137:LEU:CD2	1:A:149:ILE:HD12	2.35	0.56
1:A:460:PHE:HB3	1:A:476:TRP:CE2	2.40	0.56
1:A:490:LEU:HD12	1:A:528:PHE:CZ	2.39	0.56
1:A:60:LYS:HD3	1:A:130:LYS:CG	2.35	0.56
1:A:204:VAL:HG11	1:A:244:VAL:HG21	1.87	0.56
1:A:487:THR:HG22	1:A:504:VAL:N	2.20	0.56
1:A:275:VAL:HG22	1:A:295:SER:CB	2.36	0.56
1:A:518:LEU:HD23	1:A:579:ILE:HB	1.87	0.56
1:A:476:TRP:O	1:A:479:TYR:HB2	2.06	0.56
1:A:43:ASP:OD1	1:A:43:ASP:N	2.39	0.56
1:A:80:ILE:O	1:A:139:TRP:HA	2.06	0.56
1:A:149:ILE:CG2	1:A:154:LEU:HG	2.36	0.56
1:A:379:VAL:HB	1:A:457:THR:C	2.30	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:204:VAL:O	1:A:204:VAL:HG23	2.06	0.55
1:A:274:LEU:H	1:A:274:LEU:CD2	2.15	0.55
1:A:132:TYR:C	1:A:134:GLY:H	2.14	0.55
1:A:238:TYR:CD1	1:A:248:ILE:HG13	2.41	0.55
1:A:558:THR:HG21	1:A:583:MET:SD	2.46	0.55
1:A:573:ASP:OD2	1:A:573:ASP:N	2.32	0.55
1:A:300:ASN:C	1:A:301:ILE:HG13	2.30	0.55
1:A:38:ILE:HB	1:A:208:LYS:CE	2.37	0.55
1:A:57:LEU:CG	1:A:58:GLY:H	2.20	0.55
1:A:566:LEU:O	1:A:569:THR:N	2.33	0.55
1:A:89:ARG:HG2	1:A:90:VAL:H	1.71	0.55
1:A:449:VAL:O	1:A:449:VAL:HG23	2.05	0.55
1:A:458:GLY:O	1:A:476:TRP:HB2	2.07	0.55
1:A:28:PHE:CD1	1:A:28:PHE:N	2.74	0.55
1:A:90:VAL:O	1:A:96:ILE:HA	2.07	0.55
1:A:81:LEU:HD11	1:A:92:LEU:HD11	1.88	0.55
1:A:208:LYS:HE3	1:A:208:LYS:C	2.32	0.55
1:A:233:THR:O	1:A:235:ASN:N	2.39	0.55
1:A:271:MET:HE1	1:A:274:LEU:CB	2.31	0.55
1:A:264:TYR:HD1	1:A:264:TYR:H	1.56	0.54
1:A:48:PHE:HE1	1:A:52:ASP:HB2	1.72	0.54
1:A:74:SER:C	1:A:111:GLN:HG2	2.33	0.54
1:A:137:LEU:HD21	1:A:149:ILE:HD12	1.90	0.54
1:A:192:GLY:C	1:A:193:ILE:HG12	2.30	0.54
1:A:236:ASP:HB2	1:A:237:PRO:CD	2.29	0.54
1:A:260:MET:HE1	1:A:526:LYS:HZ1	1.71	0.54
1:A:383:THR:HG21	1:A:451:LEU:CD2	2.37	0.54
1:A:489:SER:O	1:A:490:LEU:HB2	2.07	0.54
1:A:53:ILE:HD12	1:A:60:LYS:CG	2.37	0.54
1:A:255:VAL:CG1	1:A:529:ARG:HH21	2.20	0.54
1:A:271:MET:CE	1:A:274:LEU:HB3	2.30	0.54
1:A:276:VAL:HA	1:A:362:ILE:HA	1.89	0.54
1:A:303:THR:HG21	1:A:331:SER:HB3	1.89	0.54
1:A:343:THR:C	1:A:344:THR:HG23	2.32	0.54
1:A:35:LEU:HG	1:A:194:PRO:CG	2.38	0.54
1:A:31:ASP:OD1	1:A:63:LYS:HD2	2.08	0.54
1:A:43:ASP:HB3	1:A:151:SER:OG	2.07	0.54
1:A:385:ILE:HA	1:A:450:MET:O	2.08	0.53
1:A:60:LYS:HD3	1:A:130:LYS:HG3	1.89	0.53
1:A:198:GLU:OE1	1:A:226:SER:HB3	2.08	0.53
1:A:89:ARG:HA	1:A:97:PHE:O	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:460:PHE:CE2	1:A:462:LYS:HE2	2.43	0.53
1:A:117:ILE:HG22	1:A:118:ARG:N	2.20	0.53
1:A:155:LEU:HD22	1:A:468:ASN:HD21	1.73	0.53
1:A:378:ASN:HB2	1:A:459:ASN:H	1.74	0.53
1:A:519:THR:HG22	1:A:578:ILE:HD12	1.91	0.53
1:A:53:ILE:CD1	1:A:60:LYS:HB3	2.38	0.53
1:A:494:LEU:HD13	1:A:539:PHE:CE2	2.44	0.53
1:A:87:ASN:H	1:A:87:ASN:ND2	2.02	0.53
1:A:294:THR:HG22	1:A:294:THR:O	2.06	0.53
1:A:72:LYS:HB3	1:A:114:VAL:CG2	2.36	0.53
1:A:23:LEU:HD21	1:A:154:LEU:HD22	1.90	0.53
1:A:74:SER:HA	1:A:111:GLN:HG2	1.90	0.53
1:A:413:PRO:HG2	1:A:418:PRO:O	2.09	0.53
1:A:235:ASN:HD22	1:A:482:THR:CB	2.22	0.53
1:A:333:THR:HG22	1:A:334:TRP:N	2.23	0.53
1:A:392:VAL:HG23	1:A:393:ALA:N	2.24	0.53
1:A:60:LYS:O	1:A:62:ILE:N	2.42	0.52
1:A:539:PHE:O	1:A:540:HIS:HB2	2.09	0.52
1:A:579:ILE:HD11	1:A:585:ILE:CD1	2.38	0.52
1:A:198:GLU:OE1	1:A:227:ASN:O	2.26	0.52
1:A:470:VAL:HG12	1:A:470:VAL:O	2.09	0.52
1:A:119:ILE:O	1:A:119:ILE:HG22	2.08	0.52
1:A:213:ASP:O	1:A:214:ASP:O	2.28	0.52
1:A:477:GLY:O	1:A:479:TYR:N	2.42	0.52
1:A:522:GLN:O	1:A:526:LYS:HG2	2.10	0.52
1:A:103:THR:O	1:A:104:SER:HB2	2.09	0.52
1:A:98:ASN:O	1:A:99:LEU:HD22	2.09	0.52
1:A:371:THR:OG1	1:A:500:GLN:N	2.37	0.52
1:A:102:ASN:OD1	1:A:102:ASN:O	2.28	0.52
1:A:267:VAL:HG12	1:A:268:GLY:N	2.08	0.52
1:A:490:LEU:HG	1:A:528:PHE:CE2	2.45	0.52
1:A:574:ILE:HG23	1:A:574:ILE:O	2.09	0.52
1:A:76:THR:HG23	1:A:110:ILE:HG12	1.92	0.52
1:A:144:ILE:O	1:A:144:ILE:HG22	2.10	0.52
1:A:274:LEU:HD23	1:A:274:LEU:N	2.15	0.52
1:A:272:GLU:O	1:A:273:ARG:HB3	2.08	0.52
1:A:499:THR:HG22	1:A:499:THR:O	2.09	0.52
1:A:360:ALA:HB3	1:A:435:ILE:HG13	1.92	0.51
1:A:362:ILE:CG2	1:A:433:ILE:HB	2.40	0.51
1:A:453:THR:O	1:A:454:SER:O	2.28	0.51
1:A:28:PHE:CG	1:A:33:PHE:HA	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:494:LEU:HB3	1:A:539:PHE:CE2	2.44	0.51
1:A:558:THR:O	1:A:562:PHE:N	2.43	0.51
1:A:356:THR:HA	1:A:437:TYR:CG	2.44	0.51
1:A:58:GLY:O	1:A:60:LYS:N	2.38	0.51
1:A:212:TRP:HB3	1:A:216:PHE:CD1	2.45	0.51
1:A:225:VAL:HG23	1:A:260:MET:SD	2.51	0.51
1:A:399:GLU:O	1:A:400:SER:HB2	2.09	0.51
1:A:251:SER:O	1:A:408:PRO:HG2	2.10	0.51
1:A:385:ILE:HD11	1:A:395:ILE:HD11	1.93	0.51
1:A:494:LEU:CB	1:A:495:PRO:HD3	2.39	0.51
1:A:552:VAL:HG12	1:A:553:PHE:N	2.26	0.51
1:A:333:THR:CG2	1:A:334:TRP:N	2.74	0.51
1:A:25:GLY:CA	1:A:67:TRP:CD1	2.94	0.51
1:A:48:PHE:CE1	1:A:52:ASP:HB2	2.46	0.51
1:A:117:ILE:CG2	1:A:118:ARG:H	2.11	0.51
1:A:255:VAL:CG2	1:A:373:THR:HG22	2.40	0.51
1:A:304:VAL:HG12	1:A:304:VAL:O	2.11	0.51
1:A:386:VAL:HG13	1:A:391:SER:N	2.26	0.51
1:A:378:ASN:CB	1:A:459:ASN:H	2.24	0.50
1:A:464:ASN:O	1:A:468:ASN:HA	2.11	0.50
1:A:515:THR:HG22	1:A:516:PRO:CD	2.41	0.50
1:A:269:VAL:CG1	1:A:366:ILE:HD12	2.37	0.50
1:A:560:VAL:O	1:A:564:ASN:OD1	2.30	0.50
1:A:271:MET:O	1:A:334:TRP:HZ3	1.94	0.50
1:A:46:LEU:HB2	1:A:135:ILE:HG23	1.93	0.50
1:A:97:PHE:CZ	1:A:105:ASN:HB3	2.47	0.50
1:A:267:VAL:HG13	1:A:406:LEU:CD2	2.42	0.50
1:A:587:VAL:HG12	1:A:587:VAL:O	2.11	0.50
1:A:56:ILE:O	1:A:57:LEU:O	2.29	0.50
1:A:368:TYR:CD1	1:A:412:TYR:HD1	2.29	0.50
1:A:71:ILE:HD13	1:A:117:ILE:CD1	2.41	0.50
1:A:233:THR:C	1:A:235:ASN:N	2.69	0.50
1:A:38:ILE:O	1:A:207:GLN:O	2.29	0.50
1:A:76:THR:HA	1:A:110:ILE:HA	1.94	0.50
1:A:251:SER:HB2	1:A:375:PRO:HG3	1.93	0.49
1:A:252:VAL:HG13	1:A:256:ALA:HB3	1.91	0.49
1:A:521:GLU:O	1:A:524:LEU:N	2.45	0.49
1:A:38:ILE:HB	1:A:208:LYS:HE2	1.94	0.49
1:A:50:LYS:HG2	1:A:132:TYR:HE2	1.76	0.49
1:A:90:VAL:HG23	1:A:97:PHE:C	2.37	0.49
1:A:368:TYR:HB2	1:A:412:TYR:HB3	1.92	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:371:THR:OG1	1:A:371:THR:O	2.29	0.49
1:A:300:ASN:HD21	1:A:332:HIS:HB3	1.77	0.49
1:A:460:PHE:CD1	1:A:461:ALA:N	2.80	0.49
1:A:105:ASN:O	1:A:106:THR:OG1	2.28	0.49
1:A:491:THR:OG1	1:A:500:GLN:HG2	2.12	0.49
1:A:578:ILE:HG23	1:A:579:ILE:N	2.27	0.49
1:A:30:ASN:CB	1:A:34:ASN:ND2	2.75	0.49
1:A:441:LYS:O	1:A:445:ASN:OD1	2.29	0.49
1:A:492:LEU:O	1:A:493:SER:HB3	2.12	0.49
1:A:493:SER:O	1:A:493:SER:OG	2.27	0.49
1:A:25:GLY:HA2	1:A:67:TRP:CD1	2.48	0.48
1:A:214:ASP:OD1	1:A:214:ASP:N	2.45	0.48
1:A:375:PRO:HD3	1:A:408:PRO:HG3	1.95	0.48
1:A:379:VAL:CG1	1:A:380:THR:N	2.76	0.48
1:A:26:TYR:HH	1:A:159:TYR:HH	1.55	0.48
1:A:38:ILE:HG21	1:A:241:PHE:CZ	2.48	0.48
1:A:85:SER:O	1:A:86:PRO:O	2.32	0.48
1:A:334:TRP:NE1	1:A:335:GLN:O	2.46	0.48
1:A:341:ASP:O	1:A:342:ASP:HB2	2.13	0.48
1:A:555:ASP:OD2	1:A:558:THR:OG1	2.31	0.48
1:A:46:LEU:HD13	1:A:67:TRP:CG	2.49	0.48
1:A:89:ARG:HG3	1:A:96:ILE:HG23	1.95	0.48
1:A:264:TYR:OH	1:A:502:ALA:HB2	2.13	0.48
1:A:270:GLN:HA	1:A:300:ASN:ND2	2.28	0.48
1:A:30:ASN:HB2	1:A:34:ASN:ND2	2.19	0.48
1:A:149:ILE:HG21	1:A:154:LEU:CG	2.41	0.48
1:A:266:ILE:HD13	1:A:372:GLY:HA2	1.94	0.48
1:A:25:GLY:CA	1:A:67:TRP:HD1	2.26	0.48
1:A:27:TYR:HE2	1:A:67:TRP:CZ2	2.31	0.48
1:A:219:ASN:ND2	1:A:221:TYR:HE2	2.10	0.48
1:A:571:ASN:O	1:A:573:ASP:N	2.46	0.48
1:A:477:GLY:C	1:A:479:TYR:N	2.72	0.48
1:A:38:ILE:HG21	1:A:241:PHE:CE1	2.49	0.48
1:A:393:ALA:CB	1:A:433:ILE:HG12	2.40	0.48
1:A:398:GLN:HB3	1:A:401:LEU:HD11	1.95	0.48
1:A:504:VAL:O	1:A:505:ALA:HB2	2.14	0.47
1:A:67:TRP:CZ2	1:A:135:ILE:HG21	2.49	0.47
1:A:362:ILE:HG22	1:A:433:ILE:HB	1.95	0.47
1:A:359:SER:O	1:A:360:ALA:HB2	2.14	0.47
1:A:387:ILE:O	1:A:389:LYS:N	2.47	0.47
1:A:266:ILE:HG22	1:A:266:ILE:O	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:373:THR:HG23	1:A:501:VAL:HG22	1.97	0.47
1:A:395:ILE:HG12	1:A:422:LEU:HD22	1.96	0.47
1:A:238:TYR:CG	1:A:248:ILE:HD11	2.48	0.47
1:A:244:VAL:HG22	1:A:245:SER:N	2.30	0.47
1:A:79:TYR:CE1	1:A:109:LEU:HB2	2.50	0.47
1:A:386:VAL:HG12	1:A:390:GLN:C	2.40	0.47
1:A:530:LEU:HB2	1:A:537:PHE:CZ	2.49	0.47
1:A:570:ALA:O	1:A:573:ASP:OD2	2.33	0.47
1:A:189:ASP:O	1:A:190:ARG:HB2	2.14	0.47
1:A:215:LYS:NZ	1:A:219:ASN:HD21	2.13	0.47
1:A:233:THR:HG22	1:A:504:VAL:HG21	1.97	0.47
1:A:245:SER:HB2	1:A:247:GLN:OE1	2.14	0.47
1:A:267:VAL:CG1	1:A:268:GLY:H	2.11	0.47
1:A:45:ASN:OD1	1:A:136:LYS:HG2	2.15	0.46
1:A:67:TRP:HE3	1:A:119:ILE:CG2	2.28	0.46
1:A:392:VAL:CG2	1:A:393:ALA:N	2.77	0.46
1:A:402:ILE:HD12	1:A:405:TYR:HA	1.96	0.46
1:A:490:LEU:HD12	1:A:490:LEU:C	2.40	0.46
1:A:518:LEU:HG	1:A:519:THR:N	2.29	0.46
1:A:382:THR:O	1:A:382:THR:HG22	2.13	0.46
1:A:383:THR:HA	1:A:453:THR:HA	1.97	0.46
1:A:23:LEU:O	1:A:41:THR:OG1	2.30	0.46
1:A:255:VAL:HG12	1:A:529:ARG:HH21	1.79	0.46
1:A:491:THR:HG22	1:A:492:LEU:H	1.80	0.46
1:A:69:GLY:O	1:A:117:ILE:HG13	2.16	0.46
1:A:197:TRP:HZ3	1:A:208:LYS:HZ1	1.61	0.46
1:A:586:LEU:HD21	1:A:588:LYS:NZ	2.30	0.46
1:A:214:ASP:O	1:A:216:PHE:N	2.48	0.46
1:A:555:ASP:OD1	1:A:557:ASN:HB2	2.16	0.46
1:A:556:ARG:HG2	1:A:556:ARG:NH2	2.29	0.46
1:A:53:ILE:C	1:A:55:SER:H	2.22	0.46
1:A:544:ILE:HD13	1:A:550:ILE:HD13	1.98	0.46
1:A:28:PHE:CD2	1:A:34:ASN:N	2.84	0.46
1:A:356:THR:HA	1:A:437:TYR:CD2	2.51	0.46
1:A:492:LEU:HD21	1:A:494:LEU:CD1	2.46	0.46
1:A:35:LEU:O	1:A:36:ASN:HB2	2.14	0.45
1:A:518:LEU:HD21	1:A:523:ALA:HB2	1.98	0.45
1:A:25:GLY:HA3	1:A:67:TRP:CD1	2.51	0.45
1:A:32:PHE:CD2	1:A:122:LEU:HD11	2.51	0.45
1:A:70:LEU:HD23	1:A:116:ASP:CA	2.43	0.45
1:A:363:ASN:HD22	1:A:363:ASN:HA	1.60	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:383:THR:O	1:A:394:THR:HG23	2.17	0.45
1:A:530:LEU:CB	1:A:537:PHE:CZ	2.99	0.45
1:A:578:ILE:CG2	1:A:579:ILE:N	2.79	0.45
1:A:189:ASP:N	1:A:189:ASP:OD1	2.44	0.45
1:A:32:PHE:CE2	1:A:122:LEU:HD11	2.51	0.45
1:A:28:PHE:HD2	1:A:34:ASN:N	2.14	0.45
1:A:34:ASN:O	1:A:35:LEU:HB2	2.15	0.45
1:A:38:ILE:O	1:A:38:ILE:HG22	2.15	0.45
1:A:92:LEU:HD12	1:A:107:VAL:HG11	1.98	0.45
1:A:159:TYR:HB2	1:A:242:GLU:HG3	1.97	0.45
1:A:387:ILE:HD12	1:A:448:THR:O	2.16	0.45
1:A:492:LEU:CG	1:A:493:SER:N	2.75	0.45
1:A:579:ILE:HD11	1:A:585:ILE:HD12	1.98	0.45
1:A:53:ILE:HD12	1:A:60:LYS:CB	2.47	0.45
1:A:506:PRO:HD3	1:A:515:THR:HB	1.99	0.45
1:A:70:LEU:HB3	1:A:114:VAL:HG11	1.97	0.45
1:A:240:ASP:O	1:A:244:VAL:HG13	2.17	0.45
1:A:369:TYR:CD2	1:A:370:ASN:N	2.82	0.45
1:A:307:GLU:N	1:A:307:GLU:OE2	2.50	0.45
1:A:483:ILE:O	1:A:487:THR:OG1	2.30	0.45
1:A:490:LEU:CD1	1:A:528:PHE:CZ	3.00	0.45
1:A:88:CYS:O	1:A:99:LEU:HD13	2.16	0.45
1:A:132:TYR:C	1:A:134:GLY:N	2.75	0.45
1:A:216:PHE:C	1:A:218:ALA:N	2.73	0.45
1:A:573:ASP:O	1:A:574:ILE:HG22	2.16	0.45
1:A:74:SER:CA	1:A:111:GLN:HG2	2.47	0.44
1:A:525:VAL:HG22	1:A:530:LEU:O	2.17	0.44
1:A:197:TRP:O	1:A:202:TYR:HD1	1.99	0.44
1:A:269:VAL:HG22	1:A:368:TYR:CD2	2.52	0.44
1:A:506:PRO:O	1:A:581:ARG:HG3	2.17	0.44
1:A:255:VAL:CG1	1:A:529:ARG:NH2	2.81	0.44
1:A:260:MET:CE	1:A:526:LYS:CD	2.95	0.44
1:A:88:CYS:O	1:A:98:ASN:HB3	2.18	0.44
1:A:519:THR:HG23	1:A:578:ILE:HD12	1.97	0.44
1:A:89:ARG:CZ	1:A:96:ILE:HG13	2.47	0.44
1:A:215:LYS:NZ	1:A:219:ASN:OD1	2.51	0.44
1:A:50:LYS:HA	1:A:53:ILE:HG12	1.99	0.44
1:A:303:THR:HG21	1:A:331:SER:HB2	1.99	0.44
1:A:487:THR:CG2	1:A:504:VAL:HA	2.44	0.44
1:A:579:ILE:HA	1:A:583:MET:CE	2.48	0.44
1:A:243:LYS:NZ	1:A:258:ASP:O	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:395:ILE:HG12	1:A:422:LEU:CD2	2.47	0.44
1:A:39:SER:CB	1:A:207:GLN:NE2	2.81	0.44
1:A:42:LEU:O	1:A:151:SER:OG	2.31	0.44
1:A:18:PHE:O	1:A:21:ASN:HB2	2.18	0.44
1:A:145:ILE:O	1:A:145:ILE:HG22	2.17	0.44
1:A:362:ILE:HG23	1:A:362:ILE:O	2.17	0.44
1:A:529:ARG:NH2	1:A:529:ARG:CG	2.79	0.44
1:A:550:ILE:O	1:A:550:ILE:HG12	2.18	0.44
1:A:29:GLU:HB2	1:A:36:ASN:HD21	1.75	0.43
1:A:69:GLY:HA2	1:A:157:PRO:HD3	2.00	0.43
1:A:155:LEU:CB	1:A:468:ASN:ND2	2.81	0.43
1:A:216:PHE:C	1:A:218:ALA:H	2.25	0.43
1:A:24:MET:CE	1:A:247:GLN:NE2	2.79	0.43
1:A:70:LEU:HD13	1:A:114:VAL:CG1	2.30	0.43
1:A:234:ALA:HB3	1:A:236:ASP:OD2	2.18	0.43
1:A:489:SER:OG	1:A:490:LEU:N	2.51	0.43
1:A:586:LEU:CD1	1:A:587:VAL:N	2.77	0.43
1:A:331:SER:OG	1:A:452:SER:HA	2.18	0.43
1:A:586:LEU:CG	1:A:587:VAL:N	2.81	0.43
1:A:105:ASN:O	1:A:105:ASN:ND2	2.52	0.43
1:A:205:MET:C	1:A:207:GLN:N	2.76	0.43
1:A:387:ILE:HD11	1:A:449:VAL:CG1	2.45	0.43
1:A:438:ASN:O	1:A:442:SER:OG	2.35	0.43
1:A:491:THR:CG2	1:A:492:LEU:N	2.80	0.43
1:A:97:PHE:HZ	1:A:105:ASN:HB3	1.81	0.43
1:A:150:PRO:C	1:A:152:GLU:H	2.26	0.43
1:A:161:ASN:OD1	1:A:231:PRO:HG2	2.18	0.43
1:A:355:ASN:OD1	1:A:355:ASN:N	2.52	0.43
1:A:586:LEU:O	1:A:587:VAL:HG23	2.17	0.43
1:A:219:ASN:HB2	1:A:221:TYR:CZ	2.53	0.43
1:A:441:LYS:O	1:A:441:LYS:HG2	2.18	0.43
1:A:555:ASP:HB3	1:A:584:ASN:HB3	2.00	0.43
1:A:262:SER:OG	1:A:263:ALA:N	2.51	0.43
1:A:132:TYR:O	1:A:134:GLY:N	2.41	0.43
1:A:191:ASP:OD1	1:A:193:ILE:HG13	2.18	0.43
1:A:555:ASP:OD2	1:A:584:ASN:O	2.36	0.43
1:A:125:GLU:CB	1:A:127:GLN:HE21	2.28	0.43
1:A:189:ASP:HB3	1:A:228:PRO:O	2.19	0.42
1:A:215:LYS:HZ1	1:A:219:ASN:HD21	1.66	0.42
1:A:266:ILE:HD12	1:A:372:GLY:HA3	2.01	0.42
1:A:539:PHE:CD2	1:A:542:MET:HE3	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:63:LYS:CD	1:A:126:ASN:HD21	2.32	0.42
1:A:72:LYS:HE2	1:A:468:ASN:ND2	2.35	0.42
1:A:143:ASP:C	1:A:145:ILE:N	2.77	0.42
1:A:202:TYR:HE1	1:A:226:SER:HB2	1.84	0.42
1:A:73:PRO:HG2	1:A:110:ILE:O	2.19	0.42
1:A:193:ILE:HA	1:A:194:PRO:HD3	1.79	0.42
1:A:363:ASN:HD21	1:A:423:ASN:C	2.26	0.42
1:A:205:MET:C	1:A:207:GLN:H	2.20	0.42
1:A:458:GLY:C	1:A:459:ASN:HD22	2.26	0.42
1:A:83:THR:HB	1:A:136:LYS:O	2.20	0.42
1:A:195:ASP:CG	1:A:228:PRO:HB3	2.45	0.42
1:A:210:VAL:HG22	1:A:211:ALA:H	1.83	0.42
1:A:460:PHE:HB3	1:A:476:TRP:NE1	2.34	0.42
1:A:101:LEU:HD22	1:A:102:ASN:N	2.33	0.42
1:A:107:VAL:O	1:A:107:VAL:HG13	2.20	0.42
1:A:143:ASP:O	1:A:145:ILE:N	2.52	0.42
1:A:275:VAL:HG22	1:A:295:SER:HA	2.01	0.42
1:A:378:ASN:HB3	1:A:379:VAL:H	1.66	0.42
1:A:96:ILE:O	1:A:97:PHE:CD1	2.73	0.42
1:A:266:ILE:O	1:A:267:VAL:O	2.37	0.42
1:A:275:VAL:HG22	1:A:295:SER:OG	2.19	0.42
1:A:586:LEU:HD21	1:A:588:LYS:HZ1	1.85	0.42
1:A:260:MET:HE1	1:A:526:LYS:CD	2.50	0.42
1:A:552:VAL:HG12	1:A:553:PHE:H	1.85	0.42
1:A:554:LEU:HD23	1:A:585:ILE:CG1	2.31	0.42
1:A:36:ASN:C	1:A:37:ILE:HG13	2.45	0.42
1:A:227:ASN:ND2	1:A:514:LYS:C	2.78	0.42
1:A:26:TYR:OH	1:A:159:TYR:OH	2.29	0.41
1:A:99:LEU:HB2	1:A:100:SER:H	1.69	0.41
1:A:386:VAL:CG1	1:A:391:SER:N	2.83	0.41
1:A:238:TYR:CG	1:A:248:ILE:HG13	2.55	0.41
1:A:406:LEU:CD1	1:A:412:TYR:CB	2.98	0.41
1:A:24:MET:HE3	1:A:247:GLN:HE21	1.84	0.41
1:A:87:ASN:ND2	1:A:87:ASN:N	2.66	0.41
1:A:136:LYS:CE	1:A:148:ILE:HD11	2.39	0.41
1:A:235:ASN:ND2	1:A:482:THR:HB	2.32	0.41
1:A:70:LEU:O	1:A:71:ILE:HG23	2.19	0.41
1:A:242:GLU:HA	1:A:247:GLN:OE1	2.21	0.41
1:A:276:VAL:HG13	1:A:362:ILE:CD1	2.49	0.41
1:A:460:PHE:CE1	1:A:462:LYS:HG2	2.55	0.41
1:A:31:ASP:OD1	1:A:63:LYS:HB3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:359:SER:HA	1:A:435:ILE:O	2.20	0.41
1:A:402:ILE:O	1:A:402:ILE:HG13	2.19	0.41
1:A:149:ILE:HG22	1:A:154:LEU:HD12	2.02	0.41
1:A:261:ILE:HG12	1:A:526:LYS:HB2	2.03	0.41
1:A:490:LEU:CD1	1:A:528:PHE:CE2	3.03	0.41
1:A:551:GLN:HG2	1:A:590:ILE:HG23	2.02	0.41
1:A:99:LEU:N	1:A:99:LEU:CD1	2.76	0.41
1:A:149:ILE:CG2	1:A:154:LEU:CD1	2.99	0.41
1:A:515:THR:HA	1:A:516:PRO:HD3	1.64	0.41
1:A:31:ASP:C	1:A:32:PHE:CG	2.98	0.41
1:A:60:LYS:HD3	1:A:130:LYS:HG2	2.02	0.41
1:A:215:LYS:NZ	1:A:219:ASN:ND2	2.69	0.41
1:A:242:GLU:HB3	1:A:247:GLN:O	2.21	0.41
1:A:341:ASP:OD1	1:A:341:ASP:N	2.53	0.41
1:A:406:LEU:CD1	1:A:412:TYR:HB3	2.51	0.41
1:A:203:THR:C	1:A:204:VAL:HG13	2.46	0.41
1:A:230:LYS:C	1:A:232:CYS:N	2.77	0.41
1:A:377:TYR:HB2	1:A:459:ASN:O	2.21	0.41
1:A:393:ALA:CB	1:A:433:ILE:CD1	2.99	0.41
1:A:67:TRP:CE3	1:A:119:ILE:CG2	3.04	0.40
1:A:111:GLN:CD	1:A:112:GLY:N	2.79	0.40
1:A:244:VAL:CG2	1:A:245:SER:N	2.82	0.40
1:A:369:TYR:CD2	1:A:369:TYR:C	2.99	0.40
1:A:485:SER:O	1:A:581:ARG:HD3	2.21	0.40
1:A:110:ILE:HG22	1:A:111:GLN:N	2.35	0.40
1:A:414:ILE:C	1:A:416:GLY:N	2.77	0.40
1:A:539:PHE:HD2	1:A:542:MET:HE3	1.86	0.40
1:A:24:MET:SD	1:A:40:PRO:HB3	2.62	0.40
1:A:48:PHE:CZ	1:A:53:ILE:CG2	3.05	0.40
1:A:248:ILE:HG12	1:A:249:ASP:H	1.86	0.40
1:A:355:ASN:HB2	1:A:356:THR:H	1.52	0.40
1:A:573:ASP:C	1:A:575:MET:N	2.79	0.40
1:A:490:LEU:HG	1:A:528:PHE:CZ	2.56	0.40
1:A:558:THR:CG2	1:A:583:MET:SD	3.09	0.40
1:A:260:MET:C	1:A:261:ILE:HD13	2.47	0.40
1:A:370:ASN:O	1:A:409:GLY:HA2	2.22	0.40
1:A:462:LYS:NZ	1:A:474:ASN:H	2.19	0.40
1:A:482:THR:O	1:A:486:THR:HG23	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	489/721 (68%)	311 (64%)	108 (22%)	70 (14%)	0 1

All (70) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	33	PHE
1	A	57	LEU
1	A	85	SER
1	A	86	PRO
1	A	213	ASP
1	A	214	ASP
1	A	215	LYS
1	A	247	GLN
1	A	262	SER
1	A	267	VAL
1	A	329	ASN
1	A	454	SER
1	A	493	SER
1	A	543	GLU
1	A	572	LYS
1	A	589	VAL
1	A	36	ASN
1	A	43	ASP
1	A	61	ILE
1	A	98	ASN
1	A	107	VAL
1	A	118	ARG
1	A	144	ILE
1	A	234	ALA
1	A	248	ILE
1	A	304	VAL
1	A	328	ALA
1	A	342	ASP

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Mol	Chain	Res	Type
1	A	405	TYR
1	A	477	GLY
1	A	490	LEU
1	A	557	ASN
1	A	571	ASN
1	A	59	ASN
1	A	84	ASN
1	A	131	ASN
1	A	378	ASN
1	A	381	PRO
1	A	388	ASP
1	A	478	PRO
1	A	31	ASP
1	A	100	SER
1	A	119	ILE
1	A	161	ASN
1	A	162	THR
1	A	187	ASP
1	A	206	ASN
1	A	207	GLN
1	A	254	MET
1	A	273	ARG
1	A	355	ASN
1	A	481	GLY
1	A	506	PRO
1	A	529	ARG
1	A	588	LYS
1	A	73	PRO
1	A	99	LEU
1	A	208	LYS
1	A	375	PRO
1	A	516	PRO
1	A	117	ILE
1	A	473	GLY
1	A	475	ASN
1	A	574	ILE
1	A	483	ILE
1	A	228	PRO
1	A	419	PRO
1	A	364	PRO
1	A	495	PRO
1	A	505	ALA

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	451/648 (70%)	320 (71%)	131 (29%)	0 1

All (131) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	PHE
1	A	20	ILE
1	A	23	LEU
1	A	28	PHE
1	A	35	LEU
1	A	43	ASP
1	A	46	LEU
1	A	56	ILE
1	A	59	ASN
1	A	61	ILE
1	A	64	SER
1	A	71	ILE
1	A	74	SER
1	A	80	ILE
1	A	87	ASN
1	A	89	ARG
1	A	90	VAL
1	A	91	GLU
1	A	92	LEU
1	A	96	ILE
1	A	98	ASN
1	A	99	LEU
1	A	101	LEU
1	A	109	LEU
1	A	117	ILE
1	A	123	MET
1	A	124	SER
1	A	128	LEU
1	A	135	ILE
1	A	137	LEU

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Mol	Chain	Res	Type
1	A	138	TYR
1	A	142	SER
1	A	144	ILE
1	A	151	SER
1	A	155	LEU
1	A	162	THR
1	A	188	THR
1	A	190	ARG
1	A	193	ILE
1	A	205	MET
1	A	208	LYS
1	A	214	ASP
1	A	215	LYS
1	A	222	LYS
1	A	225	VAL
1	A	226	SER
1	A	233	THR
1	A	244	VAL
1	A	245	SER
1	A	254	MET
1	A	260	MET
1	A	261	ILE
1	A	262	SER
1	A	264	TYR
1	A	270	GLN
1	A	271	MET
1	A	274	LEU
1	A	276	VAL
1	A	277	SER
1	A	299	THR
1	A	301	ILE
1	A	308	VAL
1	A	325	SER
1	A	329	ASN
1	A	331	SER
1	A	339	THR
1	A	340	VAL
1	A	341	ASP
1	A	344	THR
1	A	354	ILE
1	A	355	ASN
1	A	356	THR

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Mol	Chain	Res	Type
1	A	363	ASN
1	A	365	ASN
1	A	366	ILE
1	A	367	ARG
1	A	369	TYR
1	A	371	THR
1	A	376	VAL
1	A	380	THR
1	A	382	THR
1	A	384	THR
1	A	385	ILE
1	A	386	VAL
1	A	389	LYS
1	A	398	GLN
1	A	405	TYR
1	A	407	ASN
1	A	414	ILE
1	A	415	ILE
1	A	424	THR
1	A	435	ILE
1	A	442	SER
1	A	450	MET
1	A	451	LEU
1	A	459	ASN
1	A	469	LEU
1	A	470	VAL
1	A	475	ASN
1	A	484	LYS
1	A	485	SER
1	A	486	THR
1	A	490	LEU
1	A	492	LEU
1	A	493	SER
1	A	499	THR
1	A	501	VAL
1	A	514	LYS
1	A	515	THR
1	A	518	LEU
1	A	519	THR
1	A	520	LEU
1	A	524	LEU
1	A	525	VAL

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Mol	Chain	Res	Type
1	A	526	LYS
1	A	538	TYR
1	A	544	ILE
1	A	545	SER
1	A	550	ILE
1	A	554	LEU
1	A	560	VAL
1	A	567	LYS
1	A	569	THR
1	A	573	ASP
1	A	574	ILE
1	A	577	CYS
1	A	578	ILE
1	A	579	ILE
1	A	583	MET
1	A	587	VAL
1	A	589	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	ASN
1	A	93	ASN
1	A	98	ASN
1	A	105	ASN
1	A	113	ASN
1	A	127	GLN
1	A	200	ASN
1	A	207	GLN
1	A	302	ASN
1	A	329	ASN
1	A	363	ASN
1	A	407	ASN
1	A	423	ASN
1	A	455	GLN
1	A	459	ASN
1	A	468	ASN
1	A	500	GLN
1	A	507	ASN
1	A	551	GLN
1	A	568	ASN
1	A	571	ASN

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Mol	Chain	Res	Type
1	A	576	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	A	505/721 (70%)	2.09	222 (43%) 0 0	22, 43, 63, 71	0

All (222) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	562	PHE	8.6
1	A	566	LEU	8.5
1	A	344	THR	7.8
1	A	62	ILE	7.1
1	A	48	PHE	6.9
1	A	378	ASN	6.8
1	A	556	ARG	6.7
1	A	58	GLY	6.7
1	A	305	GLY	6.3
1	A	50	LYS	6.2
1	A	328	ALA	6.1
1	A	343	THR	5.8
1	A	591	THR	5.8
1	A	586	LEU	5.7
1	A	49	SER	5.7
1	A	130	LYS	5.7
1	A	395	ILE	5.6
1	A	359	SER	5.6
1	A	304	VAL	5.3
1	A	332	HIS	5.1
1	A	295	SER	5.0
1	A	507	ASN	4.9
1	A	423	ASN	4.9
1	A	53	ILE	4.8
1	A	306	ALA	4.6
1	A	409	GLY	4.5
1	A	307	GLU	4.5

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Mol	Chain	Res	Type	RSRZ
1	A	302	ASN	4.5
1	A	568	ASN	4.4
1	A	453	THR	4.4
1	A	412	TYR	4.4
1	A	47	THR	4.3
1	A	440	LEU	4.3
1	A	571	ASN	4.3
1	A	398	GLN	4.2
1	A	565	GLN	4.2
1	A	52	ASP	4.2
1	A	64	SER	4.2
1	A	391	SER	4.2
1	A	579	ILE	4.2
1	A	536	LYS	4.1
1	A	436	ASN	4.1
1	A	401	LEU	4.1
1	A	162	THR	4.0
1	A	299	THR	4.0
1	A	438	ASN	4.0
1	A	55	SER	3.9
1	A	303	THR	3.8
1	A	244	VAL	3.8
1	A	435	ILE	3.8
1	A	330	TYR	3.8
1	A	541	GLY	3.7
1	A	437	TYR	3.7
1	A	300	ASN	3.6
1	A	19	THR	3.6
1	A	463	TYR	3.6
1	A	422	LEU	3.6
1	A	588	LYS	3.6
1	A	32	PHE	3.6
1	A	400	SER	3.6
1	A	419	PRO	3.6
1	A	190	ARG	3.5
1	A	567	LYS	3.5
1	A	208	LYS	3.5
1	A	494	LEU	3.5
1	A	383	THR	3.5
1	A	495	PRO	3.5
1	A	443	ILE	3.5
1	A	163	ASN	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	361	TYR	3.4
1	A	448	THR	3.4
1	A	334	TRP	3.3
1	A	339	THR	3.3
1	A	93	ASN	3.3
1	A	42	LEU	3.3
1	A	327	SER	3.3
1	A	577	CYS	3.3
1	A	308	VAL	3.3
1	A	472	ASP	3.3
1	A	329	ASN	3.3
1	A	298	SER	3.2
1	A	471	THR	3.2
1	A	86	PRO	3.2
1	A	408	PRO	3.2
1	A	469	LEU	3.2
1	A	445	ASN	3.2
1	A	35	LEU	3.2
1	A	274	LEU	3.2
1	A	392	VAL	3.2
1	A	396	LYS	3.2
1	A	336	ASN	3.2
1	A	264	TYR	3.2
1	A	114	VAL	3.2
1	A	402	ILE	3.1
1	A	575	MET	3.1
1	A	353	SER	3.1
1	A	405	TYR	3.1
1	A	293	SER	3.1
1	A	477	GLY	3.0
1	A	269	VAL	3.0
1	A	230	LYS	3.0
1	A	85	SER	3.0
1	A	234	ALA	3.0
1	A	439	GLN	3.0
1	A	504	VAL	3.0
1	A	101	LEU	3.0
1	A	369	TYR	3.0
1	A	454	SER	3.0
1	A	576	ASN	2.9
1	A	157	PRO	2.9
1	A	156	LYS	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	540	HIS	2.9
1	A	131	ASN	2.9
1	A	376	VAL	2.9
1	A	146	LYS	2.9
1	A	484	LYS	2.9
1	A	56	ILE	2.8
1	A	356	THR	2.8
1	A	59	ASN	2.8
1	A	415	ILE	2.8
1	A	407	ASN	2.7
1	A	563	GLU	2.7
1	A	404	ASP	2.7
1	A	468	ASN	2.7
1	A	381	PRO	2.7
1	A	297	SER	2.7
1	A	252	VAL	2.7
1	A	590	ILE	2.7
1	A	358	GLU	2.7
1	A	534	ASN	2.7
1	A	301	ILE	2.7
1	A	410	GLY	2.7
1	A	464	ASN	2.7
1	A	433	ILE	2.6
1	A	544	ILE	2.6
1	A	363	ASN	2.6
1	A	38	ILE	2.6
1	A	296	HIS	2.6
1	A	338	SER	2.6
1	A	247	GLN	2.6
1	A	34	ASN	2.6
1	A	160	SER	2.5
1	A	442	SER	2.5
1	A	61	ILE	2.5
1	A	187	ASP	2.5
1	A	248	ILE	2.5
1	A	333	THR	2.5
1	A	141	THR	2.5
1	A	66	ARG	2.5
1	A	137	LEU	2.5
1	A	126	ASN	2.5
1	A	515	THR	2.4
1	A	222	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	517	ARG	2.4
1	A	236	ASP	2.4
1	A	122	LEU	2.4
1	A	105	ASN	2.4
1	A	498	THR	2.4
1	A	380	THR	2.3
1	A	149	ILE	2.3
1	A	462	LYS	2.3
1	A	532	LYS	2.3
1	A	578	ILE	2.3
1	A	29	GLU	2.3
1	A	231	PRO	2.3
1	A	83	THR	2.3
1	A	84	ASN	2.3
1	A	161	ASN	2.3
1	A	267	VAL	2.3
1	A	60	LYS	2.3
1	A	63	LYS	2.3
1	A	240	ASP	2.3
1	A	500	GLN	2.3
1	A	45	ASN	2.3
1	A	108	ASN	2.3
1	A	480	LEU	2.3
1	A	492	LEU	2.3
1	A	572	LYS	2.3
1	A	37	ILE	2.2
1	A	516	PRO	2.2
1	A	425	MET	2.2
1	A	233	THR	2.2
1	A	379	VAL	2.2
1	A	542	MET	2.2
1	A	129	LEU	2.2
1	A	360	ALA	2.2
1	A	418	PRO	2.2
1	A	451	LEU	2.2
1	A	243	LYS	2.2
1	A	499	THR	2.2
1	A	331	SER	2.2
1	A	489	SER	2.2
1	A	200	ASN	2.2
1	A	89	ARG	2.2
1	A	270	GLN	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	483	ILE	2.2
1	A	574	ILE	2.2
1	A	205	MET	2.2
1	A	210	VAL	2.1
1	A	589	VAL	2.1
1	A	441	LYS	2.1
1	A	493	SER	2.1
1	A	413	PRO	2.1
1	A	554	LEU	2.1
1	A	97	PHE	2.1
1	A	508	PHE	2.1
1	A	537	PHE	2.1
1	A	539	PHE	2.1
1	A	71	ILE	2.1
1	A	117	ILE	2.1
1	A	155	LEU	2.1
1	A	549	LYS	2.1
1	A	558	THR	2.1
1	A	545	SER	2.1
1	A	27	TYR	2.1
1	A	294	THR	2.1
1	A	33	PHE	2.1
1	A	434	PRO	2.1
1	A	57	LEU	2.1
1	A	444	ASP	2.0
1	A	386	VAL	2.0
1	A	195	ASP	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.