



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 12:20 AM UTC

PDB ID : 2IE3 / pdb_00002ie3
Title : Structure of the Protein Phosphatase 2A Core Enzyme Bound to Tumor-inducing Toxins
Authors : Xing, Y.; Xu, Y.; Chen, Y.; Jeffrey, P.D.; Chao, Y.; Shi, Y.
Deposited on : 2006-09-17
Resolution : 2.80 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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

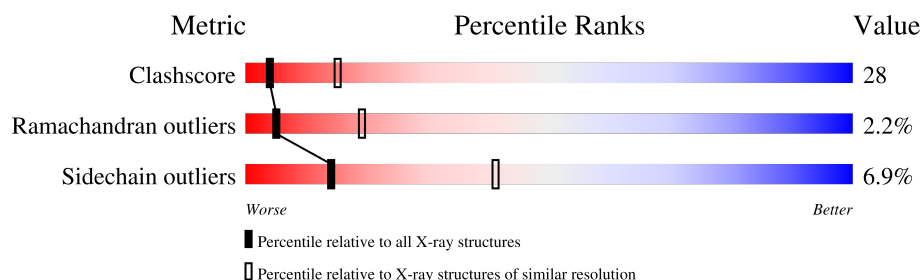
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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))
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	589	
2	C	309	
3	I	7	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6922 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 Protein Phosphatase 2, regulatory subunit A (PR 65), alpha isoform.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	581	Total	C	N	O	S	0	0	0
			4527	2877	763	860	27			

- Molecule 2 is a protein called Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	288	Total	C	N	O	S	0	0	0
			2322	1471	396	440	15			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	5	LEU	VAL	conflict	UNP P67775

- Molecule 3 is a protein called microcystin LR.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	I	7	Total	C	N	O	0	0	0
			71	49	10	12			

- Molecule 4 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

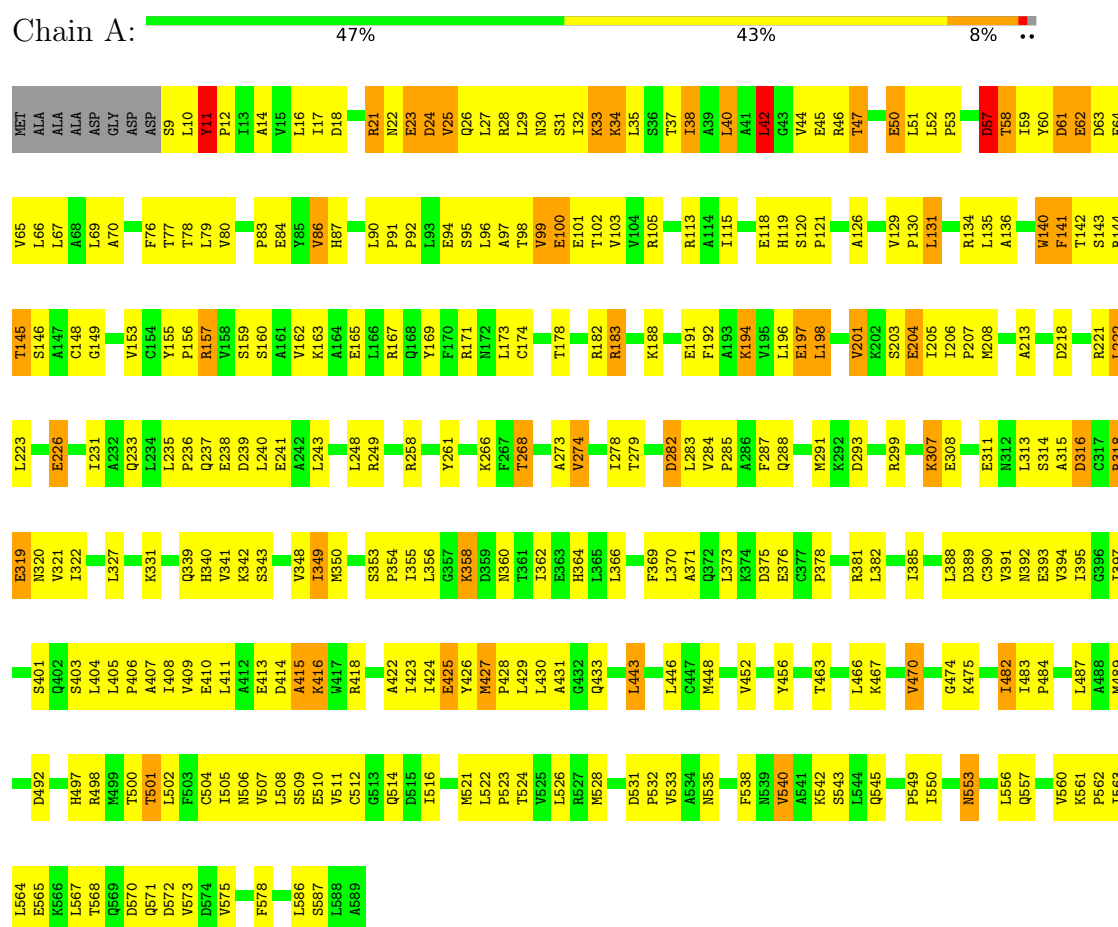
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	2	Total	Mn	0	0
			2	2		

3 Residue-property plots

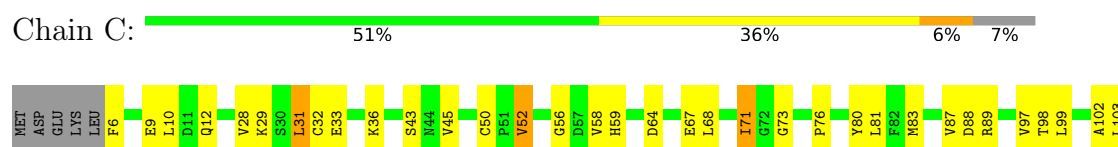
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

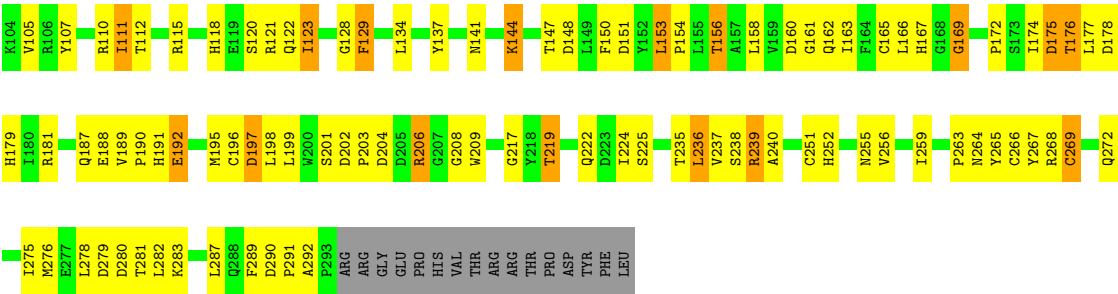
Note EDS was not executed.

- Molecule 1: Protein Phosphatase 2, regulatory subunit A (PR 65), alpha isoform

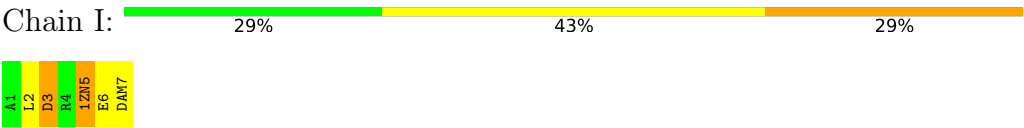


- Molecule 2: Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform





● Molecule 3: microcystin LR



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	93.07Å 195.09Å 201.91Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.80	Depositor
% Data completeness (in resolution range)	92.9 (30.00-2.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.221 , 0.264	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6922	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FGA, DAL, ACB, MN, 1ZN, DAM

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	0.56	0/4601	1.11	24/6246 (0.4%)
2	C	0.59	0/2379	1.12	18/3227 (0.6%)
3	I	0.53	0/17	0.73	0/19
All	All	0.57	0/6997	1.11	42/9492 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	I	0	2

There are no bond length outliers.

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	11	TYR	CA-C-N	-18.08	99.15	118.85
1	A	11	TYR	C-N-CA	-18.08	99.15	118.85
2	C	206	ARG	N-CA-C	-9.41	94.06	109.40
1	A	11	TYR	N-CA-C	8.68	129.00	109.81
1	A	349	ILE	N-CA-C	8.46	119.24	110.36
1	A	482	ILE	N-CA-C	8.17	118.08	111.62
2	C	153	LEU	CA-C-N	7.70	127.75	119.90
2	C	153	LEU	C-N-CA	7.70	127.75	119.90
1	A	34	LYS	N-CA-C	-7.66	101.83	112.25
2	C	255	ASN	N-CA-C	-7.52	104.25	113.50
1	A	42	LEU	N-CA-C	-6.89	98.99	109.95
2	C	71	ILE	N-CA-C	6.83	118.44	111.00
1	A	340	HIS	N-CA-C	-6.76	103.91	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	137	TYR	N-CA-C	-6.61	96.72	110.80
1	A	62	GLU	N-CA-C	-6.34	104.80	113.30
2	C	169	GLY	N-CA-C	6.27	119.33	110.74
2	C	219	THR	N-CA-C	-6.13	100.20	109.95
2	C	269	CYS	N-CA-C	-5.89	102.20	110.50
1	A	235	LEU	N-CA-C	5.88	118.03	110.39
2	C	197	ASP	N-CA-C	5.87	118.43	111.33
1	A	201	VAL	N-CA-C	-5.84	104.82	110.72
1	A	573	VAL	N-CA-C	5.78	116.24	110.23
2	C	272	GLN	N-CA-C	-5.77	102.39	110.35
1	A	38	ILE	N-CA-C	-5.69	104.07	112.04
1	A	47	THR	N-CA-C	-5.69	105.00	111.14
1	A	474	GLY	N-CA-C	5.55	119.67	112.68
1	A	33	LYS	N-CA-C	-5.51	106.68	113.41
2	C	28	VAL	N-CA-C	-5.46	105.40	110.53
2	C	167	HIS	N-CA-C	5.40	116.85	110.97
2	C	222	GLN	N-CA-C	5.39	117.58	111.11
1	A	203	SER	N-CA-C	5.38	119.00	112.23
1	A	153	VAL	N-CA-C	5.35	115.56	110.53
1	A	126	ALA	N-CA-C	5.28	117.04	111.28
1	A	282	ASP	N-CA-C	5.28	119.79	112.45
1	A	283	LEU	N-CA-C	5.24	117.90	111.82
1	A	243	LEU	N-CA-C	5.19	119.67	113.23
2	C	43	SER	N-CA-C	5.19	117.76	110.14
1	A	470	VAL	N-CA-C	-5.16	105.50	110.72
2	C	141	ASN	N-CA-C	5.13	116.56	110.97
1	A	553	ASN	N-CA-C	5.07	117.70	111.82
2	C	64	ASP	N-CA-C	-5.05	106.28	112.90
2	C	201	SER	N-CA-C	5.02	117.15	110.53

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	I	5	1ZN	Mainchain,Peptide

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	4527	0	4633	280	0
2	C	2322	0	2223	112	0
3	I	71	0	61	3	0
4	C	2	0	0	0	0
All	All	6922	0	6917	387	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 28.

All (387) 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:99:VAL:HG12	1:A:100:GLU:H	1.05	1.11
2:C:190:PRO:HD3	2:C:195:MET:HE2	1.42	0.99
1:A:526:LEU:HD22	1:A:563:ILE:HG13	1.51	0.91
2:C:115:ARG:HH12	2:C:151:ASP:HA	1.33	0.90
1:A:99:VAL:HG12	1:A:100:GLU:N	1.83	0.90
2:C:115:ARG:HH21	2:C:189:VAL:HG23	1.37	0.90
1:A:99:VAL:CG1	1:A:100:GLU:H	1.85	0.89
2:C:115:ARG:NH1	2:C:151:ASP:HA	1.88	0.88
2:C:118:HIS:CG	2:C:123:ILE:HD11	2.09	0.87
2:C:45:VAL:HA	2:C:156:THR:HG22	1.55	0.86
1:A:311:GLU:HG2	1:A:355:ILE:HD11	1.56	0.85
1:A:194:LYS:HD2	1:A:194:LYS:O	1.77	0.84
1:A:416:LYS:HD3	1:A:416:LYS:H	1.42	0.83
1:A:59:ILE:HG23	1:A:66:LEU:HD21	1.61	0.82
2:C:81:LEU:HD12	2:C:112:THR:HB	1.61	0.81
1:A:213:ALA:O	1:A:221:ARG:HD2	1.80	0.81
2:C:118:HIS:ND1	2:C:123:ILE:HD11	1.97	0.80
1:A:373:LEU:HD11	1:A:385:ILE:HD11	1.64	0.80
1:A:381:ARG:HD2	1:A:426:TYR:OH	1.82	0.80
2:C:281:THR:HG22	2:C:281:THR:O	1.83	0.79
1:A:27:LEU:HD13	1:A:32:ILE:HD11	1.64	0.79
2:C:276:MET:HE3	2:C:278:LEU:HD21	1.64	0.79
2:C:175:ASP:H	2:C:179:HIS:HD2	1.30	0.78
2:C:176:THR:HG22	2:C:179:HIS:H	1.48	0.77
2:C:67:GLU:HB2	2:C:292:ALA:HB2	1.66	0.76
1:A:339:GLN:O	1:A:343:SER:HB2	1.86	0.75
1:A:105:ARG:HH21	1:A:145:THR:HG21	1.51	0.75
1:A:97:ALA:O	1:A:105:ARG:HD2	1.87	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:176:THR:CG2	2:C:178:ASP:H	2.00	0.74
1:A:29:LEU:HD11	1:A:64:GLU:HG2	1.69	0.74
1:A:226:GLU:OE2	1:A:266:LYS:HE3	1.88	0.74
1:A:42:LEU:HB2	1:A:46:ARG:HB2	1.69	0.73
1:A:57:ASP:O	1:A:59:ILE:HG13	1.89	0.72
2:C:275:ILE:HG22	2:C:287:LEU:HB2	1.71	0.72
1:A:564:LEU:O	1:A:568:THR:HG23	1.89	0.72
1:A:416:LYS:HD3	1:A:416:LYS:N	2.04	0.72
1:A:67:LEU:HD13	1:A:103:VAL:HG12	1.71	0.72
1:A:388:LEU:H	1:A:433:GLN:HE22	1.38	0.70
2:C:118:HIS:HA	2:C:123:ILE:CD1	2.22	0.70
1:A:28:ARG:HH11	1:A:30:ASN:HB2	1.58	0.69
1:A:204:GLU:O	1:A:208:MET:HG3	1.93	0.69
1:A:131:LEU:HD12	1:A:131:LEU:C	2.18	0.68
1:A:52:LEU:HB2	1:A:53:PRO:HD3	1.76	0.68
1:A:285:PRO:HA	1:A:288:GLN:HE21	1.57	0.68
2:C:264:ASN:ND2	2:C:267:TYR:HA	2.09	0.68
2:C:290:ASP:HB3	2:C:291:PRO:HD2	1.74	0.68
1:A:409:VAL:HG22	1:A:446:LEU:HD21	1.75	0.68
1:A:446:LEU:HD12	1:A:446:LEU:H	1.58	0.68
2:C:122:GLN:HE22	2:C:191:HIS:HE1	1.40	0.67
2:C:176:THR:HG22	2:C:178:ASP:N	2.09	0.67
1:A:452:VAL:HG22	1:A:497:HIS:CE1	2.30	0.67
1:A:159:SER:OG	1:A:162:VAL:HG23	1.95	0.66
1:A:62:GLU:HA	1:A:62:GLU:OE2	1.96	0.65
1:A:29:LEU:C	1:A:29:LEU:HD23	2.22	0.65
1:A:284:VAL:O	1:A:288:GLN:HG3	1.97	0.65
2:C:283:LYS:HE2	2:C:283:LYS:HA	1.78	0.65
2:C:81:LEU:CD1	2:C:112:THR:HB	2.27	0.65
2:C:204:ASP:O	2:C:252:HIS:HE1	1.79	0.64
2:C:268:ARG:HB3	2:C:268:ARG:NH1	2.11	0.64
1:A:467:LYS:HB2	1:A:507:VAL:CG1	2.28	0.64
1:A:136:ALA:O	1:A:144:ARG:HG3	1.98	0.64
1:A:23:GLU:HG3	1:A:26:GLN:CD	2.23	0.64
1:A:378:PRO:HA	1:A:381:ARG:NH1	2.13	0.63
2:C:191:HIS:C	2:C:192:GLU:HG3	2.23	0.63
1:A:205:ILE:HD13	1:A:208:MET:HE3	1.81	0.63
1:A:183:ARG:HG3	1:A:183:ARG:HH11	1.64	0.63
1:A:358:LYS:O	1:A:362:ILE:HG13	1.98	0.63
1:A:514:GLN:HG3	1:A:550:ILE:O	1.99	0.63
1:A:62:GLU:O	1:A:64:GLU:N	2.31	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:40:LEU:N	1:A:40:LEU:HD22	2.13	0.62
1:A:538:PHE:HB2	1:A:578:PHE:HD2	1.64	0.62
1:A:29:LEU:HD21	1:A:33:LYS:HE3	1.82	0.62
2:C:208:GLY:C	2:C:224:ILE:HD11	2.25	0.62
1:A:23:GLU:HG3	1:A:26:GLN:OE1	1.99	0.61
1:A:96:LEU:O	1:A:99:VAL:HG23	1.99	0.61
2:C:89:ARG:HD2	2:C:266:CYS:SG	2.39	0.61
2:C:176:THR:HG22	2:C:178:ASP:H	1.65	0.61
1:A:183:ARG:HG3	1:A:183:ARG:NH1	2.15	0.61
1:A:409:VAL:O	1:A:413:GLU:HG2	2.00	0.61
1:A:350:MET:HB3	1:A:391:VAL:HG23	1.83	0.60
1:A:489:MET:HE1	1:A:500:THR:HG22	1.84	0.60
1:A:37:THR:HA	1:A:40:LEU:HD23	1.83	0.60
2:C:281:THR:O	2:C:281:THR:CG2	2.49	0.60
1:A:155:TYR:HB3	1:A:156:PRO:HD3	1.84	0.60
1:A:349:ILE:HG23	1:A:350:MET:N	2.16	0.60
2:C:176:THR:HG23	2:C:178:ASP:H	1.67	0.60
1:A:475:LYS:HB2	1:A:516:ILE:HD12	1.84	0.59
1:A:390:CYS:O	1:A:394:VAL:HG23	2.01	0.59
2:C:115:ARG:NH1	2:C:150:PHE:O	2.33	0.59
2:C:225:SER:OG	2:C:252:HIS:HD2	1.84	0.59
1:A:129:VAL:HB	1:A:130:PRO:HD3	1.84	0.59
1:A:165:GLU:O	1:A:169:TYR:HD1	1.86	0.59
2:C:177:LEU:O	2:C:181:ARG:HG3	2.01	0.59
1:A:240:LEU:HD13	1:A:274:VAL:HG23	1.84	0.59
1:A:392:ASN:O	1:A:395:ILE:O	2.20	0.59
1:A:446:LEU:HD12	1:A:446:LEU:N	2.18	0.59
1:A:62:GLU:HB3	1:A:65:VAL:HB	1.83	0.59
1:A:535:ASN:HA	1:A:538:PHE:CE2	2.39	0.58
2:C:50:CYS:HA	2:C:52:VAL:HG22	1.85	0.58
1:A:509:SER:O	1:A:550:ILE:HD13	2.02	0.58
2:C:188:GLU:HG3	2:C:189:VAL:N	2.17	0.58
1:A:37:THR:OG1	1:A:38:ILE:HD12	2.03	0.58
1:A:307:LYS:O	1:A:311:GLU:HG3	2.03	0.58
2:C:276:MET:HE3	2:C:278:LEU:CD2	2.31	0.58
1:A:507:VAL:O	1:A:510:GLU:HB2	2.04	0.58
1:A:241:GLU:OE2	1:A:249:ARG:NH2	2.37	0.57
1:A:489:MET:HB2	1:A:501:THR:OG1	2.05	0.57
1:A:136:ALA:O	1:A:144:ARG:CG	2.52	0.57
1:A:318:ARG:O	1:A:321:VAL:HG22	2.05	0.57
2:C:176:THR:CG2	2:C:178:ASP:HB2	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:424:ILE:O	1:A:427:MET:HB2	2.05	0.57
1:A:427:MET:HE1	1:A:443:LEU:HG	1.86	0.57
1:A:388:LEU:H	1:A:433:GLN:NE2	2.04	0.56
2:C:158:LEU:HD21	2:C:161:GLY:HA2	1.87	0.56
2:C:59:HIS:HE1	2:C:118:HIS:CD2	2.23	0.56
1:A:46:ARG:HD2	1:A:50:GLU:CD	2.31	0.56
1:A:206:ILE:HB	1:A:207:PRO:HD3	1.86	0.56
1:A:205:ILE:HD13	1:A:208:MET:CE	2.35	0.56
1:A:370:LEU:HD21	1:A:403:SER:O	2.06	0.56
2:C:68:LEU:HG	2:C:275:ILE:HD12	1.88	0.56
1:A:492:ASP:O	1:A:498:ARG:HD3	2.05	0.55
2:C:203:PRO:HD2	2:C:239:ARG:CZ	2.35	0.55
1:A:381:ARG:O	1:A:385:ILE:HG12	2.05	0.55
1:A:236:PRO:HG2	1:A:239:ASP:OD2	2.07	0.55
1:A:356:LEU:O	1:A:360:ASN:HB2	2.06	0.55
1:A:44:VAL:HG23	1:A:80:VAL:C	2.30	0.55
2:C:197:ASP:OD1	2:C:217:GLY:HA2	2.05	0.55
1:A:28:ARG:NH1	1:A:30:ASN:HD22	2.04	0.55
1:A:586:LEU:O	1:A:587:SER:HB2	2.05	0.55
1:A:57:ASP:O	1:A:58:THR:C	2.47	0.55
1:A:373:LEU:HD11	1:A:385:ILE:CD1	2.35	0.55
1:A:197:GLU:CD	1:A:197:GLU:H	2.15	0.55
2:C:118:HIS:HA	2:C:123:ILE:HD11	1.88	0.55
1:A:59:ILE:HG22	1:A:59:ILE:O	2.06	0.54
1:A:350:MET:SD	1:A:369:PHE:HB2	2.47	0.54
2:C:263:PRO:O	2:C:264:ASN:C	2.49	0.54
1:A:542:LYS:NZ	1:A:578:PHE:CE1	2.76	0.54
1:A:502:LEU:HD11	1:A:540:VAL:HG23	1.90	0.54
1:A:141:PHE:C	1:A:141:PHE:CD1	2.84	0.54
1:A:353:SER:OG	1:A:391:VAL:HG22	2.08	0.54
1:A:553:ASN:O	1:A:557:GLN:HG2	2.08	0.54
2:C:268:ARG:HB3	2:C:268:ARG:HH11	1.73	0.54
1:A:194:LYS:O	1:A:194:LYS:CD	2.52	0.53
1:A:86:VAL:HG11	1:A:118:GLU:CB	2.39	0.53
1:A:205:ILE:HA	1:A:208:MET:HE3	1.91	0.53
1:A:28:ARG:NH1	1:A:30:ASN:HB2	2.22	0.53
2:C:190:PRO:HD3	2:C:195:MET:CE	2.26	0.53
1:A:60:TYR:O	1:A:62:GLU:N	2.41	0.53
1:A:155:TYR:CZ	1:A:196:LEU:HD22	2.44	0.53
1:A:205:ILE:HG22	1:A:231:ILE:HD13	1.90	0.53
2:C:169:GLY:O	2:C:198:LEU:HA	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:113:ARG:NH1	1:A:149:GLY:O	2.42	0.53
1:A:131:LEU:C	1:A:131:LEU:CD1	2.81	0.53
1:A:572:ASP:OD2	2:C:110:ARG:NH2	2.42	0.53
2:C:266:CYS:SG	3:I:2:LEU:HD12	2.48	0.53
2:C:118:HIS:HA	2:C:123:ILE:HD13	1.90	0.52
1:A:233:GLN:HG3	1:A:273:ALA:CB	2.40	0.52
1:A:470:VAL:HG11	1:A:511:VAL:HG23	1.90	0.52
2:C:87:VAL:O	2:C:88:ASP:HB2	2.09	0.52
1:A:86:VAL:HG11	1:A:118:GLU:HB2	1.91	0.52
1:A:233:GLN:HG3	1:A:273:ALA:HB1	1.92	0.52
1:A:258:ARG:O	1:A:261:TYR:HB3	2.09	0.52
1:A:59:ILE:HG23	1:A:66:LEU:CD2	2.34	0.52
2:C:162:GLN:HB3	2:C:235:THR:OG1	2.10	0.52
1:A:21:ARG:NH1	1:A:26:GLN:OE1	2.43	0.52
1:A:115:ILE:O	1:A:119:HIS:HD2	1.93	0.52
1:A:505:ILE:HG23	1:A:521:MET:HB3	1.91	0.52
1:A:32:ILE:HG22	1:A:32:ILE:O	2.09	0.52
1:A:466:LEU:HD22	1:A:482:ILE:HD13	1.91	0.52
1:A:467:LYS:HB2	1:A:507:VAL:HG13	1.92	0.52
1:A:83:PRO:O	1:A:86:VAL:HG22	2.10	0.51
1:A:404:LEU:HD11	1:A:408:ILE:HD11	1.91	0.51
2:C:268:ARG:NH1	3:I:2:LEU:HD21	2.25	0.51
1:A:102:THR:CG2	1:A:105:ARG:HH12	2.22	0.51
1:A:44:VAL:HG13	1:A:45:GLU:N	2.26	0.51
1:A:90:LEU:HB2	1:A:91:PRO:HD3	1.92	0.51
1:A:282:ASP:O	1:A:285:PRO:HD2	2.11	0.51
2:C:165:CYS:HA	2:C:238:SER:O	2.10	0.51
1:A:506:ASN:HD21	1:A:543:SER:CB	2.24	0.51
2:C:80:TYR:HB2	2:C:111:ILE:HG22	1.93	0.51
1:A:11:TYR:O	1:A:12:PRO:C	2.47	0.51
1:A:40:LEU:N	1:A:40:LEU:CD2	2.73	0.51
2:C:89:ARG:HG3	2:C:265:TYR:OH	2.11	0.50
2:C:121:ARG:HG2	2:C:147:THR:HB	1.93	0.50
2:C:176:THR:HG21	2:C:178:ASP:HB2	1.92	0.50
1:A:145:THR:HG22	1:A:146:SER:N	2.26	0.50
1:A:58:THR:O	1:A:58:THR:HG22	2.11	0.50
1:A:155:TYR:CE1	1:A:163:LYS:HB3	2.46	0.50
2:C:189:VAL:HA	2:C:195:MET:HE3	1.93	0.50
1:A:350:MET:HB3	1:A:391:VAL:CG2	2.41	0.50
2:C:279:ASP:OD2	2:C:283:LYS:HB2	2.11	0.50
1:A:35:LEU:C	1:A:37:THR:H	2.18	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:157:ARG:HG2	1:A:157:ARG:HH11	1.77	0.50
1:A:287:PHE:CD2	1:A:291:MET:HE2	2.47	0.50
1:A:411:LEU:C	1:A:413:GLU:H	2.20	0.50
1:A:102:THR:HA	1:A:105:ARG:NH1	2.27	0.50
2:C:283:LYS:HE2	2:C:283:LYS:CA	2.42	0.50
2:C:187:GLN:HG2	2:C:195:MET:HE1	1.94	0.49
1:A:313:LEU:HD13	1:A:321:VAL:CG2	2.42	0.49
1:A:354:PRO:HD3	1:A:390:CYS:SG	2.52	0.49
2:C:176:THR:HG22	2:C:179:HIS:N	2.23	0.49
1:A:136:ALA:O	1:A:144:ARG:HD2	2.12	0.49
2:C:83:MET:HE3	2:C:240:ALA:HB2	1.93	0.49
2:C:251:CYS:O	2:C:252:HIS:HB2	2.12	0.49
1:A:452:VAL:CG2	1:A:497:HIS:CE1	2.95	0.49
2:C:237:VAL:HB	2:C:256:VAL:HG22	1.95	0.49
1:A:87:HIS:HA	1:A:90:LEU:HG	1.95	0.49
2:C:31:LEU:HD21	2:C:102:ALA:HA	1.94	0.49
1:A:80:VAL:HG12	1:A:80:VAL:O	2.12	0.49
2:C:115:ARG:NH2	2:C:189:VAL:HG23	2.18	0.49
1:A:38:ILE:HD12	1:A:38:ILE:N	2.27	0.49
1:A:47:THR:HG23	1:A:51:LEU:HD23	1.94	0.49
1:A:542:LYS:NZ	1:A:578:PHE:CD1	2.81	0.49
2:C:264:ASN:HA	2:C:269:CYS:O	2.13	0.48
1:A:42:LEU:HB2	1:A:46:ARG:CB	2.41	0.48
1:A:327:LEU:HG	1:A:331:LYS:HE3	1.95	0.48
2:C:187:GLN:HG3	2:C:188:GLU:O	2.13	0.48
1:A:78:THR:C	1:A:80:VAL:H	2.21	0.48
1:A:105:ARG:HH11	1:A:105:ARG:HG3	1.76	0.48
2:C:144:LYS:HE3	2:C:148:ASP:OD2	2.13	0.48
2:C:190:PRO:CD	2:C:195:MET:HE2	2.28	0.48
1:A:25:VAL:HG12	1:A:25:VAL:O	2.13	0.48
1:A:9:SER:O	1:A:10:LEU:HD23	2.14	0.48
1:A:94:GLU:OE1	1:A:134:ARG:NH2	2.43	0.48
1:A:17:ILE:HG22	1:A:18:ASP:N	2.29	0.48
1:A:38:ILE:HD12	1:A:38:ILE:H	1.79	0.48
1:A:293:ASP:O	1:A:299:ARG:HD3	2.14	0.48
1:A:353:SER:N	1:A:354:PRO:HD2	2.29	0.48
1:A:522:LEU:N	1:A:523:PRO:CD	2.77	0.48
1:A:411:LEU:C	1:A:413:GLU:N	2.72	0.48
1:A:37:THR:CA	1:A:40:LEU:HD23	2.42	0.47
1:A:46:ARG:HD2	1:A:50:GLU:OE2	2.14	0.47
1:A:174:CYS:O	1:A:182:ARG:HD2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:122:GLN:HG3	2:C:188:GLU:OE2	2.13	0.47
1:A:456:TYR:CD1	2:C:73:GLY:HA2	2.49	0.47
1:A:183:ARG:HH11	1:A:183:ARG:CG	2.27	0.47
1:A:509:SER:HB2	1:A:550:ILE:HD12	1.97	0.47
1:A:92:PRO:O	1:A:95:SER:HB3	2.14	0.47
2:C:176:THR:O	2:C:179:HIS:HB2	2.15	0.47
1:A:240:LEU:HD13	1:A:274:VAL:CG2	2.44	0.47
1:A:307:LYS:HE2	1:A:311:GLU:OE1	2.15	0.47
1:A:533:VAL:HG21	2:C:280:ASP:OD2	2.14	0.47
1:A:140:TRP:CD1	1:A:140:TRP:N	2.82	0.47
1:A:188:LYS:HD2	1:A:191:GLU:OE2	2.14	0.47
1:A:538:PHE:HB3	1:A:575:VAL:HA	1.96	0.47
1:A:567:LEU:O	1:A:570:ASP:HB2	2.15	0.46
1:A:538:PHE:CD1	1:A:538:PHE:C	2.93	0.46
1:A:561:LYS:HB3	1:A:562:PRO:HD3	1.98	0.46
1:A:10:LEU:O	1:A:14:ALA:HB2	2.16	0.46
1:A:32:ILE:O	1:A:32:ILE:CG2	2.63	0.46
2:C:120:SER:HB3	2:C:123:ILE:HG23	1.97	0.46
1:A:463:THR:HG23	1:A:504:CYS:SG	2.55	0.46
1:A:69:LEU:HD12	1:A:69:LEU:O	2.15	0.46
1:A:141:PHE:CD1	1:A:142:THR:N	2.84	0.46
2:C:191:HIS:O	2:C:192:GLU:HG3	2.16	0.46
1:A:311:GLU:CG	1:A:355:ILE:HD11	2.38	0.46
1:A:376:GLU:O	1:A:378:PRO:HD3	2.16	0.46
1:A:411:LEU:HB2	1:A:423:ILE:HG13	1.97	0.46
1:A:279:THR:O	1:A:284:VAL:HG23	2.16	0.46
1:A:307:LYS:HB3	1:A:307:LYS:NZ	2.31	0.46
1:A:369:PHE:O	1:A:373:LEU:HB2	2.16	0.46
1:A:422:ALA:O	1:A:425:GLU:HG2	2.15	0.46
1:A:102:THR:HG22	1:A:105:ARG:HH12	1.80	0.45
1:A:314:SER:C	1:A:316:ASP:N	2.73	0.45
1:A:322:ILE:HG21	1:A:356:LEU:HD21	1.98	0.45
1:A:483:ILE:N	1:A:484:PRO:CD	2.79	0.45
1:A:100:GLU:O	1:A:101:GLU:C	2.59	0.45
1:A:171:ARG:HH12	1:A:204:GLU:CG	2.29	0.45
1:A:318:ARG:O	1:A:320:ASN:N	2.49	0.45
1:A:531:ASP:CG	1:A:532:PRO:HD2	2.41	0.45
1:A:369:PHE:HZ	1:A:404:LEU:HB2	1.81	0.45
2:C:268:ARG:HH11	2:C:268:ARG:CB	2.29	0.45
1:A:206:ILE:CB	1:A:207:PRO:HD3	2.47	0.45
1:A:248:LEU:O	1:A:248:LEU:HD12	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:140:TRP:CD1	1:A:140:TRP:H	2.34	0.45
1:A:284:VAL:HB	1:A:285:PRO:HD3	1.98	0.45
1:A:425:GLU:O	1:A:428:PRO:HD2	2.17	0.45
2:C:281:THR:HG22	2:C:283:LYS:HE3	1.98	0.45
1:A:44:VAL:HG13	1:A:45:GLU:H	1.81	0.45
1:A:349:ILE:CG2	1:A:350:MET:N	2.79	0.45
1:A:561:LYS:O	1:A:565:GLU:HG3	2.17	0.45
2:C:115:ARG:HB2	2:C:153:LEU:HB2	1.99	0.45
1:A:84:GLU:H	1:A:84:GLU:CD	2.24	0.45
1:A:99:VAL:CG1	1:A:100:GLU:N	2.55	0.45
1:A:378:PRO:CB	1:A:381:ARG:HH12	2.30	0.45
1:A:407:ALA:O	1:A:410:GLU:HB3	2.17	0.45
1:A:268:THR:HG21	1:A:308:GLU:CG	2.47	0.44
1:A:401:SER:O	1:A:405:LEU:HB2	2.17	0.44
1:A:429:LEU:O	1:A:430:LEU:C	2.59	0.44
1:A:34:LYS:O	1:A:38:ILE:CD1	2.65	0.44
1:A:391:VAL:O	1:A:395:ILE:HG12	2.18	0.44
2:C:89:ARG:NH2	3:I:3:ACB:O	2.47	0.44
1:A:67:LEU:CD1	1:A:103:VAL:HG12	2.43	0.44
1:A:556:LEU:HD23	1:A:560:VAL:HG21	1.99	0.44
2:C:202:ASP:O	2:C:219:THR:HA	2.17	0.44
1:A:77:THR:HG23	1:A:86:VAL:HG13	2.00	0.44
1:A:350:MET:CE	1:A:369:PHE:HB2	2.48	0.44
2:C:166:LEU:HD23	2:C:166:LEU:N	2.33	0.44
1:A:130:PRO:O	1:A:134:ARG:HG3	2.18	0.44
1:A:148:CYS:SG	1:A:173:LEU:HD13	2.57	0.44
1:A:389:ASP:O	1:A:393:GLU:OE1	2.36	0.44
1:A:414:ASP:OD1	1:A:415:ALA:N	2.51	0.44
1:A:418:ARG:NH2	2:C:67:GLU:OE1	2.51	0.44
1:A:427:MET:CE	1:A:443:LEU:HG	2.48	0.44
2:C:97:VAL:HG13	2:C:98:THR:N	2.32	0.44
1:A:155:TYR:OH	1:A:167:ARG:NH1	2.51	0.43
1:A:314:SER:O	1:A:315:ALA:C	2.61	0.43
1:A:545:GLN:O	1:A:545:GLN:HG2	2.18	0.43
2:C:29:LYS:O	2:C:33:GLU:HG3	2.17	0.43
2:C:81:LEU:HD12	2:C:112:THR:CB	2.41	0.43
1:A:198:LEU:O	1:A:201:VAL:N	2.50	0.43
1:A:80:VAL:O	1:A:80:VAL:CG1	2.66	0.43
1:A:135:LEU:HD23	1:A:143:SER:OG	2.19	0.43
1:A:218:ASP:OD1	1:A:258:ARG:NH1	2.51	0.43
1:A:446:LEU:H	1:A:446:LEU:CD1	2.28	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:318:ARG:HG2	1:A:319:GLU:N	2.33	0.43
1:A:375:ASP:O	1:A:381:ARG:NH2	2.51	0.43
1:A:571:GLN:HG2	1:A:572:ASP:N	2.34	0.43
1:A:96:LEU:HA	1:A:99:VAL:HG23	2.01	0.43
2:C:10:LEU:HD11	2:C:105:VAL:HG12	1.99	0.43
2:C:32:CYS:O	2:C:36:LYS:HG3	2.19	0.43
1:A:487:LEU:HD22	1:A:524:THR:OG1	2.19	0.43
1:A:42:LEU:H	1:A:42:LEU:HD22	1.84	0.43
1:A:61:ASP:HA	1:A:66:LEU:HD11	2.00	0.43
1:A:70:ALA:HB2	1:A:96:LEU:HD13	2.01	0.43
1:A:448:MET:HE2	1:A:448:MET:HA	2.01	0.43
1:A:508:LEU:O	1:A:512:CYS:HB2	2.18	0.43
1:A:561:LYS:N	1:A:562:PRO:CD	2.82	0.43
1:A:456:TYR:CG	2:C:73:GLY:HA2	2.54	0.43
1:A:96:LEU:C	1:A:99:VAL:HG23	2.44	0.42
1:A:313:LEU:HD13	1:A:321:VAL:HG21	1.99	0.42
2:C:282:LEU:HD23	2:C:282:LEU:HA	1.82	0.42
1:A:102:THR:HG22	1:A:105:ARG:NH1	2.34	0.42
2:C:99:LEU:O	2:C:102:ALA:HB3	2.18	0.42
2:C:115:ARG:HG2	2:C:199:LEU:HD21	2.02	0.42
1:A:392:ASN:HD21	1:A:397:ILE:HA	1.84	0.42
1:A:406:PRO:O	1:A:410:GLU:HB2	2.19	0.42
1:A:427:MET:HE3	1:A:427:MET:HA	2.02	0.42
2:C:56:GLY:HA3	2:C:259:ILE:O	2.19	0.42
1:A:24:ASP:C	1:A:25:VAL:HG23	2.44	0.42
1:A:77:THR:HG23	1:A:86:VAL:CG1	2.50	0.42
1:A:105:ARG:CZ	1:A:142:THR:HG22	2.49	0.42
1:A:222:LEU:HD23	1:A:223:LEU:N	2.34	0.42
1:A:370:LEU:O	1:A:371:ALA:C	2.62	0.42
2:C:76:PRO:HG3	2:C:107:TYR:CE1	2.55	0.42
2:C:97:VAL:CG1	2:C:98:THR:N	2.82	0.42
1:A:60:TYR:O	1:A:61:ASP:C	2.63	0.42
1:A:98:THR:O	1:A:98:THR:HG22	2.19	0.42
1:A:196:LEU:CD1	1:A:205:ILE:HD11	2.50	0.42
2:C:6:PHE:O	2:C:9:GLU:HB3	2.20	0.42
2:C:45:VAL:HG22	2:C:156:THR:CG2	2.50	0.42
1:A:222:LEU:HD23	1:A:222:LEU:C	2.44	0.42
1:A:341:VAL:O	1:A:342:LYS:C	2.62	0.42
1:A:397:ILE:O	1:A:401:SER:HB2	2.20	0.42
2:C:45:VAL:HG22	2:C:156:THR:HG21	2.01	0.42
2:C:176:THR:HB	2:C:179:HIS:CD2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:389:ASP:C	1:A:393:GLU:OE1	2.63	0.42
2:C:10:LEU:HA	2:C:10:LEU:HD23	1.83	0.42
2:C:76:PRO:HB2	2:C:110:ARG:HG3	2.02	0.42
1:A:120:SER:O	1:A:121:PRO:C	2.62	0.41
1:A:136:ALA:O	1:A:144:ARG:CD	2.67	0.41
2:C:190:PRO:O	2:C:196:CYS:HB2	2.20	0.41
1:A:192:PHE:CE1	1:A:196:LEU:HD21	2.55	0.41
1:A:238:GLU:H	1:A:238:GLU:CD	2.27	0.41
2:C:71:ILE:CD1	2:C:289:PHE:HB3	2.50	0.41
1:A:201:VAL:HA	1:A:205:ILE:CG1	2.50	0.41
1:A:498:ARG:HG2	1:A:528:MET:HE3	2.02	0.41
1:A:17:ILE:CG2	1:A:18:ASP:N	2.84	0.41
1:A:284:VAL:N	1:A:285:PRO:CD	2.84	0.41
2:C:163:ILE:HG23	2:C:236:LEU:HD23	2.03	0.41
1:A:78:THR:O	1:A:80:VAL:N	2.53	0.41
1:A:38:ILE:O	1:A:42:LEU:HD22	2.20	0.41
1:A:102:THR:O	1:A:103:VAL:C	2.63	0.41
1:A:141:PHE:O	1:A:142:THR:C	2.64	0.41
1:A:44:VAL:HG23	1:A:80:VAL:O	2.21	0.41
1:A:327:LEU:HD21	1:A:364:HIS:HB3	2.03	0.41
2:C:172:PRO:HA	2:C:209:TRP:CZ2	2.56	0.41
2:C:225:SER:OG	2:C:252:HIS:CD2	2.70	0.41
1:A:196:LEU:HD11	1:A:205:ILE:HD11	2.03	0.41
1:A:29:LEU:C	1:A:31:SER:N	2.79	0.40
2:C:9:GLU:O	2:C:12:GLN:HB3	2.21	0.40
2:C:103:LEU:O	2:C:111:ILE:HD11	2.20	0.40
2:C:128:GLY:O	2:C:129:PHE:C	2.64	0.40
1:A:318:ARG:HD3	1:A:355:ILE:CG2	2.51	0.40
1:A:240:LEU:HD12	1:A:278:ILE:HD12	2.04	0.40
1:A:318:ARG:HD3	1:A:355:ILE:HG23	2.03	0.40
2:C:115:ARG:NH1	2:C:150:PHE:C	2.80	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	579/589 (98%)	499 (86%)	62 (11%)	18 (3%)	3	12
2	C	286/309 (93%)	255 (89%)	30 (10%)	1 (0%)	36	66
3	I	1/7 (14%)	1 (100%)	0	0	100	100
All	All	866/905 (96%)	755 (87%)	92 (11%)	19 (2%)	5	19

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	61	ASP
1	A	63	ASP
1	A	319	GLU
1	A	21	ARG
1	A	23	GLU
1	A	57	ASP
1	A	79	LEU
1	A	140	TRP
1	A	316	ASP
1	A	431	ALA
2	C	129	PHE
1	A	198	LEU
1	A	415	ALA
1	A	25	VAL
1	A	58	THR
1	A	318	ARG
1	A	22	ASN
1	A	99	VAL
1	A	348	VAL

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	508/512 (99%)	472 (93%)	36 (7%)	13	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	C	254/274 (93%)	237 (93%)	17 (7%)	15	42
3	I	2/2 (100%)	2 (100%)	0	100	100
All	All	764/788 (97%)	711 (93%)	53 (7%)	14	41

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	TYR
1	A	16	LEU
1	A	24	ASP
1	A	40	LEU
1	A	42	LEU
1	A	50	GLU
1	A	57	ASP
1	A	76	PHE
1	A	86	VAL
1	A	100	GLU
1	A	131	LEU
1	A	141	PHE
1	A	145	THR
1	A	157	ARG
1	A	160	SER
1	A	178	THR
1	A	183	ARG
1	A	194	LYS
1	A	197	GLU
1	A	204	GLU
1	A	222	LEU
1	A	226	GLU
1	A	237	GLN
1	A	268	THR
1	A	274	VAL
1	A	307	LYS
1	A	358	LYS
1	A	366	LEU
1	A	382	LEU
1	A	416	LYS
1	A	425	GLU
1	A	427	MET
1	A	443	LEU
1	A	501	THR

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Mol	Chain	Res	Type
1	A	540	VAL
1	A	549	PRO
2	C	31	LEU
2	C	52	VAL
2	C	58	VAL
2	C	111	ILE
2	C	123	ILE
2	C	134	LEU
2	C	144	LYS
2	C	154	PRO
2	C	156	THR
2	C	160	ASP
2	C	174	ILE
2	C	175	ASP
2	C	176	THR
2	C	192	GLU
2	C	206	ARG
2	C	236	LEU
2	C	239	ARG

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

Mol	Chain	Res	Type
1	A	30	ASN
1	A	119	HIS
1	A	127	HIS
1	A	200	ASN
1	A	237	GLN
1	A	271	GLN
1	A	288	GLN
1	A	320	ASN
1	A	325	GLN
1	A	364	HIS
1	A	392	ASN
1	A	402	GLN
1	A	433	GLN
1	A	465	ASN
1	A	506	ASN
2	C	12	GLN
2	C	16	GLN
2	C	122	GLN
2	C	179	HIS

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Mol	Chain	Res	Type
2	C	191	HIS
2	C	252	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

5 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	DAM	I	7	3,2	4,5,6	2.31	1 (25%)	3,5,7	4.09	3 (100%)
3	FGA	I	6	3	6,8,9	2.47	2 (33%)	6,9,11	0.45	0
3	ACB	I	3	3	7,8,9	2.12	1 (14%)	8,10,12	0.90	0
3	1ZN	I	5	3	21,23,24	1.65	5 (23%)	25,29,31	1.39	4 (16%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	DAM	I	7	3,2	-	0/0/4/6	-
3	FGA	I	6	3	-	2/8/8/9	-
3	ACB	I	3	3	-	1/10/10/12	-
3	1ZN	I	5	3	-	5/23/25/27	0/1/1/1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	I	6	FGA	O-C	4.92	1.36	1.22
3	I	3	ACB	CA-N	4.77	1.60	1.47
3	I	7	DAM	C-CA	4.08	1.52	1.45
3	I	5	1ZN	C3-C2	3.71	1.57	1.52
3	I	5	1ZN	C9-C4	2.73	1.44	1.38
3	I	5	1ZN	C6-C5	2.71	1.43	1.38
3	I	6	FGA	OXT-C	-2.28	1.23	1.30
3	I	5	1ZN	C8-C9	2.12	1.42	1.38
3	I	5	1ZN	C10-C2	2.02	1.58	1.53

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	7	DAM	CM-N-CA	-5.12	116.21	123.98
3	I	5	1ZN	CA-C18-C	-4.43	105.05	110.67
3	I	7	DAM	O-C-CA	-4.37	119.64	125.33
3	I	5	1ZN	CA-C16-C15	-2.53	119.50	123.62
3	I	7	DAM	CB-CA-N	-2.21	120.41	125.84
3	I	5	1ZN	C18-CA-C16	-2.10	109.97	112.98
3	I	5	1ZN	C16-C15-C13	2.00	130.63	126.32

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	I	5	1ZN	C12-C13-C15-C16
3	I	5	1ZN	C14-C13-C15-C16
3	I	6	FGA	O-C-CA-N
3	I	3	ACB	CA-CB-CG-OD1
3	I	5	1ZN	C10-C2-C3-C4
3	I	5	1ZN	C2-C3-C4-C9
3	I	5	1ZN	C2-C3-C4-C5
3	I	6	FGA	OXT-C-CA-N

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	I	3	ACB	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.