



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 06:49 PM GMT

PDB ID : 1CPS  
Title : STRUCTURAL COMPARISON OF SULFODIIMINE AND SULFONAMIDE  
INHIBITORS IN THEIR COMPLEXES WITH ZINC ENZYMES  
Authors : Cappalonga, A.M.; Alexander, R.S.; Christianson, D.W.  
Deposited on : 1992-02-18  
Resolution : 2.25 Å(reported)

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

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

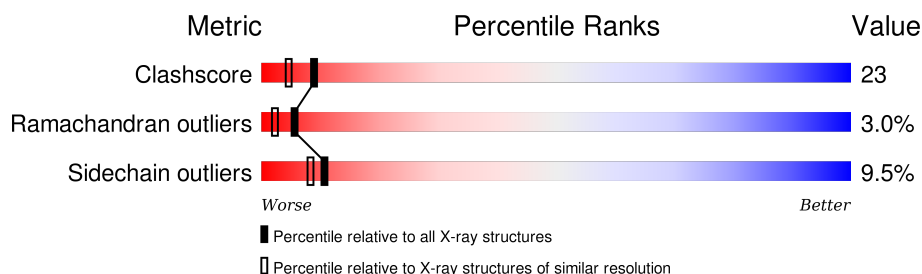
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.25 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	102246	1095 (2.26-2.26)
Ramachandran outliers	100387	1063 (2.26-2.26)
Sidechain outliers	100360	1063 (2.26-2.26)

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

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	307	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2575 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 CARBOXYPEPTIDASE A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	307	Total	C	N	O	S	0	0	0
			2436	1561	406	464	5			

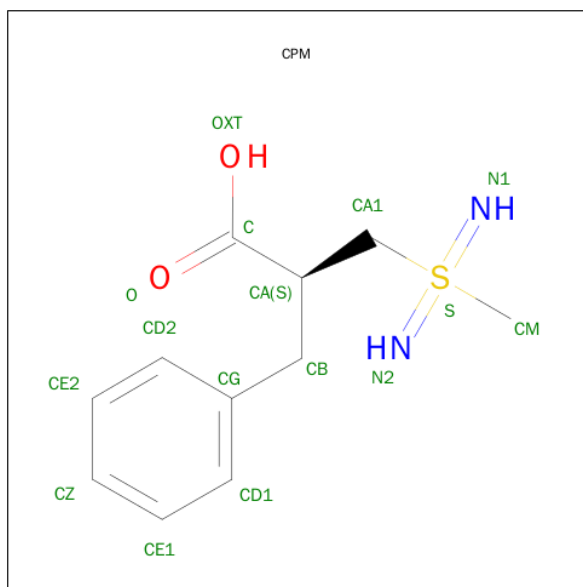
There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	89	ASN	ASP	CONFLICT	UNP P00730
A	93	ASN	ASP	CONFLICT	UNP P00730
A	114	ASN	ASP	CONFLICT	UNP P00730
A	122	GLU	GLN	CONFLICT	UNP P00730
A	185	ASN	ASP	CONFLICT	UNP P00730
A	228	ALA	GLU	CONFLICT	UNP P00730
A	305	VAL	LEU	CONFLICT	UNP P00730

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is S-(2-CARBOXY-3-PHENYLPROPYL)THIODIIMINE-S-METHANE (three-letter code: CPM) (formula: C<sub>11</sub>H<sub>16</sub>N<sub>2</sub>O<sub>2</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			16	11	2	2	1		

- Molecule 4 is water.

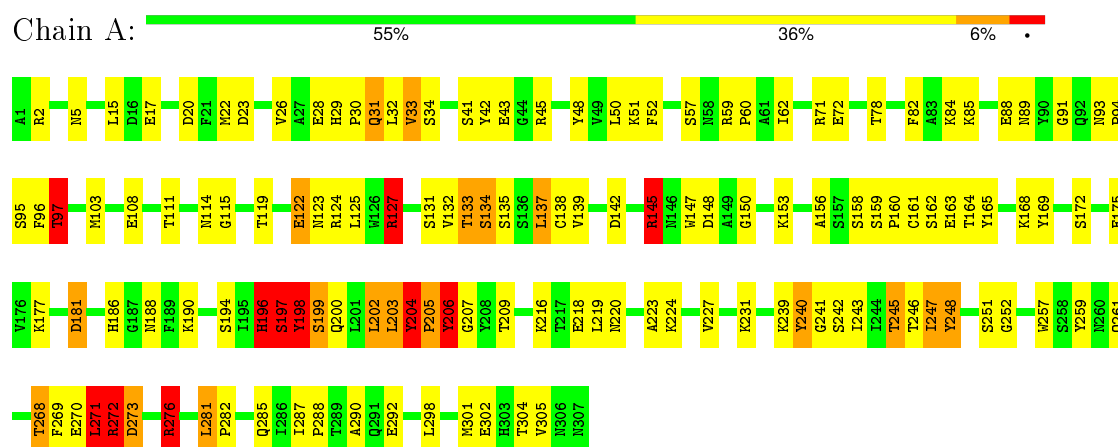
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	122	Total	O	0	0
			122	122		

### 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.

Note EDS was not executed.

#### • Molecule 1: CARBOXYPEPTIDASE A



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	51.70 Å 60.40 Å 47.20 Å 90.00° 97.40° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.25	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.25)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, $R_{free}$	0.174 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2575	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	13.0	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: ZN, CPM

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	1.41	16/2502 (0.6%)	1.91	54/3402 (1.6%)

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
1	A	0	4

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	88	GLU	CD-OE1	10.26	1.36	1.25
1	A	205	PRO	N-CA	-9.02	1.31	1.47
1	A	43	GLU	CD-OE1	8.35	1.34	1.25
1	A	28	GLU	CD-OE2	8.28	1.34	1.25
1	A	292	GLU	CD-OE1	7.83	1.34	1.25
1	A	272	ARG	N-CA	-7.70	1.30	1.46
1	A	197	SER	N-CA	-7.34	1.31	1.46
1	A	204	TYR	C-N	-7.08	1.20	1.34
1	A	17	GLU	CD-OE2	6.46	1.32	1.25
1	A	204	TYR	CA-C	-6.40	1.36	1.52
1	A	122	GLU	CD-OE1	6.23	1.32	1.25
1	A	218	GLU	CD-OE2	5.76	1.31	1.25
1	A	175	GLU	CD-OE2	5.70	1.31	1.25
1	A	207	GLY	N-CA	5.65	1.54	1.46
1	A	292	GLU	CG-CD	-5.64	1.43	1.51
1	A	196	HIS	C-N	-5.49	1.21	1.34

All (54) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	204	TYR	CA-C-O	-29.13	58.93	120.10
1	A	204	TYR	CA-C-N	21.78	178.08	117.10
1	A	196	HIS	C-N-CA	20.88	173.91	121.70
1	A	271	LEU	C-N-CA	20.55	173.07	121.70
1	A	272	ARG	N-CA-CB	19.19	145.13	110.60
1	A	127	ARG	NE-CZ-NH2	11.91	126.25	120.30
1	A	148	ASP	CB-CG-OD1	10.70	127.93	118.30
1	A	205	PRO	C-N-CA	10.44	147.80	121.70
1	A	196	HIS	O-C-N	10.03	138.75	122.70
1	A	205	PRO	CA-N-CD	-9.95	97.58	111.50
1	A	205	PRO	N-CA-CB	9.87	115.14	103.30
1	A	197	SER	C-N-CA	9.82	146.26	121.70
1	A	145	ARG	NE-CZ-NH1	9.25	124.92	120.30
1	A	271	LEU	CB-CA-C	9.07	127.44	110.20
1	A	145	ARG	CD-NE-CZ	8.69	135.77	123.60
1	A	197	SER	CA-C-O	8.64	138.24	120.10
1	A	197	SER	N-CA-C	8.64	134.32	111.00
1	A	196	HIS	N-CA-C	-8.51	88.03	111.00
1	A	205	PRO	O-C-N	-8.48	109.14	122.70
1	A	205	PRO	CA-C-O	8.31	140.13	120.20
1	A	273	ASP	CA-CB-CG	8.05	131.12	113.40
1	A	59	ARG	NE-CZ-NH2	-7.87	116.37	120.30
1	A	196	HIS	CA-C-N	-7.84	99.95	117.20
1	A	145	ARG	NE-CZ-NH2	-7.75	116.42	120.30
1	A	271	LEU	CA-C-N	-7.61	100.45	117.20
1	A	205	PRO	N-CA-C	7.27	131.01	112.10
1	A	276	ARG	NE-CZ-NH1	-7.21	116.70	120.30
1	A	124	ARG	NE-CZ-NH1	7.10	123.85	120.30
1	A	197	SER	O-C-N	-6.95	111.58	122.70
1	A	204	TYR	N-CA-C	6.92	129.69	111.00
1	A	148	ASP	CB-CG-OD2	-6.80	112.18	118.30
1	A	59	ARG	NE-CZ-NH1	6.70	123.65	120.30
1	A	204	TYR	C-N-CA	6.63	149.84	122.00
1	A	206	TYR	N-CA-CB	6.32	121.97	110.60
1	A	198	TYR	CB-CG-CD2	-6.13	117.32	121.00
1	A	197	SER	N-CA-CB	6.05	119.58	110.50
1	A	271	LEU	O-C-N	6.05	132.38	122.70
1	A	181	ASP	CB-CG-OD1	5.90	123.61	118.30
1	A	2	ARG	NE-CZ-NH2	5.90	123.25	120.30
1	A	205	PRO	N-CD-CG	5.57	111.56	103.20
1	A	198	TYR	N-CA-C	5.52	125.90	111.00
1	A	48	TYR	CA-CB-CG	5.51	123.87	113.40
1	A	82	PHE	CB-CG-CD1	-5.49	116.96	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	142	ASP	N-CA-C	-5.35	96.56	111.00
1	A	273	ASP	CB-CA-C	5.32	121.04	110.40
1	A	268	THR	N-CA-CB	5.32	120.40	110.30
1	A	269	PHE	CA-CB-CG	5.26	126.53	113.90
1	A	153	LYS	N-CA-CB	5.17	119.91	110.60
1	A	20	ASP	CB-CG-OD1	5.16	122.94	118.30
1	A	97	THR	CA-CB-CG2	5.14	119.59	112.40
1	A	240	TYR	CB-CG-CD2	5.09	124.05	121.00
1	A	197	SER	CB-CA-C	-5.08	100.45	110.10
1	A	198	TYR	CB-CG-CD1	5.07	124.04	121.00
1	A	23	ASP	CB-CG-OD2	5.00	122.80	118.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	145	ARG	Sidechain
1	A	196	HIS	Peptide
1	A	204	TYR	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	2436	0	2350	109	0
2	A	1	0	0	0	0
3	A	16	0	13	4	0
4	A	122	0	0	8	0
All	All	2575	0	2363	111	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 23.

All (111) 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:198:TYR:HA	1:A:271:LEU:O	1.48	1.13
1:A:93:ASN:O	1:A:97:THR:HG22	1.66	0.94
1:A:72:GLU:HB3	1:A:197:SER:CB	2.00	0.91
1:A:137:LEU:HD22	1:A:137:LEU:H	1.36	0.90
1:A:72:GLU:HB3	1:A:197:SER:HB3	1.54	0.89
1:A:287:ILE:HB	1:A:288:PRO:HD3	1.57	0.85
1:A:22:MET:HE3	1:A:50:LEU:HG	1.59	0.84
1:A:231:LYS:HB2	4:A:371:HOH:O	1.86	0.75
1:A:186:HIS:HD2	1:A:188:ASN:H	1.35	0.74
1:A:272:ARG:HH11	1:A:285:GLN:HE21	1.35	0.73
1:A:243:ILE:HG13	4:A:338:HOH:O	1.89	0.72
1:A:31:GLN:HB2	4:A:375:HOH:O	1.91	0.69
1:A:5:ASN:HD21	1:A:84:LYS:HZ1	1.41	0.69
1:A:198:TYR:CA	1:A:271:LEU:O	2.35	0.69
1:A:202:LEU:HD12	1:A:227:VAL:HG23	1.78	0.66
1:A:272:ARG:HH11	1:A:285:GLN:NE2	1.92	0.66
1:A:150:GLY:O	1:A:251:SER:HB2	1.96	0.66
1:A:145:ARG:HG2	1:A:251:SER:O	1.96	0.65
1:A:72:GLU:HB3	1:A:197:SER:HB2	1.78	0.65
1:A:119:THR:HA	1:A:123:ASN:O	1.96	0.64
1:A:133:THR:O	1:A:134:SER:CB	2.45	0.64
1:A:72:GLU:CB	1:A:197:SER:HB3	2.26	0.64
1:A:133:THR:O	1:A:134:SER:HB3	1.98	0.63
1:A:93:ASN:ND2	1:A:96:PHE:H	1.98	0.62
1:A:22:MET:O	1:A:26:VAL:HG23	1.99	0.61
1:A:115:GLY:O	1:A:119:THR:HG23	2.01	0.60
1:A:45:ARG:HH11	1:A:114:ASN:ND2	2.00	0.60
1:A:268:THR:HG21	3:A:588:CPM:HD1	1.84	0.60
1:A:281:LEU:CD1	1:A:285:GLN:HB2	2.31	0.59
1:A:242:SER:O	1:A:246:THR:HG23	2.02	0.59
1:A:257:TRP:O	1:A:261:GLN:HG2	2.03	0.59
1:A:281:LEU:HD13	1:A:285:GLN:HB2	1.84	0.58
1:A:137:LEU:HD22	1:A:137:LEU:N	2.13	0.57
1:A:134:SER:OG	1:A:135:SER:N	2.35	0.56
1:A:95:SER:OG	1:A:302:GLU:OE2	2.19	0.56
1:A:85:LYS:HE3	1:A:89:ASN:ND2	2.20	0.56
1:A:205:PRO:HG2	1:A:259:TYR:HB2	1.89	0.55
3:A:588:CPM:C	3:A:588:CPM:CD2	2.85	0.54
1:A:22:MET:CE	1:A:50:LEU:HG	2.33	0.54
1:A:281:LEU:HD22	1:A:282:PRO:HD2	1.88	0.54
1:A:177:LYS:NZ	4:A:324:HOH:O	2.36	0.54
1:A:196:HIS:O	1:A:271:LEU:HD13	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:33:VAL:HA	1:A:51:LYS:O	2.09	0.52
1:A:168:LYS:NZ	1:A:169:TYR:CE2	2.78	0.52
1:A:242:SER:OG	1:A:245:THR:HB	2.10	0.52
1:A:302:GLU:O	1:A:305:VAL:HG12	2.10	0.52
1:A:271:LEU:CD1	1:A:271:LEU:N	2.73	0.51
1:A:202:LEU:HD13	1:A:223:ALA:HB1	1.92	0.51
1:A:168:LYS:HE3	1:A:172:SER:HB2	1.92	0.51
1:A:145:ARG:HH11	1:A:145:ARG:HG3	1.73	0.51
1:A:198:TYR:O	1:A:199:SER:CB	2.59	0.50
1:A:198:TYR:O	1:A:199:SER:HB3	2.10	0.50
1:A:186:HIS:HD2	1:A:188:ASN:N	2.05	0.50
1:A:160:PRO:HA	1:A:165:TYR:CG	2.46	0.50
1:A:72:GLU:CG	1:A:197:SER:HB3	2.41	0.49
1:A:132:VAL:O	1:A:133:THR:CB	2.61	0.49
1:A:132:VAL:O	1:A:133:THR:HB	2.12	0.49
1:A:42:TYR:OH	1:A:132:VAL:HG22	2.12	0.49
1:A:62:ILE:HD11	1:A:304:THR:HG21	1.93	0.48
1:A:276:ARG:O	1:A:276:ARG:HD3	2.14	0.48
1:A:241:GLY:HA3	1:A:246:THR:CG2	2.43	0.48
1:A:248:TYR:O	1:A:248:TYR:HD1	1.96	0.48
1:A:91:GLY:H	1:A:97:THR:HB	1.78	0.47
1:A:247:ILE:HG22	1:A:248:TYR:CG	2.49	0.47
1:A:160:PRO:HA	1:A:165:TYR:CD2	2.49	0.47
1:A:204:TYR:HB2	1:A:219:LEU:HD23	1.97	0.46
1:A:138:CYS:SG	1:A:161:CYS:CB	3.04	0.46
1:A:203:LEU:HD21	1:A:247:ILE:HD11	1.97	0.46
1:A:5:ASN:ND2	1:A:84:LYS:HZ1	2.10	0.46
1:A:190:LYS:HE2	1:A:190:LYS:HA	1.98	0.46
1:A:248:TYR:C	1:A:248:TYR:HD1	2.19	0.46
1:A:5:ASN:ND2	1:A:84:LYS:NZ	2.64	0.45
1:A:224:LYS:HG3	1:A:240:TYR:OH	2.16	0.45
1:A:93:ASN:O	1:A:97:THR:CG2	2.53	0.45
1:A:206:TYR:HB2	4:A:322:HOH:O	2.17	0.45
1:A:127:ARG:HH12	1:A:164:THR:HG22	1.82	0.44
1:A:268:THR:HG21	3:A:588:CPM:CD1	2.47	0.44
1:A:287:ILE:HB	1:A:288:PRO:CD	2.37	0.44
1:A:147:TRP:O	1:A:252:GLY:HA2	2.18	0.44
1:A:93:ASN:HA	1:A:94:PRO:HD2	1.83	0.44
1:A:78:THR:HG23	1:A:290:ALA:HA	1.99	0.44
1:A:247:ILE:HG22	1:A:248:TYR:CD2	2.53	0.44
1:A:248:TYR:CD1	1:A:248:TYR:C	2.90	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:41:SER:OG	1:A:114:ASN:ND2	2.50	0.43
1:A:168:LYS:HG2	4:A:353:HOH:O	2.18	0.43
1:A:204:TYR:O	4:A:338:HOH:O	2.22	0.42
1:A:131:SER:O	1:A:139:VAL:HG23	2.18	0.42
1:A:127:ARG:NH1	1:A:163:GLU:O	2.50	0.42
1:A:108:GLU:OE2	1:A:111:THR:HA	2.19	0.42
1:A:287:ILE:N	1:A:288:PRO:CD	2.82	0.42
1:A:158:SER:HB3	4:A:399:HOH:O	2.19	0.42
1:A:159:SER:O	1:A:162:SER:HB3	2.20	0.42
1:A:145:ARG:HD3	1:A:156:ALA:HB2	2.02	0.42
1:A:29:HIS:N	1:A:30:PRO:CD	2.82	0.42
1:A:281:LEU:HA	1:A:282:PRO:HD3	1.77	0.41
1:A:202:LEU:HD13	1:A:223:ALA:CB	2.49	0.41
1:A:204:TYR:OH	1:A:220:ASN:ND2	2.53	0.41
3:A:588:CPM:C	3:A:588:CPM:HD2	2.51	0.41
1:A:301:MET:O	1:A:304:THR:HB	2.20	0.41
1:A:276:ARG:C	1:A:276:ARG:HD3	2.40	0.41
1:A:71:ARG:HG3	1:A:72:GLU:HG3	2.02	0.41
1:A:202:LEU:CD1	1:A:223:ALA:HA	2.51	0.41
1:A:202:LEU:O	1:A:240:TYR:HA	2.21	0.41
1:A:177:LYS:HZ3	1:A:181:ASP:CG	2.24	0.41
1:A:62:ILE:CD1	1:A:304:THR:HG21	2.51	0.41
1:A:200:GLN:HA	1:A:270:GLU:O	2.20	0.41
1:A:60:PRO:HB2	1:A:103:MET:HE3	2.03	0.40
1:A:15:LEU:HD13	1:A:15:LEU:C	2.41	0.40
1:A:177:LYS:O	1:A:177:LYS:HD2	2.21	0.40
1:A:93:ASN:HD22	1:A:96:PHE:CB	2.34	0.40
1:A:32:LEU:O	1:A:52:PHE:HA	2.21	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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	305/307 (99%)	283 (93%)	13 (4%)	9 (3%)	5 2

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	134	SER
1	A	199	SER
1	A	272	ARG
1	A	198	TYR
1	A	133	THR
1	A	197	SER
1	A	204	TYR
1	A	206	TYR
1	A	247	ILE

### 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	263/263 (100%)	238 (90%)	25 (10%)	11 8

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	GLN
1	A	33	VAL
1	A	34	SER
1	A	57	SER
1	A	97	THR
1	A	122	GLU
1	A	125	LEU
1	A	127	ARG
1	A	137	LEU
1	A	145	ARG
1	A	194	SER
1	A	197	SER

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Mol	Chain	Res	Type
1	A	198	TYR
1	A	202	LEU
1	A	203	LEU
1	A	209	THR
1	A	216	LYS
1	A	239	LYS
1	A	245	THR
1	A	248	TYR
1	A	271	LEU
1	A	273	ASP
1	A	276	ARG
1	A	281	LEU
1	A	298	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	ASN
1	A	37	GLN
1	A	93	ASN
1	A	112	ASN
1	A	171	ASN
1	A	186	HIS
1	A	220	ASN
1	A	285	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

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	CPM	A	588	2	10,16,16	8.43	9 (90%)	12,22,22	6.97	9 (75%)

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	CPM	A	588	2	-	0/6/13/13	0/1/1/1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	588	CPM	CZ-CE1	-7.81	1.18	1.38
3	A	588	CPM	CA1-CA	5.71	1.64	1.54
3	A	588	CPM	CD2-CG	5.98	1.51	1.38
3	A	588	CPM	CB-CG	6.54	1.67	1.51
3	A	588	CPM	CZ-CE2	8.47	1.59	1.38
3	A	588	CPM	CD1-CG	9.01	1.58	1.38
3	A	588	CPM	CB-CA	10.40	1.68	1.54
3	A	588	CPM	CE1-CD1	11.56	1.62	1.38
3	A	588	CPM	CE2-CD2	11.85	1.63	1.38

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	588	CPM	CB-CA-CA1	-10.62	93.78	110.69
3	A	588	CPM	CG-CB-CA	-10.49	98.73	113.92
3	A	588	CPM	CZ-CE2-CD2	-9.66	106.04	120.19
3	A	588	CPM	CE1-CD1-CG	-9.54	105.49	120.65
3	A	588	CPM	CB-CA-C	-3.96	103.28	111.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	588	CPM	CB-CG-CD1	-3.73	113.10	120.90
3	A	588	CPM	CZ-CE1-CD1	3.72	125.64	120.19
3	A	588	CPM	CD2-CG-CD1	6.72	128.89	118.13
3	A	588	CPM	CE2-CZ-CE1	9.11	135.91	119.93

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	588	CPM	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 ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.