



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:14 PM GMT

PDB ID : 1EPN
Title : A STRUCTURAL COMPARISON OF 21 INHIBITOR COMPLEXES OF
THE ASPARTIC PROTEINASE FROM ENDOTHIA PARASITICA
Authors : Crawford, M.; Cooper, J.B.; Blundell, T.L.
Deposited on : 1994-07-27
Resolution : 1.60 Å(reported)

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

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **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

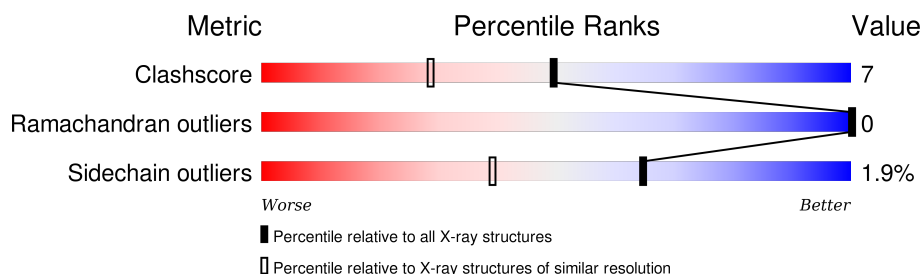
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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	2732 (1.60-1.60)
Ramachandran outliers	100387	2654 (1.60-1.60)
Sidechain outliers	100360	2653 (1.60-1.60)

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

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	E	330	

2 Entry composition [i](#)

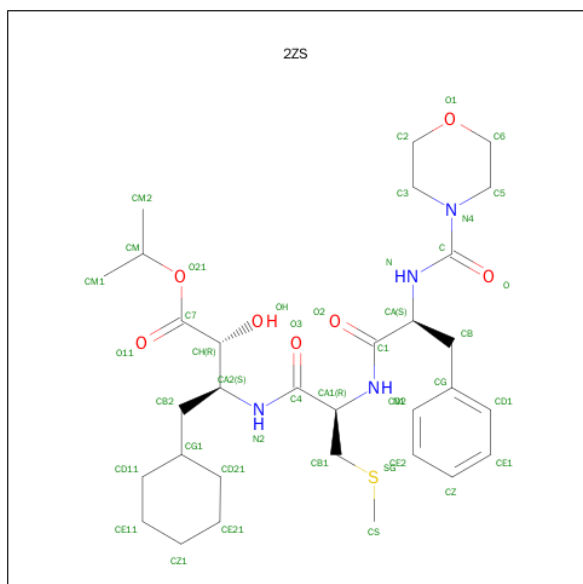
There are 4 unique types of molecules in this entry. The entry contains 2731 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ENDOTHAPEPSIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	E	330	Total	C	N	O	S	0	0	0
			2389	1514	366	507	2			

- Molecule 2 is N-(MORPHOLIN-4-YLCARBONYL)-L-PHENYLALANYL-N-[(1R,2S)-1-(CYCLOHEXYLMETHYL)-2-HYDROXY-3-(1-METHYLETHOXY)-3-OXOPROPYL]-S-METHYL-L-CYSTEINAMIDE (three-letter code: 2ZS) (formula: C₃₁H₄₈N₄O₇S).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	E	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is water.

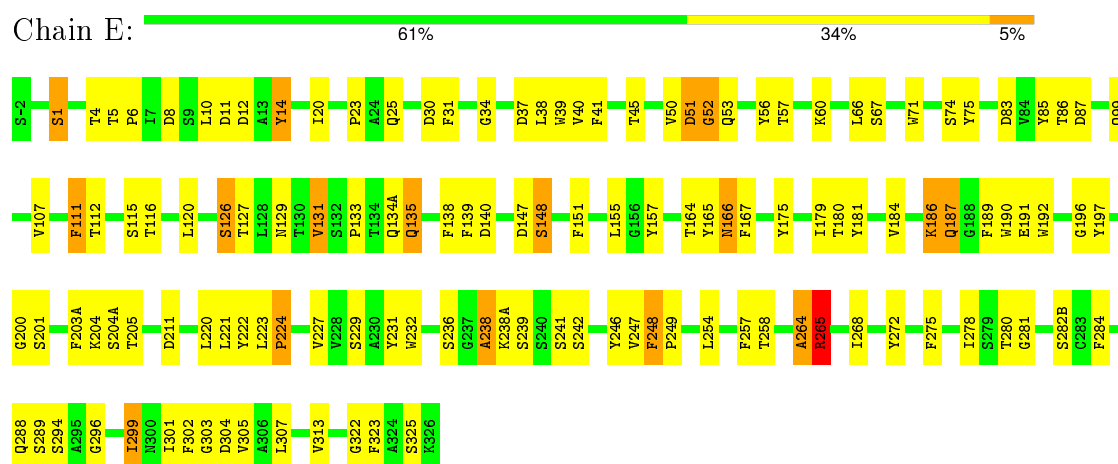
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	281	Total	O	0	0
			281	281		

3 Residue-property plots [i](#)

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: ENDOTHIAPEPSIN



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, α , β , γ	43.11 Å 76.08 Å 42.99 Å 90.00° 96.80° 90.00°	Depositor
Resolution (Å)	20.00 – 1.60	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-1.60)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	RESTRAIN	Depositor
R, R_{free}	0.170 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2731	wwPDB-VP
Average B, all atoms (Å ²)	0.0	wwPDB-VP

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: 2ZS, SO4

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	E	1.90	39/2445 (1.6%)	2.40	141/3345 (4.2%)

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	E	0	3

All (39) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	51	ASP	N-CA	8.10	1.62	1.46
1	E	200	GLY	N-CA	7.83	1.57	1.46
1	E	201	SER	CB-OG	7.63	1.52	1.42
1	E	25	GLN	CD-OE1	7.13	1.39	1.24
1	E	135	GLN	CD-OE1	6.84	1.39	1.24
1	E	75	TYR	CG-CD1	-6.42	1.30	1.39
1	E	1	SER	CB-OG	6.39	1.50	1.42
1	E	6	PRO	C-N	6.27	1.48	1.34
1	E	34	GLY	CA-C	6.10	1.61	1.51
1	E	239	SER	CB-OG	6.09	1.50	1.42
1	E	14	TYR	CG-CD2	5.91	1.46	1.39
1	E	236	SER	CA-CB	5.89	1.61	1.52
1	E	222	TYR	CB-CG	-5.88	1.42	1.51
1	E	301	ILE	CA-CB	-5.85	1.41	1.54
1	E	294	SER	N-CA	5.83	1.58	1.46
1	E	284	PHE	C-N	5.80	1.43	1.33
1	E	134(A)	GLN	CD-OE1	5.78	1.36	1.24
1	E	284	PHE	CD1-CE1	5.76	1.50	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	224	PRO	N-CD	-5.75	1.39	1.47
1	E	196	GLY	N-CA	5.73	1.54	1.46
1	E	181	TYR	CG-CD1	5.63	1.46	1.39
1	E	229	SER	C-O	5.62	1.34	1.23
1	E	74	SER	CB-OG	-5.59	1.34	1.42
1	E	71	TRP	CE2-CZ2	-5.55	1.30	1.39
1	E	257	PHE	C-O	5.54	1.33	1.23
1	E	275	PHE	N-CA	-5.47	1.35	1.46
1	E	222	TYR	CZ-OH	-5.41	1.28	1.37
1	E	166	ASN	CG-OD1	5.34	1.35	1.24
1	E	157	TYR	CE1-CZ	5.32	1.45	1.38
1	E	164	THR	CB-OG1	5.32	1.53	1.43
1	E	288	GLN	CD-OE1	5.32	1.35	1.24
1	E	325	SER	N-CA	5.27	1.56	1.46
1	E	204(A)	SER	N-CA	5.22	1.56	1.46
1	E	112	THR	C-O	-5.13	1.13	1.23
1	E	305	VAL	CB-CG1	5.10	1.63	1.52
1	E	313	VAL	N-CA	5.07	1.56	1.46
1	E	322	GLY	N-CA	5.05	1.53	1.46
1	E	126	SER	CB-OG	5.05	1.48	1.42
1	E	242	SER	CB-OG	-5.00	1.35	1.42

All (141) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	197	TYR	CB-CG-CD2	-15.18	111.89	121.00
1	E	275	PHE	CB-CG-CD1	-14.93	110.35	120.80
1	E	75	TYR	CB-CG-CD2	-12.27	113.64	121.00
1	E	56	TYR	CB-CG-CD2	-11.82	113.91	121.00
1	E	151	PHE	CB-CG-CD2	-11.79	112.55	120.80
1	E	157	TYR	CG-CD2-CE2	-10.84	112.63	121.30
1	E	211	ASP	CB-CG-OD1	-10.82	108.56	118.30
1	E	157	TYR	CZ-CE2-CD2	10.81	129.53	119.80
1	E	248	PHE	CB-CG-CD1	10.45	128.11	120.80
1	E	197	TYR	CG-CD2-CE2	-10.11	113.21	121.30
1	E	31	PHE	CB-CG-CD2	-9.86	113.90	120.80
1	E	67	SER	O-C-N	9.65	139.61	123.20
1	E	257	PHE	CZ-CE2-CD2	-9.60	108.58	120.10
1	E	83	ASP	CB-CG-OD1	9.49	126.84	118.30
1	E	87	ASP	CB-CG-OD1	9.31	126.68	118.30
1	E	157	TYR	CB-CG-CD2	-9.27	115.44	121.00
1	E	203(A)	PHE	CB-CG-CD1	-9.04	114.47	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	14	TYR	CG-CD2-CE2	-9.01	114.09	121.30
1	E	222	TYR	CZ-CE2-CD2	8.93	127.84	119.80
1	E	190	TRP	CE2-CD2-CG	-8.90	100.18	107.30
1	E	265	ARG	CD-NE-CZ	8.84	135.98	123.60
1	E	304	ASP	CB-CG-OD1	-8.50	110.65	118.30
1	E	284	PHE	CB-CG-CD1	-8.41	114.91	120.80
1	E	190	TRP	CD1-CG-CD2	8.35	112.98	106.30
1	E	41	PHE	CB-CG-CD1	-8.29	115.00	120.80
1	E	197	TYR	CZ-CE2-CD2	8.24	127.21	119.80
1	E	323	PHE	CZ-CE2-CD2	-8.14	110.33	120.10
1	E	323	PHE	CE1-CZ-CE2	7.98	134.36	120.00
1	E	138	PHE	CB-CG-CD2	-7.90	115.27	120.80
1	E	275	PHE	CZ-CE2-CD2	-7.78	110.76	120.10
1	E	221	LEU	CB-CG-CD1	7.67	124.05	111.00
1	E	51	ASP	CB-CG-OD2	-7.67	111.40	118.30
1	E	181	TYR	CB-CG-CD1	-7.67	116.40	121.00
1	E	38	LEU	CB-CG-CD2	7.59	123.91	111.00
1	E	181	TYR	CG-CD2-CE2	-7.59	115.22	121.30
1	E	257	PHE	CG-CD1-CE1	-7.53	112.51	120.80
1	E	248	PHE	CG-CD1-CE1	7.41	128.95	120.80
1	E	249	PRO	CA-N-CD	7.33	121.97	111.70
1	E	45	THR	OG1-CB-CG2	-7.32	93.16	110.00
1	E	313	VAL	O-C-N	7.26	134.32	122.70
1	E	197	TYR	CB-CG-CD1	7.26	125.36	121.00
1	E	281	GLY	O-C-N	-7.20	111.18	122.70
1	E	133	PRO	CA-N-CD	7.08	121.61	111.70
1	E	155	LEU	CB-CG-CD1	-7.04	99.04	111.00
1	E	175	TYR	CB-CG-CD2	7.04	125.22	121.00
1	E	204	LYS	O-C-N	6.97	133.84	122.70
1	E	231	TYR	CB-CG-CD1	-6.91	116.86	121.00
1	E	322	GLY	O-C-N	-6.88	111.69	122.70
1	E	246	TYR	CB-CG-CD2	-6.85	116.89	121.00
1	E	134(A)	GLN	CG-CD-OE1	-6.79	108.03	121.60
1	E	175	TYR	CG-CD2-CE2	6.76	126.71	121.30
1	E	139	PHE	CG-CD2-CE2	-6.71	113.42	120.80
1	E	258	THR	O-C-N	6.71	133.44	122.70
1	E	325	SER	N-CA-CB	-6.69	100.46	110.50
1	E	67	SER	C-N-CA	-6.68	108.26	122.30
1	E	222	TYR	CB-CG-CD1	6.63	124.98	121.00
1	E	107	VAL	CA-CB-CG2	6.61	120.81	110.90
1	E	275	PHE	CB-CG-CD2	6.58	125.40	120.80
1	E	304	ASP	OD1-CG-OD2	6.44	135.54	123.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	127	THR	O-C-N	-6.43	112.41	122.70
1	E	280	THR	CA-CB-CG2	-6.42	103.41	112.40
1	E	50	VAL	CA-CB-CG2	6.41	120.51	110.90
1	E	211	ASP	OD1-CG-OD2	6.36	135.38	123.30
1	E	57	THR	CA-CB-CG2	-6.34	103.52	112.40
1	E	189	PHE	CD1-CE1-CZ	-6.34	112.49	120.10
1	E	272	TYR	CB-CG-CD1	6.32	124.79	121.00
1	E	60	LYS	O-C-N	-6.23	112.73	122.70
1	E	257	PHE	CG-CD2-CE2	6.23	127.65	120.80
1	E	275	PHE	CG-CD1-CE1	-6.22	113.95	120.80
1	E	323	PHE	CB-CG-CD2	-6.22	116.44	120.80
1	E	66	LEU	CA-C-O	6.15	133.02	120.10
1	E	190	TRP	NE1-CE2-CD2	6.10	113.40	107.30
1	E	181	TYR	CD1-CG-CD2	6.10	124.61	117.90
1	E	272	TYR	CG-CD2-CE2	6.09	126.17	121.30
1	E	39	TRP	CE3-CZ3-CH2	-6.09	114.50	121.20
1	E	181	TYR	CD1-CE1-CZ	-6.08	114.33	119.80
1	E	239	SER	CA-C-O	6.08	132.86	120.10
1	E	67	SER	CA-C-N	-6.06	104.08	116.20
1	E	302	PHE	CD1-CE1-CZ	-6.03	112.87	120.10
1	E	284	PHE	CA-C-O	5.97	132.64	120.10
1	E	85	TYR	CG-CD2-CE2	-5.92	116.56	121.30
1	E	56	TYR	CG-CD2-CE2	-5.88	116.60	121.30
1	E	204	LYS	CA-CB-CG	-5.88	100.47	113.40
1	E	231	TYR	CD1-CE1-CZ	-5.88	114.51	119.80
1	E	51	ASP	CA-CB-CG	-5.87	100.48	113.40
1	E	192	TRP	CE2-CD2-CE3	5.85	125.72	118.70
1	E	299	ILE	O-C-N	5.83	132.02	122.70
1	E	8	ASP	CB-CG-OD1	5.80	123.52	118.30
1	E	180	THR	O-C-N	5.79	131.97	122.70
1	E	289	SER	O-C-N	5.78	131.95	122.70
1	E	31	PHE	CG-CD2-CE2	-5.76	114.46	120.80
1	E	249	PRO	N-CD-CG	-5.75	94.57	103.20
1	E	257	PHE	CB-CG-CD1	-5.69	116.82	120.80
1	E	20	ILE	C-N-CA	-5.66	110.42	122.30
1	E	30	ASP	CB-CG-OD1	5.66	123.39	118.30
1	E	45	THR	CA-CB-CG2	-5.66	104.48	112.40
1	E	164	THR	O-C-N	5.66	131.75	122.70
1	E	139	PHE	CB-CG-CD2	-5.65	116.84	120.80
1	E	227	VAL	CA-CB-CG1	-5.64	102.44	110.90
1	E	184	VAL	O-C-N	5.64	131.72	122.70
1	E	232	TRP	CZ3-CH2-CZ2	-5.64	114.83	121.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	23	PRO	O-C-N	-5.63	113.70	122.70
1	E	167	PHE	CG-CD2-CE2	-5.62	114.62	120.80
1	E	305	VAL	CA-CB-CG2	5.61	119.31	110.90
1	E	231	TYR	CZ-CE2-CD2	-5.61	114.75	119.80
1	E	31	PHE	CD1-CE1-CZ	-5.53	113.47	120.10
1	E	40	VAL	CA-CB-CG2	5.48	119.12	110.90
1	E	11	ASP	CB-CG-OD2	-5.46	113.39	118.30
1	E	203(A)	PHE	CD1-CE1-CZ	-5.42	113.60	120.10
1	E	246	TYR	CD1-CG-CD2	5.39	123.83	117.90
1	E	131	VAL	O-C-N	5.32	131.22	122.70
1	E	191	GLU	CA-C-O	5.32	131.27	120.10
1	E	192	TRP	CG-CD2-CE3	-5.31	129.12	133.90
1	E	191	GLU	OE1-CD-OE2	-5.28	116.97	123.30
1	E	31	PHE	CE1-CZ-CE2	5.27	129.48	120.00
1	E	75	TYR	CG-CD2-CE2	-5.27	117.09	121.30
1	E	307	LEU	CB-CG-CD1	-5.27	102.05	111.00
1	E	301	ILE	CA-C-O	-5.23	109.11	120.10
1	E	238(A)	LYS	CB-CG-CD	5.22	125.18	111.60
1	E	30	ASP	CB-CG-OD2	5.20	122.98	118.30
1	E	268	ILE	O-C-N	5.19	130.97	121.10
1	E	56	TYR	N-CA-CB	-5.19	101.26	110.60
1	E	148	SER	N-CA-CB	-5.18	102.73	110.50
1	E	71	TRP	CG-CD2-CE3	-5.17	129.25	133.90
1	E	111	PHE	O-C-N	-5.17	114.43	122.70
1	E	238	ALA	O-C-N	-5.16	114.44	122.70
1	E	323	PHE	CD1-CE1-CZ	-5.15	113.92	120.10
1	E	203(A)	PHE	CE1-CZ-CE2	5.14	129.25	120.00
1	E	30	ASP	OD1-CG-OD2	-5.13	113.55	123.30
1	E	165	TYR	CZ-CE2-CD2	-5.13	115.18	119.80
1	E	23	PRO	CA-N-CD	5.13	118.88	111.70
1	E	296	GLY	O-C-N	-5.12	114.51	122.70
1	E	71	TRP	CE2-CD2-CE3	5.12	124.84	118.70
1	E	264	ALA	O-C-N	-5.11	114.53	122.70
1	E	6	PRO	CA-N-CD	5.10	118.84	111.70
1	E	284	PHE	CD1-CG-CD2	5.08	124.90	118.30
1	E	87	ASP	OD1-CG-OD2	-5.08	113.65	123.30
1	E	138	PHE	CG-CD2-CE2	-5.08	115.22	120.80
1	E	116	THR	CA-CB-CG2	-5.07	105.30	112.40
1	E	284	PHE	CD1-CE1-CZ	-5.02	114.08	120.10
1	E	187	GLN	C-N-CA	-5.00	111.79	122.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	10	LEU	Mainchain
1	E	265	ARG	Sidechain
1	E	52	GLY	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	E	2389	0	2280	34	1
2	E	46	0	11	0	0
3	E	15	0	0	1	0
4	E	281	0	0	3	0
All	All	2731	0	2291	34	1

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 7.

All (34) 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:E:51:ASP:O	1:E:53:GLN:OE1	1.75	1.04
1:E:51:ASP:C	1:E:51:ASP:OD1	2.06	0.92
1:E:187:GLN:NE2	4:E:607:HOH:O	2.22	0.72
1:E:5:THR:HG23	4:E:357:HOH:O	1.89	0.71
1:E:205:THR:O	1:E:205:THR:HG23	1.90	0.71
1:E:51:ASP:O	1:E:51:ASP:OD1	2.13	0.65
1:E:179:ILE:N	3:E:329:SO4:O2	2.26	0.64
1:E:129:ASN:ND2	1:E:131:VAL:H	2.05	0.55
1:E:51:ASP:O	1:E:53:GLN:CD	2.45	0.54
1:E:205:THR:O	1:E:205:THR:CG2	2.56	0.53
1:E:129:ASN:ND2	1:E:135:GLN:H	2.09	0.51
1:E:1:SER:OG	1:E:166:ASN:ND2	2.48	0.47
1:E:220:LEU:O	1:E:303:GLY:HA3	2.15	0.46
1:E:223:LEU:HB3	1:E:224:PRO:HD2	1.97	0.46
1:E:126:SER:OG	1:E:140:ASP:OD2	2.23	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:52:GLY:HA3	1:E:115:SER:HB2	1.99	0.44
1:E:248:PHE:CZ	1:E:254:LEU:HD11	2.52	0.44
1:E:264:ALA:C	1:E:265:ARG:HG2	2.35	0.43
1:E:86:THR:HA	1:E:99:GLN:O	2.19	0.43
1:E:4:THR:OG1	1:E:14:TYR:HB3	2.19	0.42
1:E:223:LEU:HB3	1:E:224:PRO:CD	2.50	0.42
1:E:186:LYS:HD2	4:E:605:HOH:O	2.20	0.41
1:E:278:ILE:HD12	1:E:282(B):SER:CB	2.51	0.41
1:E:238:ALA:HA	1:E:247:VAL:O	2.21	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:51:ASP:CB	1:E:147:ASP:O[1_556]	1.99	0.21

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	E	328/330 (99%)	323 (98%)	5 (2%)	0	100 100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	E	263/263 (100%)	258 (98%)	5 (2%)	65 39

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	37	ASP
1	E	148	SER
1	E	186	LYS
1	E	241	SER
1	E	299	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	28	ASN
1	E	99	GLN
1	E	129	ASN
1	E	134(A)	GLN
1	E	135	GLN
1	E	141	ASN
1	E	166	ASN
1	E	187	GLN
1	E	300	ASN

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 ⓘ

5 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	2ZS	E	327[A]	-	45,45,45	2.37	13 (28%)	56,59,59	3.26	25 (44%)
2	2ZS	E	327[B]	-	45,45,45	2.33	13 (28%)	56,59,59	2.96	22 (39%)
3	SO4	E	328	-	4,4,4	0.63	0	6,6,6	0.46	0
3	SO4	E	329	-	4,4,4	0.35	0	6,6,6	0.55	0
3	SO4	E	330	-	4,4,4	0.32	0	6,6,6	0.24	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	2ZS	E	327[A]	-	-	0/47/63/63	0/3/3/3
2	2ZS	E	327[B]	-	-	0/47/63/63	0/3/3/3
3	SO4	E	328	-	-	0/0/0/0	0/0/0/0
3	SO4	E	329	-	-	0/0/0/0	0/0/0/0
3	SO4	E	330	-	-	0/0/0/0	0/0/0/0

All (26) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	327[B]	2ZS	CB1-SG	-7.84	1.72	1.80
2	E	327[A]	2ZS	CD21-CG1	-3.08	1.44	1.52
2	E	327[B]	2ZS	CD21-CG1	-3.08	1.44	1.52
2	E	327[A]	2ZS	C5-N4	-3.05	1.41	1.47
2	E	327[B]	2ZS	C5-N4	-3.05	1.41	1.47
2	E	327[A]	2ZS	CZ-CE2	-2.40	1.31	1.38
2	E	327[B]	2ZS	CZ-CE2	-2.40	1.31	1.38
2	E	327[A]	2ZS	CD2-CG	-2.24	1.34	1.38
2	E	327[B]	2ZS	CD2-CG	-2.24	1.34	1.38
2	E	327[A]	2ZS	O11-C7	2.16	1.26	1.21
2	E	327[B]	2ZS	O11-C7	2.16	1.26	1.21
2	E	327[A]	2ZS	C1-N1	2.45	1.39	1.34
2	E	327[B]	2ZS	C1-N1	2.45	1.39	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	327[A]	2ZS	O21-CM	2.78	1.54	1.47
2	E	327[B]	2ZS	O21-CM	2.78	1.54	1.47
2	E	327[A]	2ZS	CB2-CA2	2.99	1.57	1.53
2	E	327[B]	2ZS	CB2-CA2	2.99	1.57	1.53
2	E	327[A]	2ZS	CH-CA2	3.27	1.58	1.54
2	E	327[B]	2ZS	CH-CA2	3.27	1.58	1.54
2	E	327[A]	2ZS	O21-C7	3.87	1.43	1.34
2	E	327[B]	2ZS	O21-C7	3.87	1.43	1.34
2	E	327[A]	2ZS	CB2-CG1	4.94	1.61	1.53
2	E	327[B]	2ZS	CB2-CG1	4.94	1.61	1.53
2	E	327[A]	2ZS	C4-N2	6.21	1.48	1.34
2	E	327[B]	2ZS	C4-N2	6.21	1.48	1.34
2	E	327[A]	2ZS	CB1-SG	8.48	1.90	1.80

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	327[A]	2ZS	O3-C4-N2	-8.99	105.33	122.93
2	E	327[B]	2ZS	O3-C4-N2	-8.99	105.33	122.93
2	E	327[A]	2ZS	O21-C7-O11	-8.25	106.90	123.89
2	E	327[B]	2ZS	O21-C7-O11	-8.25	106.90	123.89
2	E	327[A]	2ZS	CS-SG-CB1	-6.97	89.88	101.21
2	E	327[A]	2ZS	CM-O21-C7	-6.01	110.31	117.87
2	E	327[B]	2ZS	CM-O21-C7	-6.01	110.31	117.87
2	E	327[A]	2ZS	O3-C4-CA1	-3.79	111.98	120.36
2	E	327[B]	2ZS	O3-C4-CA1	-3.79	111.98	120.36
2	E	327[A]	2ZS	CE1-CD1-CG	-3.59	114.94	120.65
2	E	327[B]	2ZS	CE1-CD1-CG	-3.59	114.94	120.65
2	E	327[A]	2ZS	CB2-CA2-CH	-3.28	105.06	111.71
2	E	327[B]	2ZS	CB2-CA2-CH	-3.28	105.06	111.71
2	E	327[A]	2ZS	CB-CG-CD2	-2.98	114.67	120.90
2	E	327[B]	2ZS	CB-CG-CD2	-2.98	114.67	120.90
2	E	327[A]	2ZS	O-C-N4	-2.94	117.28	121.77
2	E	327[B]	2ZS	O-C-N4	-2.94	117.28	121.77
2	E	327[A]	2ZS	CZ-CE2-CD2	-2.82	116.06	120.19
2	E	327[B]	2ZS	CZ-CE2-CD2	-2.82	116.06	120.19
2	E	327[A]	2ZS	C5-N4-C	-2.10	114.48	122.03
2	E	327[B]	2ZS	C5-N4-C	-2.10	114.48	122.03
2	E	327[A]	2ZS	O1-C2-C3	-2.05	107.14	111.84
2	E	327[B]	2ZS	O1-C2-C3	-2.05	107.14	111.84
2	E	327[A]	2ZS	O21-CM-CM1	2.31	113.08	107.12
2	E	327[B]	2ZS	O21-CM-CM1	2.31	113.08	107.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	327[A]	2ZS	O21-CM-CM2	2.31	113.09	107.12
2	E	327[B]	2ZS	O21-CM-CM2	2.31	113.09	107.12
2	E	327[A]	2ZS	CE2-CZ-CE1	2.60	124.49	119.93
2	E	327[B]	2ZS	CE2-CZ-CE1	2.60	124.49	119.93
2	E	327[A]	2ZS	CB2-CG1-CD21	2.68	118.02	111.67
2	E	327[B]	2ZS	CB2-CG1-CD21	2.68	118.02	111.67
2	E	327[A]	2ZS	C6-C5-N4	2.88	116.08	109.90
2	E	327[B]	2ZS	C6-C5-N4	2.88	116.08	109.90
2	E	327[A]	2ZS	CB1-CA1-C4	3.29	117.47	109.59
2	E	327[A]	2ZS	O11-C7-CH	3.39	131.62	123.44
2	E	327[B]	2ZS	O11-C7-CH	3.39	131.62	123.44
2	E	327[A]	2ZS	CD2-CG-CD1	3.42	123.61	118.13
2	E	327[B]	2ZS	CD2-CG-CD1	3.42	123.61	118.13
2	E	327[A]	2ZS	C5-N4-C3	5.07	121.96	112.56
2	E	327[B]	2ZS	C5-N4-C3	5.07	121.96	112.56
2	E	327[A]	2ZS	O21-C7-CH	5.41	121.47	111.14
2	E	327[B]	2ZS	O21-C7-CH	5.41	121.47	111.14
2	E	327[A]	2ZS	CA1-C4-N2	6.71	132.25	116.78
2	E	327[B]	2ZS	CA1-C4-N2	6.71	132.25	116.78
2	E	327[A]	2ZS	CB1-CA1-N1	6.83	127.65	110.83
2	E	327[A]	2ZS	CA2-N2-C4	6.84	135.85	123.13
2	E	327[B]	2ZS	CA2-N2-C4	6.84	135.85	123.13

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	329	SO4	1	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.