



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:48 PM GMT

PDB ID : 4G8O  
Title : Crystal Structure of a novel small molecule inactivator bound to plasminogen activator inhibitor-1  
Authors : Stuckey, J.A.; Lawrence, D.A.; Li, S.-H.  
Deposited on : 2012-07-23  
Resolution : 2.71 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) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

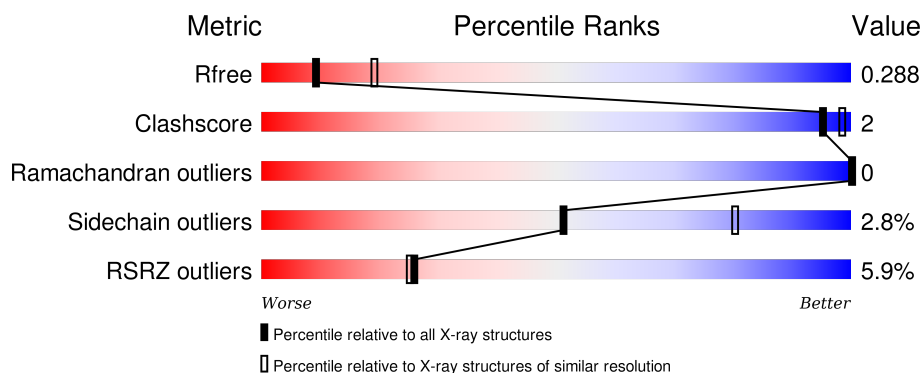
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.71 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	2439 (2.74-2.70)
Clashscore	102246	2771 (2.74-2.70)
Ramachandran outliers	100387	2726 (2.74-2.70)
Sidechain outliers	100360	2727 (2.74-2.70)
RSRZ outliers	91569	2443 (2.74-2.70)

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.

Mol	Chain	Length	Quality of chain
1	A	376	<div> <div>6%</div> <div>89% 6% 5%</div> </div>
1	B	376	<div> <div>3%</div> <div>91% • 5%</div> </div>
1	C	376	<div> <div>6%</div> <div>91% 6% •</div> </div>
1	D	376	<div> <div>7%</div> <div>89% 8% ••</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	96P	D	403	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 11723 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 Plasminogen activator inhibitor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	359	Total	C	N	O	S	0	0	0
			2841	1829	477	521	14			
1	B	359	Total	C	N	O	S	0	0	0
			2851	1835	485	517	14			
1	C	367	Total	C	N	O	S	0	0	0
			2912	1874	495	528	15			
1	D	367	Total	C	N	O	S	0	0	0
			2881	1853	486	527	15			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	4	ALA	-	EXPRESSION TAG	UNP P05121
A	150	HIS	ASN	ENGINEERED MUTATION	UNP P05121
A	154	THR	LYS	ENGINEERED MUTATION	UNP P05121
A	319	LEU	GLN	ENGINEERED MUTATION	UNP P05121
A	354	ILE	MET	ENGINEERED MUTATION	UNP P05121
B	4	ALA	-	EXPRESSION TAG	UNP P05121
B	150	HIS	ASN	ENGINEERED MUTATION	UNP P05121
B	154	THR	LYS	ENGINEERED MUTATION	UNP P05121
B	319	LEU	GLN	ENGINEERED MUTATION	UNP P05121
B	354	ILE	MET	ENGINEERED MUTATION	UNP P05121
C	4	ALA	-	EXPRESSION TAG	UNP P05121
C	150	HIS	ASN	ENGINEERED MUTATION	UNP P05121
C	154	THR	LYS	ENGINEERED MUTATION	UNP P05121
C	319	LEU	GLN	ENGINEERED MUTATION	UNP P05121
C	354	ILE	MET	ENGINEERED MUTATION	UNP P05121
D	4	ALA	-	EXPRESSION TAG	UNP P05121
D	150	HIS	ASN	ENGINEERED MUTATION	UNP P05121
D	154	THR	LYS	ENGINEERED MUTATION	UNP P05121
D	319	LEU	GLN	ENGINEERED MUTATION	UNP P05121
D	354	ILE	MET	ENGINEERED MUTATION	UNP P05121

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



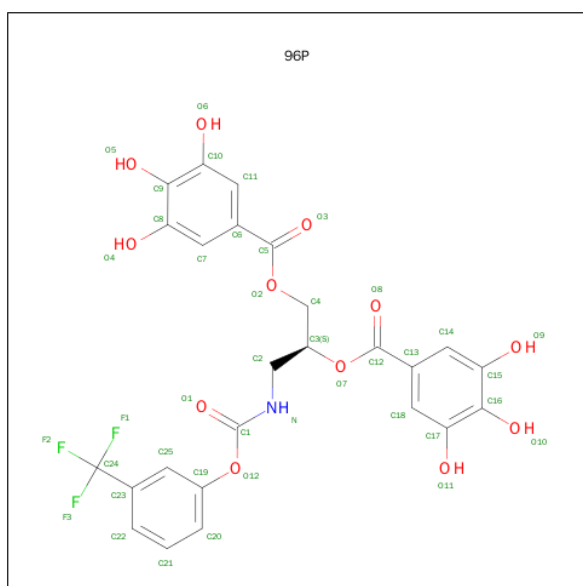
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is (2S)-3-({[3-(TRIFLUOROMETHYL)PHENOXY]CARBONYL}AMINO)PROPANE-1,2-DIYL BIS(3,4,5-TRIHYDROXYBENZOATE) (three-letter code: 96P) (formula:  $C_{25}H_{20}F_3NO_{12}$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	D	1	Total	C	F	N	O	21	0
			41	25	3	1	12		

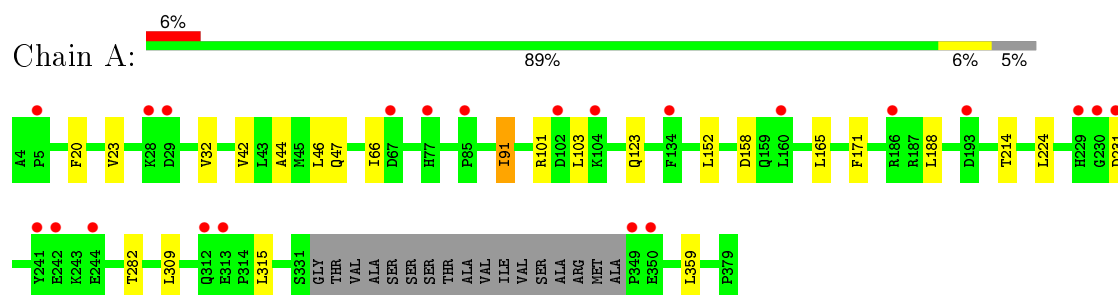
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	40	Total 40	O 40	0	0
5	B	46	Total 46	O 46	0	0
5	C	37	Total 37	O 37	0	0
5	D	40	Total 40	O 40	0	0

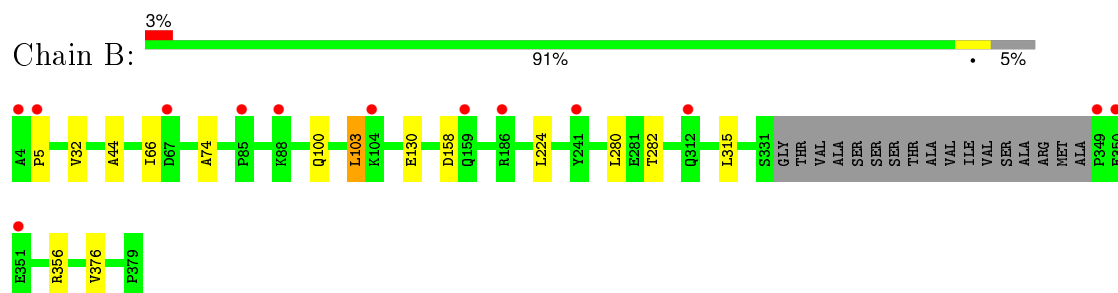
### 3 Residue-property plots [i](#)

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.

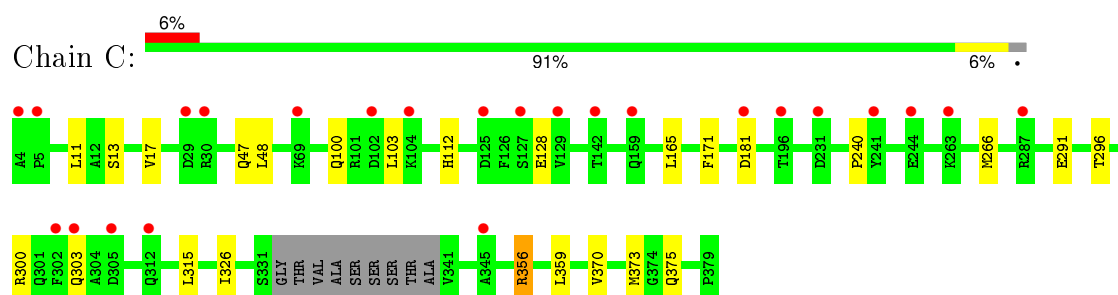
#### • Molecule 1: Plasminogen activator inhibitor 1



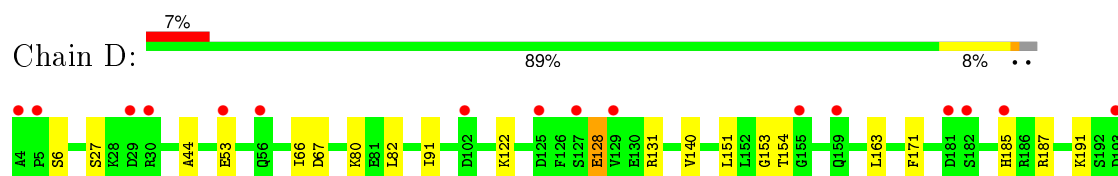
#### • Molecule 1: Plasminogen activator inhibitor 1



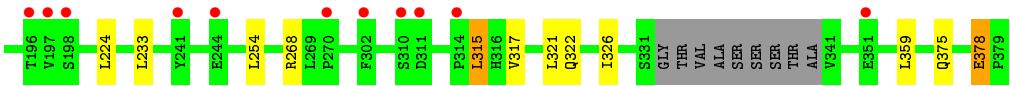
#### • Molecule 1: Plasminogen activator inhibitor 1



#### • Molecule 1: Plasminogen activator inhibitor 1







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	65.33Å 75.32Å 105.00Å 91.32° 93.49° 115.65°	Depositor
Resolution (Å)	20.00 – 2.71 20.32 – 2.71	Depositor EDS
% Data completeness (in resolution range)	87.6 (20.00-2.71) 87.7 (20.32-2.71)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.36 (at 2.71Å)	Xtriage
Refinement program	BUSTER 2.11.2	Depositor
R, $R_{free}$	0.239 , 0.268 0.253 , 0.288	Depositor DCC
$R_{free}$ test set	2158 reflections (5.33%)	DCC
Wilson B-factor (Å <sup>2</sup> )	46.1	Xtriage
Anisotropy	0.894	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 51.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 42667 reflections	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	11723	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.32% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

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

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 96P, SO4, EDO

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	0.39	0/2911	0.57	0/3951
1	B	0.39	0/2922	0.56	0/3964
1	C	0.39	0/2983	0.55	0/4046
1	D	0.40	0/2952	0.56	0/4009
All	All	0.39	0/11768	0.56	0/15970

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2841	0	2805	7	0
1	B	2851	0	2826	6	0
1	C	2912	0	2902	11	0
1	D	2881	0	2825	13	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	10	0	0	0	0
2	D	10	0	0	0	0
3	A	4	0	6	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	41	0	14	1	0
5	A	40	0	0	0	0
5	B	46	0	0	0	0
5	C	37	0	0	0	0
5	D	40	0	0	0	0
All	All	11723	0	11378	36	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 2.

All (36) 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:C:171:PHE:HB3	1:C:326:ILE:HD13	1.87	0.56
1:D:163:LEU:HD23	1:D:317:VAL:HG22	1.89	0.55
1:D:191:LYS:HD3	1:D:378:GLU:HG3	1.87	0.55
1:B:130:GLU:HG2	1:C:11:LEU:HD23	1.87	0.54
1:C:300:ARG:HB3	1:C:303:GLN:HB2	1.88	0.54
1:C:240:PRO:HD2	1:C:356:ARG:HE	1.73	0.53
1:B:44:ALA:HB1	1:B:66:ILE:HD13	1.91	0.51
1:D:268:ARG:HH12	4:D:403:96P:H14	1.75	0.51
1:A:44:ALA:HB1	1:A:66:ILE:HD13	1.95	0.49
1:D:140:VAL:HG21	1:D:151:LEU:HD11	1.95	0.48
1:C:359:LEU:HD12	1:C:375:GLN:HB3	1.94	0.48
1:A:91:ILE:HG23	1:A:171:PHE:HD1	1.78	0.47
1:C:103:LEU:HD21	1:C:315:LEU:HD11	1.95	0.47
1:C:370:VAL:HG11	1:C:373:MET:HE3	1.97	0.47
1:A:32:VAL:HG23	1:A:282:THR:HG21	1.96	0.47
1:D:171:PHE:HB3	1:D:326:ILE:HD13	1.96	0.46
1:A:46:LEU:HD13	1:A:165:LEU:HD13	1.96	0.46
1:D:151:LEU:HB2	1:D:154:THR:HG23	1.97	0.46
1:C:291:GLU:HG2	1:C:296:THR:HA	1.98	0.45
1:C:13:SER:O	1:C:17:VAL:HG23	2.17	0.45
1:B:100:GLN:HB3	1:B:103:LEU:HD13	1.99	0.45
1:D:163:LEU:HB2	1:D:315:LEU:HD21	1.99	0.44
1:A:101:ARG:HA	1:A:123:GLN:HB3	1.99	0.44
1:A:309:LEU:HD23	1:A:315:LEU:HD13	2.00	0.44
1:B:5:PRO:HA	1:B:74:ALA:HB1	2.00	0.43
1:B:280:LEU:HD11	1:B:376:VAL:HG22	2.00	0.43
1:D:91:ILE:HD11	1:D:233:LEU:HD11	1.99	0.43
1:D:185:HIS:CE1	1:D:187:ARG:HE	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:359:LEU:HD12	1:D:375:GLN:HB3	2.01	0.42
1:D:44:ALA:HB1	1:D:66:ILE:HD13	2.02	0.42
1:B:32:VAL:HG23	1:B:282:THR:HG21	2.02	0.42
1:D:128:GLU:HB3	1:D:131:ARG:HB3	2.02	0.42
1:D:153:GLY:HA3	1:D:321:LEU:HD21	2.03	0.41
1:C:100:GLN:HB3	1:C:103:LEU:HB2	2.03	0.41
1:C:48:LEU:HD21	1:C:112:HIS:HD2	1.86	0.41
1:A:20:PHE:HA	1:A:23:VAL:HG22	2.02	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	355/376 (94%)	344 (97%)	11 (3%)	0	100	100
1	B	355/376 (94%)	344 (97%)	11 (3%)	0	100	100
1	C	363/376 (96%)	350 (96%)	13 (4%)	0	100	100
1	D	363/376 (96%)	353 (97%)	10 (3%)	0	100	100
All	All	1436/1504 (96%)	1391 (97%)	45 (3%)	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	A	310/329 (94%)	299 (96%)	11 (4%)	43	73
1	B	311/329 (94%)	306 (98%)	5 (2%)	70	90
1	C	319/329 (97%)	313 (98%)	6 (2%)	65	88
1	D	310/329 (94%)	297 (96%)	13 (4%)	36	66
All	All	1250/1316 (95%)	1215 (97%)	35 (3%)	51	80

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	42	VAL
1	A	47	GLN
1	A	91	ILE
1	A	103	LEU
1	A	152	LEU
1	A	158	ASP
1	A	188	LEU
1	A	214	THR
1	A	224	LEU
1	A	231	ASP
1	A	359	LEU
1	B	103	LEU
1	B	158	ASP
1	B	224	LEU
1	B	315	LEU
1	B	356	ARG
1	C	47	GLN
1	C	128	GLU
1	C	165	LEU
1	C	181	ASP
1	C	266	MET
1	C	356	ARG
1	D	6	SER
1	D	27	SER
1	D	53	GLU
1	D	67	ASP
1	D	80	LYS
1	D	82	LEU
1	D	122	LYS
1	D	128	GLU
1	D	224	LEU
1	D	254	LEU
1	D	315	LEU

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Mol	Chain	Res	Type
1	D	322	GLN
1	D	378	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	316	HIS
1	C	112	HIS
1	C	190	HIS
1	D	59	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

8 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	SO4	A	401	-	4,4,4	0.14	0	6,6,6	0.07	0
3	EDO	A	402	-	3,3,3	0.59	0	2,2,2	0.46	0
2	SO4	B	401	-	4,4,4	0.18	0	6,6,6	0.15	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	SO4	C	401	-	4,4,4	0.18	0	6,6,6	0.07	0
2	SO4	C	402	-	4,4,4	0.11	0	6,6,6	0.10	0
2	SO4	D	401	-	4,4,4	0.10	0	6,6,6	0.07	0
2	SO4	D	402	-	4,4,4	0.15	0	6,6,6	0.10	0
4	96P	D	403	-	43,43,43	0.27	0	61,62,62	0.83	1 (1%)

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	SO4	A	401	-	-	0/0/0/0	0/0/0/0
3	EDO	A	402	-	-	0/1/1/1	0/0/0/0
2	SO4	B	401	-	-	0/0/0/0	0/0/0/0
2	SO4	C	401	-	-	0/0/0/0	0/0/0/0
2	SO4	C	402	-	-	0/0/0/0	0/0/0/0
2	SO4	D	401	-	-	0/0/0/0	0/0/0/0
2	SO4	D	402	-	-	0/0/0/0	0/0/0/0
4	96P	D	403	-	-	0/32/32/32	0/3/3/3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	403	96P	O7-C3-C2	5.52	116.41	106.72

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
4	D	403	96P	1	0

## 5.7 Other polymers ⓘ

There are no such residues in this entry.



## 5.8 Polymer linkage issues ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	359/376 (95%)	0.37	22 (6%) 25 24	37, 53, 65, 69	0
1	B	359/376 (95%)	0.34	13 (3%) 46 47	38, 53, 66, 73	0
1	C	367/376 (97%)	0.54	24 (6%) 22 21	38, 57, 86, 125	0
1	D	367/376 (97%)	0.50	27 (7%) 17 16	40, 57, 66, 73	0
All	All	1452/1504 (96%)	0.44	86 (5%) 26 25	37, 55, 72, 125	0

All (86) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	5	PRO	7.0
1	D	5	PRO	5.0
1	A	102	ASP	4.7
1	D	125	ASP	4.7
1	C	4	ALA	4.4
1	D	302	PHE	4.3
1	C	196	THR	4.3
1	D	241	TYR	4.1
1	C	181	ASP	4.0
1	D	181	ASP	4.0
1	C	159	GLN	3.9
1	D	197	VAL	3.8
1	C	303	GLN	3.8
1	C	241	TYR	3.7
1	C	125	ASP	3.7
1	B	4	ALA	3.6
1	B	85	PRO	3.6
1	C	104	LYS	3.5
1	A	5	PRO	3.5
1	D	310	SER	3.4
1	D	4	ALA	3.4

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Mol	Chain	Res	Type	RSRZ
1	D	102	ASP	3.3
1	D	196	THR	3.0
1	C	231	ASP	3.0
1	C	244	GLU	3.0
1	D	53	GLU	2.9
1	A	312	GLN	2.9
1	B	241	TYR	2.9
1	A	241	TYR	2.7
1	B	312	GLN	2.6
1	A	231	ASP	2.6
1	D	244	GLU	2.6
1	B	186	ARG	2.6
1	A	134	PHE	2.6
1	C	127	SER	2.5
1	D	182	SER	2.5
1	D	351	GLU	2.5
1	D	314	PRO	2.5
1	D	129	VAL	2.5
1	C	102	ASP	2.5
1	C	345	ALA	2.5
1	C	29	ASP	2.5
1	A	186	ARG	2.4
1	C	312	GLN	2.4
1	B	104	LYS	2.4
1	A	313	GLU	2.4
1	A	350	GLU	2.4
1	D	127	SER	2.4
1	B	88	LYS	2.4
1	D	155	GLY	2.3
1	A	160	LEU	2.3
1	A	242	GLU	2.3
1	B	67	ASP	2.3
1	C	69	LYS	2.3
1	B	5	PRO	2.3
1	C	302	PHE	2.3
1	A	29	ASP	2.3
1	D	270	PRO	2.3
1	A	104	LYS	2.3
1	A	349	PRO	2.2
1	B	349	PRO	2.2
1	A	28	LYS	2.2
1	D	193	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	287	ARG	2.2
1	A	229	HIS	2.2
1	C	142	THR	2.2
1	A	85	PRO	2.2
1	D	159	GLN	2.2
1	D	311	ASP	2.2
1	D	56	GLN	2.2
1	D	185	HIS	2.2
1	B	159	GLN	2.2
1	B	351	GLU	2.2
1	A	77	HIS	2.1
1	A	193	ASP	2.1
1	C	129	VAL	2.1
1	D	29	ASP	2.1
1	C	305	ASP	2.1
1	C	30	ARG	2.1
1	D	30	ARG	2.1
1	A	230	GLY	2.1
1	B	350	GLU	2.1
1	C	263	LYS	2.0
1	A	244	GLU	2.0
1	D	198	SER	2.0
1	A	67	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 carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	96P	D	403	41/41	0.68	0.47	3.66	85,85,85,85	41
2	SO4	D	402	5/5	0.95	0.20	-0.20	77,78,78,78	0
2	SO4	C	402	5/5	0.95	0.12	-1.36	81,81,81,81	0
2	SO4	D	401	5/5	0.93	0.15	-1.79	86,86,87,87	0
2	SO4	C	401	5/5	0.96	0.10	-1.96	69,70,70,70	0
2	SO4	B	401	5/5	0.96	0.12	-2.28	68,68,68,69	0
2	SO4	A	401	5/5	0.98	0.08	-2.61	67,67,67,67	0
3	EDO	A	402	4/4	0.90	0.16	-	40,40,40,40	0

## 6.5 Other polymers

There are no such residues in this entry.