

Full wwPDB X-ray Structure Validation Report (i)

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PDB ID	:	1SZK
Title	:	The structure of gamma-aminobutyrate aminotransferase mutant: E211S
Authors	:	Liu, W.; Peterson, P.E.; Langston, J.A.; Jin, X.; Fisher, A.J.; Toney, M.D.
Deposited on	:	2004-04-05
Resolution	:	2.52 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 (i) 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 (1)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 2.52 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R _{free}	130704	5743 (2.54-2.50)
Clashscore	141614	6463 (2.54-2.50)
Ramachandran outliers	138981	6335 (2.54-2.50)
Sidechain outliers	138945	6337 (2.54-2.50)
RSRZ outliers	127900	5630(2.54-2.50)

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 <=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	А	426	3% 79%	19%	
1	В	426	78%	21%	•
1	С	426	73%	25%	
1	D	426	71%	27%	•

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



residues in	n protein,	DNA,	RNA	chains	that	are	outliers	for	geometric o	or e	electron-o	lensity-f	it crite-
ria:													

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	D	711	-	-	-	Х
3	EDO	D	805	-	-	Х	-



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 13688 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.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace		
1 A	495	Total	С	Ν	0	\mathbf{S}	0 1	1	0			
	420	3209	2027	562	602	18		1				
1	В	425	Total	С	Ν	0	S	0	0	0	0	0
1	D	420	3203	2024	561	600	18		0	0		
1	C	425	Total	С	Ν	0	S	0	0	0		
	U	420	3203	2024	561	600	18	0	U	0		
1	Л	495	Total	С	Ν	0	S	0	1	Ο		
1	D	420	3209	2027	562	602	18	0		0		

• Molecule 1 is a protein called 4-aminobutyrate aminotransferase.

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	211	SER	GLU	engineered mutation	UNP P22256
В	211	SER	GLU	engineered mutation	UNP P22256
С	211	SER	GLU	engineered mutation	UNP P22256
D	211	SER	GLU	engineered mutation	UNP P22256

• Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
2	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
2	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
2	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
2	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
2	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
2	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
2	С	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
2	С	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
2	С	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
2	D	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
2	D	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
2	D	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
2	D	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	D	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0

• Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 4 2 2 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 4 2 2 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 4 2 2 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 4 2 2 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 4 2 2 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 4 2 2 \end{array}$	0	0
3	С	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 4 2 2 \end{array}$	0	0
3	С	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 4 2 2 \end{array}$	0	0
3	С	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
3	D	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0



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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	D	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
3	D	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
3	D	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0

• Molecule 4 is 4'-DEOXY-4'-AMINOPYRIDOXAL-5'-PHOSPHATE (three-letter code: PMP) (formula: $C_8H_{13}N_2O_5P$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf					
4	Λ	1	Total	С	Ν	Ο	Р	0	0			
4	A	L	16	8	2	5	1	0	0			
4	р	1	Total	С	Ν	Ο	Р	0	0			
4	D	D	D	D	1	16	8	2	5	1	0	0
4	С	1	Total	С	Ν	Ο	Р	0	0			
4	U	1	16	8	2	5	1	0	U			
4	р	1	Total	С	Ν	Ο	Р	0	0			
4	D		16	8	2	5	1	0	U			

• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	179	Total O 179 179	0	0
5	В	177	Total O 177 177	0	0



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 Mol
 Chain
 Besidues
 Atoms

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	С	142	Total O 142 142	0	0
5	D	175	Total O 175 175	0	0



3 Residue-property plots (i)

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



• Molecule 1: 4-aminobutyrate aminotransferase

D362 G363 D364 H365 N366 K367 P368 4380 V279 I 303 355 E415 E415 E415 1416 1417 S418 S418 Y394 N395 V396 L397 R398 S389 C390 F421 D422 E423 A424 K425 D426 D426

• Molecule 1: 4-aminobutyrate aminotransferase

Q41





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants	108.26Å 108.26Å 300.83Å	Deperitor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
$\mathbf{P}_{\text{acclution}}(\hat{\mathbf{A}})$	30.00 - 2.52	Depositor
Resolution (A)	47.63 - 2.50	EDS
% Data completeness	(Not available) $(30.00-2.52)$	Depositor
(in resolution range)	97.5 (47.63 - 2.50)	EDS
R _{merge}	(Not available)	Depositor
R _{sym}	0.08	Depositor
$< I/\sigma(I) > 1$	$2.65 (at 2.51 \text{\AA})$	Xtriage
Refinement program	CNS	Depositor
D D.	0.187 , 0.240	Depositor
Π, Π_{free}	0.182 , 0.234	DCC
R_{free} test set	3519 reflections $(5.03%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	33.8	Xtriage
Anisotropy	0.407	Xtriage
Bulk solvent $k_{sol}(e/A^3)$, $B_{sol}(A^2)$	0.34 , 49.8	EDS
L-test for twinning ²	$< L > = 0.47, < L^2 > = 0.30$	Xtriage
Estimated twinning fraction	0.029 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13688	wwPDB-VP
Average B, all atoms $(Å^2)$	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.94% of the height of the origin peak. No significant pseudotranslation is detected.

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



¹Intensities estimated from amplitudes.

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: PMP, 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).

Mal	Chain	Bond	lengths	Bond angles	
		RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.37	0/3268	0.62	0/4423
1	В	0.38	0/3262	0.62	0/4415
1	С	0.36	0/3262	0.61	0/4415
1	D	0.38	0/3268	0.63	0/4423
All	All	0.37	0/13060	0.62	0/17676

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	А	3209	0	3224	71	0
1	В	3203	0	3220	75	0
1	С	3203	0	3220	82	0
1	D	3209	0	3224	84	0
2	А	15	0	0	1	0
2	В	20	0	0	0	0
2	С	15	0	0	1	0
2	D	25	0	0	0	0
3	A	12	0	18	3	0



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	В	12	0	18	4	0
3	С	12	0	18	1	0
3	D	16	0	24	5	0
4	А	16	0	10	1	0
4	В	16	0	10	1	0
4	С	16	0	10	0	0
4	D	16	0	10	1	0
5	А	179	0	0	7	0
5	В	177	0	0	6	0
5	С	142	0	0	5	0
5	D	175	0	0	3	0
All	All	13688	0	13006	296	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 11.

All (296) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:D:25:ILE:HD11	1:D:381:ARG:HD3	1.43	1.00
1:B:25:ILE:HD11	1:B:381:ARG:HD3	1.45	0.98
1:C:348:VAL:HG22	1:C:357:ILE:HG22	1.61	0.82
1:C:334:GLY:HA3	1:C:414:LEU:HD13	1.63	0.80
1:D:401:VAL:HG21	1:D:405:ILE:HD12	1.65	0.78
1:C:17:ARG:HH11	1:D:291:PRO:HD3	1.51	0.75
1:A:401:VAL:HG21	1:A:405:ILE:HD12	1.68	0.74
1:A:165:HIS:H	3:C:803:EDO:H11	1.53	0.74
1:C:350:GLY:HA3	1:C:355:ILE:HD13	1.74	0.70
1:D:364:ASP:OD2	1:D:367:LYS:HG3	1.91	0.70
5:A:857:HOH:O	1:C:157:ALA:HA	1.93	0.68
1:B:156:SER:HA	1:B:159:MET:CE	2.24	0.68
1:A:151:LYS:HD3	1:A:155:TYR:CE1	2.29	0.68
1:A:66:VAL:HG13	1:A:303:ILE:HG23	1.74	0.68
1:B:307:ALA:O	1:B:311:VAL:HG23	1.93	0.67
1:A:72:LYS:HE2	5:B:936:HOH:O	1.95	0.67
1:A:284:GLU:CD	1:A:284:GLU:H	1.99	0.66
1:B:151:LYS:HD3	1:B:155:TYR:CE1	2.31	0.65
1:B:151:LYS:HE3	1:B:153:ASN:O	1.95	0.65
1:D:88:GLU:O	1:D:92:ILE:HG13	1.97	0.65
1:C:196:ALA:HB1	1:C:198:GLU:OE2	1.98	0.63
1:A:366:ASN:N	1:A:366:ASN:HD22	1.96	0.63



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:C:17:ARG:NH1	1:D:291:PRO:HD3	2.13	0.63
1:C:76:THR:HB	3:D:805:EDO:H22	1.81	0.63
1:C:246:GLY:HA2	1:C:250:THR:O	1.99	0.63
1:C:151:LYS:HE3	1:C:153:ASN:O	1.99	0.62
1:D:406:GLU:HB2	1:D:409:GLN:OE1	2.00	0.62
1:A:364:ASP:CG	1:A:366:ASN:HD21	2.03	0.61
1:B:192:LYS:HD2	5:B:951:HOH:O	2.00	0.61
1:A:63:VAL:O	1:A:67:GLU:HG3	2.01	0.60
1:C:256:GLN:OE1	1:C:351:LEU:HD21	2.01	0.60
1:D:157:ALA:HA	5:D:940:HOH:O	2.00	0.60
1:B:426:GLN:N	1:B:426:GLN:NE2	2.50	0.59
1:C:265:THR:HG22	1:C:279:VAL:HG22	1.83	0.59
1:A:276:LEU:HB2	1:A:304:ALA:HB1	1.84	0.59
1:D:358:GLU:HG2	1:D:360:PHE:CE2	2.38	0.59
1:C:224:ARG:HD2	5:C:879:HOH:O	2.03	0.59
1:D:41:ARG:HH22	1:D:382:ASP:C	2.05	0.59
1:B:315:PHE:CD2	1:B:320:LEU:HB2	2.38	0.59
1:B:303:ILE:O	1:B:306:VAL:HG22	2.03	0.59
1:C:66:VAL:HG13	1:C:303:ILE:HG23	1.86	0.58
1:D:76:THR:O	1:D:77:CYS:HB3	2.04	0.58
1:A:72:LYS:HD2	3:A:810:EDO:H12	1.85	0.58
1:B:157:ALA:HA	5:B:839:HOH:O	2.02	0.58
1:C:63:VAL:O	1:C:67:GLU:HG3	2.04	0.58
1:C:106:LEU:HD22	1:C:294:LEU:HD13	1.86	0.58
1:C:41:ARG:HG2	1:C:43:TYR:CE1	2.38	0.58
1:D:47:ALA:HB3	3:D:805:EDO:O1	2.03	0.57
1:A:76:THR:HB	3:B:801:EDO:H11	1.86	0.57
1:A:313:LYS:HB3	1:A:317:GLN:HE21	1.69	0.57
1:B:229:CYS:HB3	1:B:234:ILE:O	2.06	0.56
1:C:412:GLN:O	1:C:416:ILE:HG13	2.06	0.56
1:C:32:ASN:C	1:C:32:ASN:HD22	2.07	0.56
1:C:229:CYS:HB3	1:C:234:ILE:O	2.06	0.56
1:B:361:GLU:HB2	1:B:367:LYS:CB	2.36	0.56
1:A:209:GLN:O	1:A:214:PHE:HA	2.06	0.55
1:B:426:GLN:N	1:B:426:GLN:HE21	2.04	0.55
1:D:350:GLY:HA3	1:D:355:ILE:HD13	1.87	0.55
1:B:361:GLU:HB2	1:B:367:LYS:HB3	1.88	0.55
1:D:209:GLN:O	1:D:214:PHE:HA	2.06	0.55
1:A:5:LYS:O	1:A:9:GLN:HG3	2.07	0.55
1:A:246:GLY:HA2	1:A:250:THR:O	2.07	0.55
1:A:162:MET:HB3	1:A:163:PRO:HD2	1.88	0.54



	to as pagem	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:B:15:ILE:HG23	1:B:16:PRO:HD2	1.89	0.54
1:A:106:LEU:HD22	1:A:294:LEU:HD13	1.90	0.54
1:D:360:PHE:HB3	1:D:364:ASP:O	2.07	0.54
1:B:241:VAL:HG13	1:B:267:ALA:HB3	1.90	0.54
1:C:263:LEU:HD23	1:C:281:GLY:HA3	1.90	0.54
1:A:295:GLY:HA2	5:A:921:HOH:O	2.08	0.54
1:A:239:ASP:HA	1:A:265:THR:OG1	2.09	0.53
1:A:282:ARG:NH2	5:A:968:HOH:O	2.41	0.53
1:B:209:GLN:O	1:B:214:PHE:HA	2.09	0.53
1:A:50:ILE:HG21	2:A:712:SO4:O2	2.09	0.53
5:C:923:HOH:O	1:D:58:LEU:HD13	2.07	0.53
1:A:366:ASN:N	1:A:366:ASN:ND2	2.57	0.53
1:B:37:ASP:OD2	1:B:41:ARG:HB3	2.08	0.53
1:C:211:SER:HB3	2:C:714:SO4:O3	2.08	0.52
1:A:76:THR:O	1:A:77:CYS:HB3	2.10	0.52
1:D:415:GLU:O	1:D:419:GLN:HG3	2.08	0.52
1:D:51:ALA:HB2	1:D:400:LEU:HD22	1.92	0.52
1:C:359:LEU:HD21	1:C:421:PHE:HZ	1.75	0.52
1:D:390:CYS:SG	1:D:398:ARG:HD3	2.49	0.52
1:D:359:LEU:HD12	1:D:373:THR:HA	1.91	0.52
1:D:422:ASP:O	1:D:425:LYS:HG2	2.10	0.52
1:A:2:ASN:N	5:A:966:HOH:O	2.43	0.51
1:C:5:LYS:O	1:C:9:GLN:HG3	2.10	0.51
1:C:110:THR:OG1	1:C:113:GLU:HG3	2.11	0.51
1:B:76:THR:O	1:B:77:CYS:HB3	2.11	0.51
1:D:316:GLU:HA	1:D:316:GLU:OE1	2.10	0.50
1:B:69:GLN:HG3	1:B:303:ILE:HD13	1.93	0.50
1:D:239:ASP:HA	1:D:265:THR:OG1	2.10	0.50
1:D:389:SER:HA	1:D:396:VAL:O	2.11	0.50
1:A:383:LYS:HE3	1:A:419:GLN:HB3	1.92	0.50
1:B:66:VAL:HG13	1:B:303:ILE:HG23	1.94	0.50
1:A:138:TYR:HE2	4:A:750:PMP:HNA1	1.54	0.50
1:B:383:LYS:HE3	1:B:419:GLN:HB3	1.93	0.50
1:B:426:GLN:NE2	1:B:426:GLN:H	2.09	0.50
1:D:303:ILE:O	1:D:306:VAL:HG22	2.12	0.49
1:D:406:GLU:O	1:D:410:ILE:HG13	2.12	0.49
1:C:390:CYS:SG	1:C:398:ARG:HD3	2.51	0.49
1:D:360:PHE:CD1	1:D:365:HIS:HA	2.47	0.49
1:A:108:VAL:HG12	5:A:930:HOH:O	2.12	0.49
1:B:214:PHE:HZ	1:B:400:LEU:HD21	1.77	0.49
1:C:17:ARG:NH1	1:D:291:PRO:CD	2.75	0.49



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:C:55:THR:HG21	1:C:311:VAL:HG13	1.95	0.49
1:C:180:GLU:HG2	1:C:221:PHE:HB2	1.94	0.49
1:C:276:LEU:HG	1:C:277:ALA:N	2.26	0.49
1:C:380:ALA:HB1	1:C:385:LEU:HB3	1.93	0.49
1:C:138:TYR:HA	1:C:149:THR:HG23	1.94	0.49
1:A:252:PHE:O	1:A:255:GLU:HG3	2.12	0.49
1:C:276:LEU:HB2	1:C:304:ALA:HB1	1.94	0.49
1:C:66:VAL:HG13	1:C:303:ILE:CG2	2.43	0.49
1:A:77:CYS:SG	1:A:79:GLN:HG2	2.53	0.49
1:B:74:SER:O	1:B:302:PRO:HD2	2.12	0.49
1:C:17:ARG:NH1	1:D:290:ALA:HA	2.27	0.49
1:D:394:TYR:CD1	1:D:394:TYR:N	2.80	0.49
1:A:96:LYS:HB3	1:A:251:LEU:HD23	1.94	0.49
1:D:268:LYS:NZ	4:D:753:PMP:N4A	2.60	0.49
1:C:34:ARG:NH1	5:C:909:HOH:O	2.46	0.48
1:A:366:ASN:HD22	1:A:366:ASN:H	1.59	0.48
1:B:79:GLN:HG3	5:B:862:HOH:O	2.12	0.48
1:C:116:GLU:O	1:C:120:LYS:HG3	2.13	0.48
1:A:15:ILE:C	1:B:104:LYS:HD3	2.34	0.48
1:B:268:LYS:CE	4:B:751:PMP:H4A2	2.43	0.48
1:D:94:ASN:HD21	1:D:104:LYS:C	2.17	0.48
1:D:97:VAL:HB	1:D:280:THR:HG21	1.96	0.48
1:A:412:GLN:O	1:A:416:ILE:HG13	2.12	0.48
1:C:344:GLU:H	1:C:344:GLU:CD	2.17	0.48
1:C:76:THR:O	1:C:77:CYS:HB3	2.13	0.48
1:A:81:LEU:HD22	3:B:801:EDO:H12	1.96	0.47
1:D:11:ARG:HH11	1:D:11:ARG:HG2	1.79	0.47
1:A:282:ARG:HG2	1:A:284:GLU:OE1	2.14	0.47
1:B:89:LEU:HA	1:B:309:LEU:HD21	1.95	0.47
1:D:79:GLN:HG3	5:D:855:HOH:O	2.15	0.47
1:D:52:VAL:HG22	1:D:268:LYS:HA	1.96	0.47
1:D:167:TYR:HA	3:D:812:EDO:H11	1.97	0.47
1:C:164:GLY:O	1:C:165:HIS:HB2	2.14	0.47
1:D:36:TRP:HA	1:D:41:ARG:O	2.14	0.47
1:C:126:THR:O	1:C:127:LYS:HB2	2.13	0.47
1:C:214:PHE:CZ	1:C:398:ARG:HB2	2.50	0.47
1:C:248:THR:HB	1:C:351:LEU:HD22	1.97	0.47
1:D:32:ASN:ND2	1:D:404:THR:OG1	2.47	0.47
1:B:239:ASP:HA	1:B:265:THR:OG1	2.15	0.47
1:C:243:SER:HA	1:C:354:MET:CE	2.44	0.47
1:A:334:GLY:O	1:A:338:ILE:HG13	2.14	0.47



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:C:51:ALA:HB2	1:C:400:LEU:HD22	1.97	0.47
1:C:152:VAL:HG13	1:C:156:SER:HB2	1.96	0.47
1:B:364:ASP:OD1	1:B:367:LYS:HE3	2.15	0.47
1:D:108:VAL:HG23	1:D:277:ALA:HB3	1.96	0.47
1:D:83:TYR:CE1	1:D:86:TYR:HB2	2.51	0.46
1:B:426:GLN:HG2	1:B:426:GLN:O	2.15	0.46
1:D:151:LYS:HE2	1:D:153:ASN:O	2.15	0.46
1:A:15:ILE:HG23	1:A:16:PRO:HD2	1.96	0.46
1:D:66:VAL:HG13	1:D:303:ILE:HG23	1.97	0.46
1:D:219:PRO:HD2	5:D:862:HOH:O	2.14	0.46
1:B:83:TYR:CE1	1:B:86:TYR:HB2	2.49	0.46
1:B:94:ASN:HD21	1:B:104:LYS:C	2.19	0.46
1:D:175:LEU:O	1:D:175:LEU:HG	2.14	0.46
1:D:263:LEU:HD23	1:D:281:GLY:HA3	1.96	0.46
1:B:156:SER:HA	1:B:159:MET:HE1	1.97	0.46
1:B:422:ASP:O	1:B:425:LYS:HB2	2.16	0.46
1:D:138:TYR:HA	1:D:149:THR:HG23	1.97	0.46
1:A:11:ARG:HH22	1:A:19:VAL:HG12	1.81	0.46
1:A:59:HIS:O	1:A:63:VAL:HG23	2.16	0.46
1:A:282:ARG:NH1	5:A:913:HOH:O	2.33	0.46
1:B:47:ALA:HB3	3:B:801:EDO:O2	2.16	0.46
1:A:49:GLY:HA2	1:B:76:THR:O	2.15	0.45
1:A:119:VAL:O	1:A:123:ARG:HG3	2.15	0.45
1:D:347:ASP:O	1:D:357:ILE:HA	2.16	0.45
1:A:364:ASP:OD2	1:A:366:ASN:ND2	2.41	0.45
1:B:108:VAL:HG23	1:B:277:ALA:HB3	1.98	0.45
1:D:59:HIS:O	1:D:63:VAL:HG23	2.16	0.45
1:A:162:MET:HB3	1:A:163:PRO:CD	2.46	0.45
1:D:91:GLU:O	1:D:95:GLN:HG2	2.16	0.45
1:A:151:LYS:HE3	1:A:153:ASN:O	2.17	0.45
1:B:170:LEU:HD21	1:D:189:ARG:HD3	1.99	0.45
1:C:155:TYR:O	1:C:159:MET:HE1	2.15	0.45
1:A:241:VAL:HG12	1:A:268:LYS:HE2	1.99	0.45
1:B:66:VAL:HG13	1:B:303:ILE:CG2	2.47	0.45
1:B:91:GLU:O	1:B:95:GLN:HG2	2.17	0.45
1:C:319:ASN:ND2	5:C:855:HOH:O	2.50	0.45
1:B:11:ARG:HG2	1:B:11:ARG:HH11	1.82	0.45
1:B:364:ASP:C	1:B:366:ASN:H	2.20	0.45
1:A:107:LEU:O	1:A:299:ALA:HB1	2.17	0.44
1:C:81:LEU:HD22	3:D:805:EDO:H21	1.99	0.44
1:D:73:LEU:HD12	1:D:73:LEU:O	2.17	0.44



	is as pagem	Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:A:74:SER:HA	1:A:303:ILE:CD1	2.47	0.44	
1:A:108:VAL:HG11	1:A:117:ASN:ND2	2.33	0.44	
1:B:228:LEU:C	1:B:228:LEU:HD23	2.38	0.44	
1:D:172:PRO:HG3	1:D:221:PHE:CD2	2.53	0.44	
1:D:284:GLU:OE2	1:D:284:GLU:N	2.39	0.44	
1:B:51:ALA:HB2	1:B:400:LEU:HD22	2.00	0.44	
1:B:276:LEU:HB2	1:B:304:ALA:HB1	1.99	0.44	
1:B:282:ARG:HD3	5:B:950:HOH:O	2.18	0.44	
1:C:373:THR:OG1	1:C:395:ASN:HA	2.18	0.44	
1:A:106:LEU:HD13	1:B:19:VAL:CG2	2.48	0.44	
1:B:301:ASN:HA	1:B:302:PRO:HD3	1.87	0.44	
1:B:121:ILE:HD13	1:B:286:MET:CE	2.48	0.43	
3:B:804:EDO:H11	1:D:165:HIS:H	1.83	0.43	
1:A:229:CYS:HB3	1:A:234:ILE:O	2.19	0.43	
1:C:249:GLY:O	1:C:321:LEU:HD22	2.18	0.43	
1:A:379:ARG:NE	1:A:424:ALA:HB2	2.34	0.43	
1:B:170:LEU:HD21	1:D:189:ARG:CD	2.48	0.43	
1:C:357:ILE:O	1:C:357:ILE:HG13	2.17	0.43	
1:D:32:ASN:C	1:D:32:ASN:HD22	2.21	0.43	
1:B:151:LYS:HZ2	1:D:192:LYS:NZ	2.17	0.43	
1:C:94:ASN:HD21	1:C:104:LYS:C	2.21	0.43	
1:C:94:ASN:HD22	1:C:94:ASN:HA	1.66	0.43	
1:C:239:ASP:HA	1:C:265:THR:OG1	2.19	0.43	
1:C:385:LEU:CD2	1:C:387:LEU:HD21	2.48	0.43	
1:B:326:ASP:O	1:B:330:LYS:HG3	2.19	0.43	
1:C:338:ILE:HD13	1:C:418:SER:HA	2.00	0.43	
1:D:179:SER:O	1:D:182:ASP:N	2.51	0.43	
1:A:189:ARG:O	1:A:193:ASN:HB2	2.19	0.43	
1:D:281:GLY:O	1:D:282:ARG:C	2.57	0.43	
1:A:47:ALA:HB3	3:A:808:EDO:O2	2.19	0.43	
1:C:55:THR:HG23	5:C:870:HOH:O	2.18	0.43	
1:C:34:ARG:HG3	1:C:34:ARG:HH11	1.83	0.42	
1:C:41:ARG:HG2	1:C:43:TYR:CZ	2.53	0.42	
1:C:214:PHE:CE1	1:C:398:ARG:HD2	2.54	0.42	
1:C:334:GLY:HA3	1:C:414:LEU:CD1	2.43	0.42	
1:A:361:GLU:O	1:A:362:ASP:HB2	2.20	0.42	
1:B:61:LYS:HE3	1:B:317:GLN:OE1	2.20	0.42	
1:B:390:CYS:SG	1:B:398:ARG:HD3	2.59	0.42	
1:C:86:TYR:C	1:C:86:TYR:CD2	2.92	0.42	
1:C:359:LEU:HD12	1:C:373:THR:HA	2.02	0.42	
1:D:49:GLY:HA2	3:D:805:EDO:H12	2.00	0.42	



	to do pagon	Interatomic	Clash		
Atom-1	Atom-2	distance (Å)	overlap (Å)		
1:C:319:ASN:HD22	1:C:319:ASN:HA	1.68	0.42		
1:A:74:SER:O	1:A:302:PRO:HD2	2.20	0.42		
1:A:347:ASP:O	1:A:357:ILE:HA	2.19	0.42		
1:A:224:ARG:HD2	5:A:914:HOH:O	2.20	0.42		
1:A:303:ILE:HD12	1:A:303:ILE:H	1.85	0.42		
3:A:808:EDO:C1	1:B:81:LEU:HD12	2.50	0.42		
1:D:86:TYR:CD2	1:D:107:LEU:HD12	2.55	0.42		
1:D:332:LYS:HG3	1:D:348:VAL:HG12	2.00	0.42		
1:C:22:ILE:HB	1:D:80:VAL:HA	2.02	0.42		
1:A:76:THR:O	1:B:49:GLY:HA2	2.19	0.42		
1:B:357:ILE:HD11	1:B:397:LEU:HD12	2.02	0.42		
1:C:364:ASP:C	1:C:366:ASN:H	2.23	0.42		
1:D:322:GLN:HA	1:D:322:GLN:NE2	2.34	0.42		
1:B:121:ILE:HD13	1:B:286:MET:HE3	2.02	0.42		
1:C:291:PRO:HA	1:D:17:ARG:O	2.20	0.42		
1:D:226:ARG:HG2	1:D:259:VAL:HG22	2.01	0.42		
1:D:422:ASP:O	1:D:426:GLN:HG3	2.20	0.42		
1:C:228:LEU:C	1:C:228:LEU:HD23	2.41	0.41		
1:B:59:HIS:CE1	1:B:61:LYS:HB2	2.56	0.41		
1:C:73:LEU:HD12	1:C:73:LEU:C	2.40	0.41		
1:D:191:PHE:HA	1:D:195:ALA:O	2.20	0.41		
1:A:303:ILE:HD12	1:A:303:ILE:N	2.35	0.41		
1:B:281:GLY:O	1:B:282:ARG:C	2.58	0.41		
1:B:357:ILE:HG13	1:B:357:ILE:O	2.21	0.41		
1:D:152:VAL:HG13	1:D:156:SER:HB2	2.03	0.41		
1:A:251:LEU:HD12	1:A:251:LEU:HA	1.91	0.41		
1:C:17:ARG:HH12	1:D:290:ALA:HA	1.84	0.41		
1:D:331:LEU:O	1:D:335:LEU:HG	2.21	0.41		
1:D:357:ILE:HD11	1:D:397:LEU:HD12	2.02	0.41		
1:A:364:ASP:O	1:A:366:ASN:N	2.42	0.41		
1:B:156:SER:HA	1:B:159:MET:HE3	1.99	0.41		
1:B:401:VAL:HG21	1:B:405:ILE:HD12	2.02	0.41		
1:A:32:ASN:C	1:A:32:ASN:HD22	2.24	0.41		
1:A:87:LEU:HD21	1:B:10:ARG:HB2	2.01	0.41		
1:A:348:VAL:HG22	1:A:357:ILE:HG22	2.03	0.41		
1:C:74:SER:O	1:C:302:PRO:HD2	2.20	0.41		
1:D:307:ALA:O	1:D:311:VAL:HG23	2.20	0.41		
1:B:335:LEU:HD13	1:B:357:ILE:CG2	2.51	0.41		
1:C:348:VAL:HG22	1:C:357:ILE:CG2	2.42	0.41		
1:C:389:SER:HA	1:C:396:VAL:O	2.20	0.41		
1:D:76:THR:O	1:D:77:CYS:CB	2.69	0.41		



A 4 a m 1	A4	Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
1:A:51:ALA:HB2	1:A:400:LEU:HD22	2.03	0.41
1:A:153:ASN:HA	1:A:154:PRO:HA	1.89	0.41
1:B:151:LYS:HZ2	1:D:192:LYS:HZ3	1.68	0.41
1:B:162:MET:HB3	1:B:163:PRO:CD	2.51	0.41
1:B:162:MET:HB3	1:B:163:PRO:HD2	2.03	0.41
1:B:313:LYS:O	1:B:317:GLN:HG2	2.21	0.41
1:C:32:ASN:C	1:C:32:ASN:ND2	2.73	0.41
1:C:307:ALA:O	1:C:311:VAL:HG23	2.20	0.41
1:D:332:LYS:O	1:D:336:LEU:HG	2.21	0.41
1:B:11:ARG:NH1	5:B:920:HOH:O	2.54	0.41
1:B:73:LEU:HD12	1:B:73:LEU:C	2.42	0.41
1:D:246:GLY:HA2	1:D:250:THR:O	2.20	0.41
1:D:276:LEU:HB2	1:D:304:ALA:HB1	2.03	0.41
1:B:43:TYR:CD1	1:B:43:TYR:N	2.89	0.40
1:C:252:PHE:O	1:C:255:GLU:HG3	2.21	0.40
1:C:330:LYS:NZ	1:C:407:ASP:OD1	2.53	0.40
1:D:73:LEU:HD12	1:D:73:LEU:C	2.41	0.40
1:C:209:GLN:O	1:C:214:PHE:HA	2.21	0.40
1:D:274:PHE:HA	1:D:275:PRO:HD3	1.91	0.40
1:D:351:LEU:HD23	1:D:351:LEU:HA	1.97	0.40
1:A:59:HIS:HE1	1:A:61:LYS:HG2	1.86	0.40
1:A:379:ARG:HE	1:A:424:ALA:HB2	1.86	0.40
1:B:364:ASP:OD1	1:B:367:LYS:HG3	2.21	0.40
1:D:315:PHE:CD2	1:D:320:LEU:HB2	2.56	0.40
1:C:357:ILE:HD11	1:C:397:LEU:HD12	2.02	0.40
1:C:86:TYR:C	1:C:86:TYR:HD2	2.25	0.40
1:C:251:LEU:HD12	1:C:251:LEU:HA	1.94	0.40
1:D:119:VAL:O	1:D:123:ARG:HG3	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	Perce	entiles
1	А	424/426~(100%)	395~(93%)	23~(5%)	6 (1%)	11	19
1	В	423/426~(99%)	393~(93%)	26~(6%)	4 (1%)	17	30
1	С	423/426~(99%)	394~(93%)	26~(6%)	3~(1%)	22	37
1	D	424/426~(100%)	391~(92%)	30~(7%)	3(1%)	22	37
All	All	1694/1704~(99%)	1573 (93%)	105 (6%)	16 (1%)	17	30

All (16) Ramachandran outliers are listed below:

\mathbf{Mol}	Chain	Res	Type
1	А	365	HIS
1	В	155	TYR
1	В	365	HIS
1	D	50	ILE
1	В	267	ALA
1	А	50	ILE
1	А	77	CYS
1	А	366	ASN
1	В	50	ILE
1	С	275	PRO
1	D	267	ALA
1	С	267	ALA
1	D	108	VAL
1	A	275	PRO
1	С	50	ILE
1	А	108	VAL

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	Percer	ntiles
1	А	330/330~(100%)	324~(98%)	6(2%)	59	80
1	В	329/330~(100%)	325~(99%)	4 (1%)	71	87
1	С	329/330~(100%)	321~(98%)	8 (2%)	49	73
1	D	330/330~(100%)	323~(98%)	7(2%)	53	76



Continued from previous page...

Mol	Chain	Analysed Rotameric Outliers		Percentiles	
All	All	1318/1320~(100%)	1293~(98%)	25~(2%)	57 79

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

Mol	Chain	Res	Type
1	А	32	ASN
1	А	86	TYR
1	А	319	ASN
1	А	354	MET
1	А	362	ASP
1	А	366	ASN
1	В	32	ASN
1	В	154	PRO
1	В	415	GLU
1	В	426	GLN
1	С	32	ASN
1	С	86	TYR
1	С	163	PRO
1	С	319	ASN
1	С	351	LEU
1	С	362	ASP
1	С	394	TYR
1	С	415	GLU
1	D	32	ASN
1	D	86	TYR
1	D	89	LEU
1	D	154	PRO
1	D	259	VAL
1	D	319	ASN
1	D	394	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	2	ASN
1	А	9	GLN
1	А	13	GLN
1	А	32	ASN
1	А	94	ASN
1	А	317	GLN
1	А	319	ASN



Mol	Chain	Res	Type
1	A	329	GLN
1	А	342	HIS
1	А	366	ASN
1	В	32	ASN
1	В	94	ASN
1	В	242	GLN
1	В	366	ASN
1	В	426	GLN
1	С	32	ASN
1	С	94	ASN
1	С	317	GLN
1	С	319	ASN
1	С	365	HIS
1	D	32	ASN
1	D	94	ASN
1	D	242	GLN
1	D	319	ASN
1	D	322	GLN
1	D	365	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

32 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



Mal	Trune	Chain	Dec	Tinle	Bo	ond leng	ths	В	ond ang	les
	туре	Unam	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	А	810	-	3,3,3	0.54	0	2,2,2	0.34	0
2	SO4	В	713	-	4,4,4	1.86	2(50%)	$6,\!6,\!6$	0.90	0
2	SO4	В	703	-	4,4,4	1.87	1 (25%)	6,6,6	0.93	0
3	EDO	А	813	-	3,3,3	0.54	0	2,2,2	0.37	0
3	EDO	С	809	-	3,3,3	0.55	0	2,2,2	0.29	0
3	EDO	В	804	-	3,3,3	0.58	0	2,2,2	0.34	0
2	SO4	С	704	-	4,4,4	1.90	2 (50%)	$6,\!6,\!6$	0.90	0
2	SO4	В	708	-	4,4,4	1.88	2(50%)	6,6,6	0.89	0
2	SO4	D	715	-	4,4,4	1.89	2 (50%)	6,6,6	0.89	0
3	EDO	С	803	-	3,3,3	0.57	0	2,2,2	0.33	0
3	EDO	В	801	-	3,3,3	0.57	0	2,2,2	0.28	0
2	SO4	С	714	-	4,4,4	1.88	2(50%)	$6,\!6,\!6$	0.91	0
2	SO4	D	706	-	4,4,4	1.87	2 (50%)	6,6,6	0.92	0
3	EDO	D	806	-	3,3,3	0.58	0	2,2,2	0.35	0
2	SO4	А	701	-	4,4,4	1.90	2 (50%)	6,6,6	0.88	0
4	PMP	D	753	-	16,16,16	4.75	4 (25%)	21,23,23	1.51	2 (9%)
2	SO4	В	702	-	4,4,4	1.92	2 (50%)	6,6,6	0.88	0
2	SO4	D	705	-	4,4,4	1.90	2 (50%)	6,6,6	0.92	0
2	SO4	D	709	-	4,4,4	1.89	2 (50%)	6,6,6	0.87	0
2	SO4	D	711	-	4,4,4	1.88	2 (50%)	6,6,6	0.90	0
3	EDO	А	808	-	3,3,3	0.53	0	2,2,2	0.30	0
4	PMP	А	750	-	16,16,16	4.75	4 (25%)	21,23,23	1.53	1 (4%)
3	EDO	D	805	-	3,3,3	0.50	0	2,2,2	0.36	0
2	SO4	А	707	-	4,4,4	1.88	2 (50%)	6,6,6	0.89	0
2	SO4	А	712	-	4,4,4	1.84	2 (50%)	6,6,6	0.90	0
3	EDO	С	811	-	3,3,3	0.58	0	2,2,2	0.37	0
4	PMP	В	751	-	16,16,16	4.84	5 (31%)	21,23,23	1.60	3 (14%)
2	SO4	С	710	-	4,4,4	1.88	2(50%)	6,6,6	0.91	0
3	EDO	В	802	-	3,3,3	0.61	0	2,2,2	0.32	0
4	PMP	C	752	-	16,16,16	4.87	4 (25%)	21,23,23	1.51	1 (4%)
3	EDO	D	807	-	3,3,3	0.51	0	2,2,2	0.37	0
3	EDO	D	812	-	3,3,3	0.48	0	2,2,2	0.41	0

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).

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.



1S	Ζ	K

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4		D	75.9				0/1/1/1
4	PMP	D	753	-	-	2/8/8/8	0/1/1/1
3	EDO	С	811	-	-	1/1/1/1	-
3	EDO	А	810	-	-	1/1/1/1	-
3	EDO	С	803	-	-	1/1/1/1	-
4	PMP	В	751	-	-	0/8/8/8	0/1/1/1
3	EDO	А	808	-	-	0/1/1/1	-
3	EDO	В	802	-	-	0/1/1/1	-
4	PMP	А	750	-	-	0/8/8/8	0/1/1/1
3	EDO	В	801	-	-	0/1/1/1	-
3	EDO	D	805	-	-	0/1/1/1	-
3	EDO	А	813	-	-	0/1/1/1	-
4	PMP	С	752	-	-	2/8/8/8	0/1/1/1
3	EDO	С	809	-	-	1/1/1/1	-
3	EDO	D	807	-	-	0/1/1/1	-
3	EDO	D	812	-	-	1/1/1/1	-
3	EDO	В	804	-	-	1/1/1/1	-
3	EDO	D	806	-	-	1/1/1/1	-

'-' means no outliers of that kind were identified.

All (46) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	753	PMP	C5-C4	13.92	1.60	1.40
4	А	750	PMP	C5-C4	13.75	1.59	1.40
4	С	752	PMP	C5-C4	13.74	1.59	1.40
4	В	751	PMP	C5-C4	13.64	1.59	1.40
4	С	752	PMP	C3-C2	11.89	1.52	1.40
4	В	751	PMP	C3-C2	11.36	1.52	1.40
4	А	750	PMP	C3-C2	11.21	1.52	1.40
4	D	753	PMP	C3-C2	10.43	1.51	1.40
4	В	751	PMP	C6-N1	5.10	1.45	1.34
4	D	753	PMP	C6-N1	4.87	1.44	1.34
4	С	752	PMP	C6-N1	4.62	1.44	1.34
4	А	750	PMP	C6-N1	4.35	1.43	1.34
4	D	753	PMP	C2-N1	4.16	1.41	1.33
4	В	751	PMP	C2-N1	4.11	1.41	1.33
4	А	750	PMP	C2-N1	3.92	1.41	1.33
4	С	752	PMP	C2-N1	3.88	1.41	1.33
2	В	702	SO4	O1-S	3.21	1.63	1.46
2	D	705	SO4	O1-S	3.18	1.63	1.46
2	А	701	SO4	O1-S	3.18	1.63	1.46
2	С	704	SO4	O1-S	3.18	1.63	1.46



Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
2	В	703	SO4	O1-S	3.15	1.63	1.46
2	D	709	SO4	O1-S	3.15	1.63	1.46
2	D	711	SO4	O1-S	3.15	1.63	1.46
2	С	710	SO4	O1-S	3.14	1.63	1.46
2	В	708	SO4	O1-S	3.13	1.63	1.46
2	А	707	SO4	O1-S	3.13	1.63	1.46
2	D	715	SO4	O1-S	3.10	1.62	1.46
2	С	714	SO4	O1-S	3.10	1.62	1.46
2	D	706	SO4	O1-S	3.10	1.62	1.46
2	В	713	SO4	O1-S	3.05	1.62	1.46
2	А	712	SO4	O1-S	2.98	1.62	1.46
4	В	751	PMP	C2A-C2	2.45	1.54	1.50
2	D	715	SO4	O3-S	-2.11	1.30	1.47
2	В	713	SO4	O3-S	-2.11	1.30	1.47
2	А	712	SO4	O3-S	-2.10	1.30	1.47
2	D	709	SO4	O3-S	-2.07	1.30	1.47
2	С	714	SO4	O3-S	-2.06	1.30	1.47
2	В	702	SO4	O3-S	-2.06	1.31	1.47
2	В	708	SO4	O3-S	-2.05	1.31	1.47
2	С	704	SO4	O3-S	-2.05	1.31	1.47
2	А	707	SO4	O3-S	-2.05	1.31	1.47
2	С	710	SO4	O3-S	-2.04	1.31	1.47
2	D	711	SO4	03-S	-2.04	1.31	1.47
2	D	706	SO4	O3-S	-2.04	1.31	1.47
2	А	701	SO4	O3-S	-2.02	1.31	1.47
2	D	705	SO4	O3-S	-2.02	1.31	1.47

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
4	В	751	PMP	C2A-C2-C3	4.70	126.69	120.89
4	А	750	PMP	C2A-C2-C3	4.70	126.69	120.89
4	С	752	PMP	C2A-C2-C3	4.47	126.41	120.89
4	D	753	PMP	C2A-C2-C3	4.20	126.08	120.89
4	В	751	PMP	C3-C2-N1	-2.30	117.80	120.77
4	D	753	PMP	C6-N1-C2	2.16	123.16	119.17
4	В	751	PMP	C6-N1-C2	2.02	122.91	119.17

There are no chirality outliers.

All (11) torsion outliers are listed below:



Mol	Chain	Res	Type	Atoms
4	С	752	PMP	C3-C4-C4A-N4A
4	С	752	PMP	C5-C4-C4A-N4A
4	D	753	PMP	C3-C4-C4A-N4A
3	А	810	EDO	O1-C1-C2-O2
3	С	811	EDO	O1-C1-C2-O2
4	D	753	PMP	C5-C4-C4A-N4A
3	D	812	EDO	O1-C1-C2-O2
3	С	803	EDO	O1-C1-C2-O2
3	В	804	EDO	O1-C1-C2-O2
3	D	806	EDO	O1-C1-C2-O2
3	С	809	EDO	O1-C1-C2-O2

There are no ring outliers.

12 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	А	810	EDO	1	0
3	В	804	EDO	1	0
3	С	803	EDO	1	0
3	В	801	EDO	3	0
2	С	714	SO4	1	0
4	D	753	PMP	1	0
3	А	808	EDO	2	0
4	А	750	PMP	1	0
3	D	805	EDO	4	0
2	А	712	SO4	1	0
4	В	751	PMP	1	0
3	D	812	EDO	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 (i)

6.1 Protein, DNA and RNA chains (i)

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^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ $>$	#RSRZ>2	$OWAB(Å^2)$	Q<0.9
1	А	425/426~(99%)	-0.24	11 (2%) 56 59	18, 32, 57, 86	0
1	В	425/426~(99%)	-0.18	12 (2%) 53 57	17, 32, 69, 97	0
1	С	425/426~(99%)	0.01	22 (5%) 27 29	17, 39, 79, 100	0
1	D	425/426~(99%)	-0.15	13 (3%) 49 53	16, 31, 66, 94	0
All	All	1700/1704~(99%)	-0.14	58 (3%) 45 49	16, 33, 70, 100	0

All (58) RSRZ outliers are listed below:

Mol	Chain	\mathbf{Res}	Type	RSRZ
1	С	426	GLN	5.9
1	С	362	ASP	5.5
1	В	426	GLN	5.3
1	D	365	HIS	4.3
1	D	360	PHE	4.2
1	D	366	ASN	4.2
1	D	426	GLN	4.1
1	С	363	GLY	4.1
1	А	426	GLN	3.9
1	С	424	ALA	3.8
1	А	362	ASP	3.5
1	А	425	LYS	3.5
1	С	341	LYS	3.5
1	В	424	ALA	3.4
1	D	362	ASP	3.4
1	D	363	GLY	3.3
1	D	364	ASP	3.2
1	С	360	PHE	3.2
1	В	362	ASP	3.2
1	С	364	ASP	3.1
1	А	368	PRO	3.0



Mol	Chain	Res	Type	RSRZ
1	D	393	TYR	2.9
1	А	361	GLU	2.9
1	С	368	PRO	2.9
1	В	363	GLY	2.8
1	А	424	ALA	2.8
1	С	366	ASN	2.8
1	В	343	PRO	2.8
1	С	343	PRO	2.8
1	С	367	LYS	2.8
1	С	425	LYS	2.8
1	В	365	HIS	2.8
1	В	341	LYS	2.7
1	А	360	PHE	2.7
1	В	367	LYS	2.7
1	С	421	PHE	2.7
1	С	361	GLU	2.7
1	А	365	HIS	2.6
1	В	425	LYS	2.6
1	С	339	ALA	2.6
1	В	368	PRO	2.6
1	D	425	LYS	2.5
1	A	364	ASP	2.5
1	В	421	PHE	2.5
1	A	2	ASN	2.5
1	D	341	LYS	2.5
1	С	365	HIS	2.4
1	С	380	ALA	2.3
1	С	415	GLU	2.3
1	С	338	ILE	2.3
1	А	366	ASN	2.3
1	С	376	ILE	2.3
1	С	422	ASP	2.2
1	D	361	GLU	2.2
1	С	371	LYS	2.2
1	D	340	GLU	2.2
1	В	366	ASN	2.1
1	D	114	ALA	2.1

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 monosaccharides 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. The B-factors column lists the minimum, median, 95^{th} 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	B -factors($Å^2$)	Q<0.9
2	SO4	D	711	5/5	0.66	0.46	130,130,130,131	0
2	SO4	А	712	5/5	0.75	0.28	120,120,120,120	0
2	SO4	В	702	5/5	0.85	0.17	94,94,95,95	0
2	SO4	В	708	5/5	0.86	0.18	106,107,107,107	0
2	SO4	С	704	5/5	0.86	0.21	100,100,101,101	0
2	SO4	D	706	5/5	0.86	0.16	110,110,110,110	0
2	SO4	А	707	5/5	0.86	0.17	113,113,114,114	0
2	SO4	В	703	5/5	0.88	0.27	96,97,97,98	0
3	EDO	С	803	4/4	0.89	0.28	50,50,51,55	0
2	SO4	С	714	5/5	0.90	0.18	106,107,107,107	0
3	EDO	В	804	4/4	0.90	0.26	50,50,51,54	0
2	SO4	А	701	5/5	0.90	0.20	114,114,114,115	0
3	EDO	А	810	4/4	0.91	0.20	53,56,57,57	0
3	EDO	В	802	4/4	0.91	0.13	38,41,43,43	0
2	SO4	D	709	5/5	0.91	0.23	101,101,102,102	0
2	SO4	В	713	5/5	0.91	0.28	117,117,118,118	0
3	EDO	В	801	4/4	0.92	0.20	47,47,48,48	0
2	SO4	D	715	5/5	0.92	0.24	119,120,120,120	0
2	SO4	D	705	5/5	0.93	0.23	88,88,88,88	0
3	EDO	D	812	4/4	0.93	0.16	33,34,37,37	0
3	EDO	С	809	4/4	0.95	0.23	$53,\!55,\!56,\!57$	0
3	EDO	С	811	4/4	0.95	0.15	31,32,33,34	0
3	EDO	D	805	4/4	0.95	0.18	42,42,43,45	0
3	EDO	D	807	4/4	0.95	0.23	53,54,54,56	0
3	EDO	А	813	4/4	0.95	0.18	49,50,51,52	0
2	SO4	С	710	5/5	0.96	0.23	94,94,95,95	0
3	EDO	А	808	4/4	0.97	0.22	51,52,52,53	0
3	EDO	D	806	4/4	0.97	0.23	$52,\!55,\!55,\!57$	0
4	PMP	С	752	16/16	0.97	0.20	$25,\!31,\!36,\!37$	0
4	PMP	В	751	16/16	0.98	0.20	18,28,32,34	0
4	PMP	А	750	16/16	0.98	0.18	24,28,32,35	0
4	PMP	D	753	16/16	0.98	0.21	21,24,32,34	0



6.5 Other polymers (i)

There are no such residues in this entry.

